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<b>(54) Title:</b> BIALLELIC MARKERS  <b>(57) Abstract</b>  The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		



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## BIALLELIC MARKERS

## RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996,  
5 the entire teachings of which are incorporated herein by reference.

## BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution,  
10 generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and  
15 is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In  
20 many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism  
25 (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.



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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., W0 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include  $\beta$ -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater



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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a  
5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays  
10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for  
15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to  
20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.



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## SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.



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DETAILED DESCRIPTION OF THE INVENTION  
DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.

Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.

Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for



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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 5 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with 15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same 20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site 25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include 30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,



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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. -The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent



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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

#### I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,



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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference  
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being  
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table  
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the  
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are  
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

## II. Analysis of Polymorphisms

### A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid  
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue



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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For  
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); *PCR* (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),  
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification  
25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

#### 30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,



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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

#### 1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe



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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

## 2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference



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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

### 3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in  
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows  
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of  
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

### 4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of  
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,  
30 1988)).



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## 5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

## 10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

## 25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.



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## A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See  
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in  
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population  
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic  
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of  
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime  
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a



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match of suspect and crime scene sample would occur by chance.

$p(\text{ID})$  is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies  $x$  and  $y$ , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote:  $p(\text{AA}) = x^2$   
 Homozygote:  $p(\text{BB}) = y^2 = (1-x)^2$   
 Single Heterozygote:  $p(\text{AB}) = p(\text{BA}) = xy = x(1-x)$   
 Both Heterozygotes:  $p(\text{AB}+\text{BA}) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(\text{ID}) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity  $p(\text{ID})$  for a 3-allele system where the alleles have the frequencies in the population of  $x$ ,  $y$  and  $z$ , respectively, is equal to the sum of the squares of the genotype frequencies:

25 
$$p(\text{ID}) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

In a locus of  $n$  alleles, the appropriate binomial expansion is used to calculate  $p(\text{ID})$  and  $p(\text{exc})$ .

The cumulative probability of identity ( $\text{cum } p(\text{ID})$ ) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30 
$$\text{cum } p(\text{ID}) = p(\text{ID}_1)p(\text{ID}_2)p(\text{ID}_3) \dots p(\text{ID}_n)$$



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The cumulative probability of non-identity for  $n$  loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5        If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10        B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15        Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20        If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
- 25        attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30        The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him



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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site  $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$ ), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3})\dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

### C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the



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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance



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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of  
5 individuals who have been tested for the presence or  
absence of a phenotypic trait of interest and for  
polymorphic markers sets. To perform such analysis, the  
presence or absence of a set of polymorphisms (i.e. a  
polymorphic set) is determined for a set of the  
10 individuals, some of whom exhibit a particular trait, and  
some of which exhibit lack of the trait. The alleles of  
each polymorphism of the set are then reviewed to determine  
whether the presence or absence of a particular allele is  
associated with the trait of interest. Correlation can be  
15 performed by standard statistical methods such as a  $\chi^2$ -  
squared test and statistically significant correlations  
between polymorphic form(s) and phenotypic characteristics  
are noted. For example, it might be found that the  
presence of allele A1 at polymorphism A correlates with  
20 heart disease. As a further example, it might be found  
that the combined presence of allele A1 at polymorphism A  
and allele B1 at polymorphism B correlates with increased  
milk production of a farm animal.

Such correlations can be exploited in several ways. In  
25 the case of a strong correlation between a set of one or  
more polymorphic forms and a disease for which treatment is  
available, detection of the polymorphic form set in a human  
or animal patient may justify immediate administration of  
treatment, or at least the institution of regular  
30 monitoring of the patient. Detection of a polymorphic form  
correlated with serious disease in a couple contemplating a  
family may also be valuable to the couple in their  
reproductive decisions. For example, the female partner



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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified.

5 Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates

10 that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows.

20 To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where  $Y_{ijkpn}$  is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record;  $\mu$  is an overall mean;  $YS_i$  is the effect common to all cows calving in year-season;  $X_k$  is the effect common to cows in either the high or average selection line;  $\beta_1$  to  $\beta_{17}$  are the binomial regressions of production record on mtDNA

30



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D-loop sequence polymorphisms;  $PE_n$  is permanent environmental effect common to all records of cow  $n$ ;  $a_n$  is effect of animal  $n$  and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and  $e_p$  is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

#### D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized



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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-

5 segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the  
10 odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction  $\theta$ , versus the situation in which the two are not linked, and thus segregating independently (Thompson &  
15 Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions ( $\theta$ ),  
20 ranging from  $\theta = 0.0$  (coincident loci) to  $\theta = 0.50$  (unlinked). Thus, the likelihood at a given value of  $\theta$  is: probability of data if loci linked at  $\theta$  to probability of data if loci unlinked. The computed likelihoods are usually expressed as the  $\log_{10}$  of this ratio (i.e., a lod  
25 score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod  
30 scores for differing values of  $\theta$  (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See



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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of  $\theta$  at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of  $\theta$ ) than the possibility that the two loci are unlinked. By convention, a combined lod score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared. Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

#### IV. Modified Polypeptides and Gene Sequences

The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component) except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the



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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.



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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby,  
5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is  
10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene  
15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating  
20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292  
25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate



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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

#### V. Kits

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,



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100 or all of the polymorphisms shown in the Table.

Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means  
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15

#### EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to  
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference  
25 sequences of the fragments shown in the Table, column 1.

The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set



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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The



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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.



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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and  
5 individually indicated to be so incorporated by reference.



1	2	3	4	5	6	7
WI-7070	226	C	T	---	---	TGTGAACTCCACTTGAAGCCAAAGAAACATCAGACTTAAACACATGCCAGTTGGGAAGGTCT GAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAAGAGAGAGTTGAGACCAATCTTTATTT GTACTGGCCAAATCTGAATAACAGTTGAAGGAAAGACATTGGAAAAAGCTTTTGAGGATAATGT TACTAGACTTTATGCCATGGTCTTTC/TJAGTTTAATGCTGTGTCTCTGTCTG
WI-10744	61	G	C	---	---	AAGCCATTGACGTAAACATCTCAGAGGTTATTTGCATGGATTGACTCCTGGGACAAAAGGAC[G/C]AA AAACACTCTTCTGTGGATATCTGTGCAGATAGTACCCAAAGATCAGATGCTACCCAGATGTGTTT GATAATACATAAGCCCCCTAGGATTTAGATACAATCTTGAAGAAACTGAGACAGATAATCTCTGAAAT AAATGAGGTAAGTTTCAGGCACTCA
WI-9975	126	C	T	---	---	GGGCAAAATACCAGCAAAAAGTCAAAATACCAGCATCAAAGTCAGGTGCAAGGAGGTAGAACAA TTACAGTAACATATGTCATCTTTTGTATATTAGTATTATCTGCCAATGCCTAGAATA[C/T]AGTG GGTCCCTAATAGTTATTAGTTCCCTTTTCTCCTCTTCTCAITCTCTGAATTTATTTTATACTTAA GGGATTAGTTACCACCAAAAATGTGTATGATCAATTTGATCTTACTGAA
WI-8010	247	G	T	---	---	GCTAGGTTTGTTCTGTGGCTGCTTCACTAGACTTGAGATGACTTGATTACAGTAATCCCTATGT GATGTAACGTAGCTAGACCTTCCCTTCTCCGCAATCCAGCTCCAGGTTTCAGAAAGTATGCCACAC TCAACCTTCTCTCCAGTTCACTCTGTATTAAATTTCTCCCATATTAAATTCAAAGGGAGTGGACAGGT CCCTGGCTGAAAAGAAATAAGAGATCCCAAGTGGTGGGG[G/T]CTT
WI-5222b	85	G	C	---	---	GCCGGCCTATCTTTAAATTTAACTTGATCTTTGGTGTCTCCACTCCTAGGATCTGCCTTATAAT CTTTGTCTGTCTGTG[A/G/C]ATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGTGCCAAATCTTCAGGTCTCTTTGAAATTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA TCTCGACTCTATAACAACCTCCAACAGAA
WI-5222	52	G	C	---	---	GCCGGCCTATCTTTAAATTTAACTTGATCTTTGGTGTCTCCACTCCTA[G/C]GATTCTGCCTTAT AATCTTTGCTCTGTGTAGATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGTGCCAAATCTTCAGGTCTCTTTGAAATTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA TCTCGACTCTATAACAACCTCCAACAGAA
WI-8007	242	C	A	---	---	TATGCACCTTCCACAAAAGCGATATAATTTAAAAGTTTTTTTCATTAGAAAATAATGTATAAAAATAA ATATGTTATTATAGGCATTTATTACTAACTATAGTCTCTTGGAAAGGAACACCCCAACCAATACTT ATAAAGTACATGTAATTTATAGTAACATAATTTACTATATACATATGGAAAAATCATATTCTCACA GAAGAGCTGAACAGACATTCACCGGATACGACTGTGGAC[C/A]AGCTGCTG
WI-9823	97	C	T	---	---	TCAGTTGCAAAAATGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGATGTTTGTAG TCTATATTCACACATATAGTGAATTT[C/T]GGGGCATGGGAAATACATCTTTATGAGACATGA ACTGCTACCACACTATCATAGTATCCATTTAAACAGACCAACCAATGTATAAGAAATCCCTTTGTTTAC ATGCTTTCCAACTGATTTTGATGACTATTGTATGCCACAGTTGGATCACC



WI-9651b	105 A T ---	---	---	TCCTACATTCTATGGACAACTCCATGCCCTTTGGACATGCTGATCCCTCCTCCTGGAAATTCCTTCCT ACTTGCTCTCATGTACAAATTTTCTGCTGCTCTCA/ATGGGGAGCTTGAAGCCTCCCTTTAGAC ACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCCTATAGGCCTCTG TCTTAAACCTGTAATGGTATATTAATCCTTGGTGTTGAATGTCCTC
WI-9651	139 T C ---	---	---	TCCTACATTCTATGGACAACTCCATGCCCTTTGGACATGCTGATCCCTCCTCCTGGAAATTCCTTCCT ACTTGCTCTCATGTACAAATTTTCTGCTGCTCTCAAGGGGAGCTTGAAGCCTCCCTTTAGACACCT CT/CACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCCTATAGGCCTCTGT CTTAAACCTGTAATGGTATATTAATCCTTGGTGTTGAATGTCCTC
WI-7676b	309 A C ---	---	---	GTGACCTTCCTGCAGCGTGGAGATGGACATCCTTGTCTGCTGGGACTTGGCCCTGCTATTATTTTG TATTTATGTCTTAATCTCTCCACTGATGCATCCTCCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GCCGGCTCTCTTGGTGCTGCTGGTTCAGGGGAGGAGCGTGTGGACTGCAGCTTCTGCTGGTGC TCCCCCTCTCCTGGAGGAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---	---	---	GTGACCTTCCTGCAGCGTGGAGATGGACATCCTTGTCTGCTGGGACTTGGCCCTGCTATTATTTTG TATTTATGTCTTAATCTCTCCACTGATGCATCCTCCAAGGGTAGATGGGAGGGTCTGTGTGAAGGG GC/CTGGCTCTCTTGGTGCTGCTGGTTCAGGGGAGGAGCGTGTGGACTGCAGCTTCTGCTGGTGC GTGCTCCCCCTCTCCTGGAGGAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105 G A ---	---	---	CATTATCTTGCTTGGTGCTGTTCAATTCATCTTCTCTCTCCAATGAAGAGGATATTTAAGCATCAT CATCTGGCCCTTTTGGATTTGAATATTTTGTG/ATGACTCTATGCACATGATAAATTTGTTA TGCTTGCTCTTATCTTATCTTTTGTATAGGAGTTTGGCCATGACCCCTTATGAGGAGAAAAGGGA TCACCCCTTTTGGCTCTACAACTTATAGATATTTAAATATCTTT
WI-9986	42 T C ---	---	---	TTGGTGTGAACCTCAGAAATATAGGAAAATAGACAATTTGAAIT/A,CJGTACCCAGGAAACAAGAG CCCTGCACCTGACTCCAAAGGAGTTCTATTTCTGGCTGTTCCAGACTTTATGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGGTAGTACTCACAAGAACAATGTCA ATATCAATAGCATGCATATGGGGTGTGGATTCTTAGAACTTATGCAATT
WI-7041	174 C A ---	---	---	GTCTATTGCAGGAGAAACGTCCCTTGCCACTGCCACTCTCATCAGGCCAAGTGGAGGACTGGCCAGA GGCCCTGCACATGCAAACTCCAGTCCCTGCCCTCAGAGAGCTGAAAAGGGTCCCTCGGCTTTTATTT CAGGGCTTTGCATGCGCTCTATTTCCCTCTGCTGCTC/C/ACCCTTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGTAAACAAGCTCATTTGTACAGTGTCTGTATGTAATAA
WI-7224	134 T C ---	---	---	ATAACCCCTTGATGTATCACCACCACTCACTAATTTATCAACTTATGTGCTATCAGATATCCTCTCT ACCCTCACGTTATTTGAAGAAAATCCTAAACATCAAACTTTTCATCCATAAAATGTCAGCATTT /C/JATTAACCAACAAATAACTTTTAAAGAAAACATAAGGACACATTTTCAAAATTAATAAAATAAAG GCATTTTAAGGATGGCCTGTGATTATCTTGGGAAGCAGAGTATCATGCTAG



WI-10826	132 A C ---				TCTTATTTGCATTTACAGTAGCCCCATGAAGTAGGTATAACCCAGCCTCTATTTTAAACATGAGAAGAT GGAGGCCCTTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTTCTTAATAGCAAAGACCTGCA/A/C JCCCTGGCTTCTGACTCCAAAGCTTATCCCTTCTCATGTCTGTCTCAGCCAGGACCCCATGCGCA GAAAGCCAGCCTCTCCATCCCCCAC
TIGR- A004S25	145 G A ---				AGATCTGCCATTAGTATTTATTCCTTTGAAGATACITTTGGAGATTCAITTTCTTGAGTGGCACTGCAT GCTCATTGAGTGAACCTTTGTGGGTATAGAAATGGAATGGAGAGTTTCAAACAGCTTTGCTGAAAC TGACTTTGG[G/A]CTCCAGACTTCACTGTCTTAGGCATTGAACCATCACCTGGTTTGCATTTCTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24 A T ---				AAACACACAGAATCATCAAAGCAC[AT]ATCTGTGTTTGAGATAAATGATAGTCTGAGTCAACCTATG TAAGAACTAACTCTGAAATAGTAGGATAGTATTAATCATTTCTGTAAATAGATTACCTCTCAGCAAT TGGTCTGTTTTCAITCTATGAAACTCTCCGTACTGTAATTTTCAITCTATGGAACCTCCCCATACTGT AATTGGACAGTTTTGGTTCCAC
WI-4687	121 G T ---				TAGTATGCTACTGCCATGGTAAGGACTTTGATCACTAGGAAATAAGAACACTTTGAATGGCTTGTCO TTTCAATAAAAGAGTGACATGATTGAACATGTGTTTAGATAAAGGCACCTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGAGATTAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAATAAG GAGGCCCTGAGATCCACTGGATAATCTAAAAACCAAGAGAAAGAACTTGAT
WI-4719b	107 T G ---				TTCAATTTCCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTCTTGGGTGTGAGCGGATT ATGCTGACGCCATGGGTTCATAAGTGACTTGAGAGT[G/G]ACTGAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGATTTCATTCAACAATTCGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATCCCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70 G A ---				TTCAATTTCCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTCTTGGGTGTGAGCGGATT AT[G/A]TCTGACGCCATGGGTTCATAAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGATTTCATTCAACAATTCGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATCCCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216 G C ---				TCAACACGCCTTTTATTGCCACTTCTGGCTCCCCTCGTCCCAGCAAGATTCTACCTTTACCCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTCTCCTGTCACACTGCCAAGT TAAAGAAACCCCTGCTTGTCTGGAGAGGGAGGCCAGACAGGAGGAATTCAGGGCATGTATGGCTC AGTCCCACTTCT[G/C]ACTGCAGAGTATAGGGACCAAGGTTCCAAACTTT
WI-9484	178 G A ---				TCAACACGCCTTTTATTGCCACTTCTGGCTCCCCTCGTCCCAGCAAGATTCTACCTTTACCCCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTTCTCCTGTCACACTGCCAAGT TAAAGAAACCCCTGCTTGTCTGGAGAGGGAGGCCAGACAGG[G/A]JAGGAATTCAGGGCATGTATG GCTCAGTCCCACCTTCTGACTGCAGAGTATAGGGACCAAGGTTCCAAACTTT



WI-7330	207 C T ---	---	---	AGGATGGAAGGAGACACGGGGGAGGAGAACTCTCTTCTGCTAAATCGATAGGAGTCAGTTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAATTTCTTTTAATGTGGCATATAGGTTT GTGACACAAGAAGTCATAGTTGGTGGCTAAGTTTACTAAGGAAATAACTGAAAGATTAAAG TGAGAG[C/TT]GAAAAGAGAAATGATAATGCTTCCAAACTGTAGCTGCACAG
WI-9443	211 G A ---	---	---	TTAAAAACAGTTTCAGGTTGGTGAAGCAGAAAGGGATGTGATTACAAATTTAAATGAATCAGTCACITT GCACAAATTAATCCTCTTGGCATACACAAACTGGTTTTAATGGCAATGATGACATCATAGCATGA CCAACACTCATGGAAGGCAGTCTAGAGTCCATCACGCTCACACCTGAGGGGAAGGCACTGCACCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGATGACACCCACATGCCACATT
WI-7166	59 C T ---	---	---	TCTCTCAAAAGAGAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/TT]GGAT CATCAACAAGATTTCCTGTGCAAAATATTTGACTATTCTGTATCTTTTCATCTTGACTAAATTCGTG ATTTCAAGCAGCATCTCTGTTTAACTGTTGCTGTGAACAATTTGCGAAAGAGTCTTCCAAAT TAATGCTTTTTATATCTAGGCTACCTGTTGGTTAGATTCAAGGCCCCGAG
WI-7259b	189 T C ---	---	---	GCCTTCCCCAGGAAGCGGGTCTTGGCCTGGAACCTTCCAGAGAGGAGGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCOCTGCAACAGCTGAGGCTGCTTCTCTCTCTGAGTTCTCTGAGTCTGCGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAGT[C/TT]GGGGAGCAG AGCCAGCAGGTGGACAGGTGTTGACAGGGGCCCAACTTCCOCTGGAGCTC
WI-7259	188 G T ---	C	---	GCCTTCCCCAGGAAGCGGGTCTTGGCCTGGAACCTTCCAGAGAGGAGGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCOCTGCAACAGCTGAGGCTGCTTCTCTCTCTGAGTTCTCTGAGTCTGCGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAGT[C/TT]GGGGAGCAG GAGCCAGCAGGTGGACAGGTGTTGACAGGGGCCCAACTTCCOCTGGAGC
WI-7322	275 A G ---	---	---	GTACTTTAGGCTGTGGAGGTGGGCAITTAGTGTGACCTTGCACCCAGGGTTTCTAACAGATGAC CCTGTGAATCATAATTTAAACCTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCCCTATATG GCCATAAACTGCCTAAGCACTCAGGCTCCCACTCATCAACCCCTTTGACCAGAGAAAGCACTC TGGTTCTCTATCCCTTTGCACATAGAGAGTTTGTATGGGGCCTCTGGCTG
WI-7685	46 T C ---	---	---	TCAGTTCTAGTCTCTCTGGGGCCACACAGAAACTCTTTTGGGCTG[C/TT]TTTCTCCCTCTGGATCA AAGTAGGCAGGACCATTGGGACCAGGTCTTGGAGCTGAGCCTCTCACCTGTACTCTCCGAAAAATCCT CTTCTCTGAGGCTGGATCCTAGCCTTATCCTCTGATCTCATGGCTTCTCTCCCTCTCTGCCGACTC CTGGGTTGAGCTGTTGCCTCAGTCCCCCAACAGATGCTTTCTGTCTC
WI-563	87 G A ---	---	---	TGTGACCAATTGTTATTTTAGAGGGTTTAAACATGGCCTGACTATCACCTGATGGTCGCCAGAATTC CTGGGGGAGGGCCCTCCCTG[A/CC]CTGATCATGTCTACCTAACTGCTACTCTAACTACTACTCC TGTGGTATGGGATCCTAAGCCAAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCTCAGTAAAGGCAATTTTAAATCTCTTTGGATAACCCAGGGCACAT



WI-931c	191	C A ---	---	GACAGGGCACCAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTCCAGTCTTATCTGCTGTCAAAATGATCCTTCT GTTGCTGCACTGTCACTTACTGTTGTATGGATTATAATTATGTCACAAAAAGCC[C/A]CGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGCAGA
WI-931b	81	A G ---	---	GACAGGGCACCAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCT[AG/TT]CCCTCACCACACCTCCAGTCTTATCTGCTGTCAAAATGATCCT TCTGTTGCTGCACTGTCACTTACTGTTGTATGGATTATAATTATGTCACAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGCAGA
WI-931	31	A G ---	---	GACAGGGCACCAAGCCACGGAAGCCAC[AG/GCC]ACTAGCCCTGAACCTTGACACCCCTGGA GTTTCTCTCCCTCCCTATCCCTCACCACACCTCCAGTCTTATCTGCTGTCAAAATGATCCT TCTGTTGCTGCACTGTCACTTACTGTTGTATGGATTATAATTATGTCACAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGCAGA
WI-10870b	91	C T ---	---	GGATGACTTACCCCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAGTGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCCCTGAGTACGACCCCC TTAGCAGCAGAAATACAAGAAATCTTGGGACCTGTACTCCTGATACAAAATAAGGACATGGGTACAGC CTGAGCCACTCTTAAACCATGAACCATCACCAATTAATAACGTTGCCCCCCC
WI-10870	103	G A ---	---	GGATGACTTACCCCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAGTGGGCACTACTTAGA[AG/AT]CAGTGGAGTACCCCTGAGTACGACCCCC TTAGCAGCAGAAATACAAGAAATCTTGGGACCTGTACTCCTGATACAAAATAAGGACATGGGTACAGC CTGAGCCACTCTTAAACCATGAACCATCACCAATTAATAACGTTGCCCCCCC
WI-7719b	281	T C ---	---	AGTTTATCTTCCAGATGACCGCAGTAGACAAAATGGATACTGAGCAGAGTCTTAGGTAAGTCTT GGGAAATATTTGGGCATTTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAAACCCCTAGC TTCITAGTGAAGACAAATGTACAGTTATCC[AG/GT]TAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTTGCCCATGTATAATCTCTCACTGATGATTTCAAGCTAAAGCAA
WI-7719	163	A G ---	---	AGTTTATCTTCCAGATGACCGCAGTAGACAAAATGGATACTGAGCAGAGTCTTAGGTAAGTCTT GGGAAATATTTGGGCATTTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAAACCCCTAGC TTCITAGTGAAGACAAATGTACAGTTATCC[AG/GT]TAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTTGCCCATGTATAATCTCTCACTGATGATTTCAAGCTAAA
WI-10396	72	C A ---	---	GCCTGGAGTATATCTAAACTGTGGCCTCCACTTTCATTTTCTTGAACATTGCTATCAACTGGGAA GAGT[C/A]TGTGACTTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTGTGTTTTCTTTTGTTA TGCCATTTGAGGGATGATGTTTCTTAACTATGAAGTACTTGGCTGTCTCTCTCCATTGCTGTTACGG TTAACAGCCACCATTTGTAACACATTTGT



WI-10673	94	C G ---	---		TCCTTTATGACCCCAAGAGATATTTATTAACACCAATACGTAGCAGGCCATGGCTCATGGACC CACCCCGGTGGCACTCATGGAGGGG[C/G]TCAGGTGGAACTATGCAGTGTCTCCGGCCACACA TCCTGTGGGCCCCCTACCTGCCCAATTCATCTGCAATAACTCTGTCTATTTGTTTCATCTGTG GAGAAATGAAGGGAGGTCAAGTTGTTGTCATGATTTGTCAGAGAACCT
WI-7842	57	T C ---	---		CACAGCCATGCCCTTGAGAGCGGCCACAGATGCTGAATCCCTATCCCATTTCTGT/CJGTATGAG TCCATTTGCCCTTGCAATTAGCATTTCTCTCCCCCAAAAGAAATGTCTATGAAGCTTTCTTTCCCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGTCTTAGTACCAGAGTAGTTTTCAGCTGCTCAGAAAT TCATCTGAAGAGAGACTTAAGATGAAGCAAAATGATTCAGTCCCTTATA
WI-7721	145	A C ---	---		CTGCCTCATACGCCACTGGAGTCCACACTTGAATTTGGGCAGCTACCACGGTCTGCCATGCTCTGG AGGAGCAAGGGGGCCACATCCCCCAGCTGTACCCAGCCGGGCGAGGTGCAGCCCTTCTCTCCC TGCTCTGC/CJ/CJCTGACTCTCTTTGAGGTCCCTGTATGTCTACCTCTGACTTCTGTGGTCCCTCTG TGCTGCTCTCATCCATTCCTCTTACTGGGGCTGGGGCTCTAGCCCAA
WI-4767b	173	C A ---	---		TTCCAGTCTGTTTATCCTTTTCATTGTCAAAAGATGCTCTTAGACTGAAATTCATAAGAGTTCCT CAGGTCTGGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATGTTT CTTGCTTGAGAAATCCTAGAAAGCACAGGATGACA[C/A]AAATCACTAAGGAAATTCCTACTAAGA CTCCTCTAACCCAGAGATTTTAACT
WI-4767	50	A G ---	---		TTCCAGTCTGTTTATCCTTTTCATTGTCAAAAGATGCTCTTAGACTG[A/G]ATTCATAAAGAGTT CCTCAGGTCTGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATG TTCTTGCTTGAGAAATCCTAGAAAGCACAGGATGACACAAATCACTAAGGAAATTCCTACTAAGAC TCCTCTAACCCAGAGATTTTAACT
WI-7718f	222	C T ---	---		ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCCGGAGATAGATG ACTTTGCAGATGGAAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAAACTATGTATTAAT
WI-7718e	60	T C ---	---		ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGA[T/C]GCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCCGGAGATAG ATGACTTTGCAGATGGAAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCTATGCAGGAAGGAAAACTATGTATTAAT
WI-7718d	31	G A ---	---		ATTGCACTGAAGTTTTTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCCGGAGATAG ATGACTTTGCAGATGGAAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCTATGCAGGAAGGAAAACTATGTATTAAT



WI-7718c	91	C G ---			ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGG[C/G]TGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718b	248	A G ---			ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGATAGTG ACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATT[A/G]AT
WI-7718a	42	A T ---	C		ATTGCACTGAAGTTTTTGAAATACCTTTGTAGTTACTCAAGC[A/C]TGTTACTCCCTACACTGATGC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAA
WI-7227d	99	G C ---			AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCAATTAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTTCATCTTTAGACAAGCTTTA[G/C]AGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTAGTATCTGTTCCGGTGGTGTAAATAGGGATTAGCCCAAGAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291	G A ---			AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCAATTAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTTCATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTT GGTAGTATCTGTTCCGGTGGTGTAAATAGGGATTAGCCCAAGAGGACTGAGCTAAACAGTG TTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227b	93	G T ---			AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCAATTAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTTCATCTTTAGACAAG[G/T]CTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTTCCGGTGGTGTAAATAGGGATTAGCCCAAGAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24	A G ---			AGGGAATTGTGTTGCTCCTGGAGG[A/G]AGCCCAAGGCATCAATTAACAAGCCAGTAGGTCACTGGC TTCCGTGGACCAATTTCATCTTTAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTTCCGGTGGTGTAAATAGGGATTAGCCCAAGAGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234	A C ---			CCACAATGCCTCTCCACGATGTCAGGACTCCTGTCTGCTGGAGGTGGGAGACAAGAACCTCCG AAGAGGAAGCAAGAAAGCCGCTACTGCTATGTTGTGATCCTTCATCGAACAAACTGATCGGAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACAGGCCCCAACACACTGTAAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCA[A/C]ATGATCTTGAGATTTC



WI-7310a	64 T A ---	---	CCACAATGCGCTCTCCACGATGTCAAGGACTCCTGTGTCTGCTGGAGGTGGGAGACAAGGAACCTT/A JCCGAAGAGAGAAAGCAAGAAAGCCGTACTGTCTATGTTGTGATCCTTCATCGAACAACCTGATGCGAA AACTTGAATCTGTTACTGAAATGAGGAGAGAGACATGTCTATTGAACCTGAGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	CCAGCAACACCTACACCTTGTACCTGCTGGACTCCTATGATGGCTGCTGGTTGATAATAATCA GATCATGCCCAAGACGGGCTCCTGATAATCGTCTTGGCATGATTGCAATGGAGGGCAAAATCGTGCC CTGAGGAGAAATCTGGAGGAGCTG/GJGTGTGATGAAGTGTATGTTGGGAGGGAGCACAGTGT CTGTGGGAGCCCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAAACTA
WI-7878a	51 C G ---	---	CCAGCAACACCTACACCTTGTACCTGCTGGACTCCTATGATGGCTG/C/GJGTGTGATAATAA TCAGATCATGCCCAAGACGGGCTCCTGATAATCGTCTTGGCATGATTGCAATGGAGGGCAAAATGC GTCCCTGAGGAGAAAAATCTGGAGGAGCTGAGTGTGATGAAGTGTATGTTGGGAGGGAGCACAGTG TCTGTGGGAGCCCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAAACTA
WI-7381c	213 C T ---	---	CTCCACATTCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCCCTTTCTTTCTACC AGCCCTGCAAGTTTCTCATGACGCTCGCAGGAGCAGGCTGCAGGTTCTCGCCTATGGTGAGATC AGATGTGCCCAAGGAAAGGAGCTGTGGTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAGACA AAACGGCTC/GJGTGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---	---	CTCCACATTCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCC/C/GJCTTTCTTTCT ACCAGCCCTGCAAGTTTCTCATGACGCTCGCAGGAGCAGGCTGCAGGTTCTCGCCTATGGTGAG ATCAGATGTGCCCAAGGAAAGGAGCTGTGGTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---	---	CTCCACATTCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCC/C/GJCTTTCTTTCT ACCAGCCCTGCAAGTTTCTCATGACGCTCGCAGGAGCAGGCTGCAGGTTCTCGCCTATGGTGAG ATCAGATGTGCCCAAGGAAAGGAGCTGTGGTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---	---	AAATTGCTCTATTGCGACCTCATATTAATAAGAGCAATGAGAGCGAGGGAAAAATTGAACCTCTC AGGTACTGACTGTGGGACCAGACAAG/G/JGATGTAGATTGTCACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTTCCCATTTACAAATAAGGAGACAAAAATTAGGAGATTAATAAATCATCAC TGTTTCAAAATAAGGAGTGTGAGGTTTGTCCC
WI-1017a	92 G A ---	---	AAATTGCTCTATTGCGACCTCATATTAATAAGAGCAATGAGAGCGAGGGAAAAATTGAACCTCTC AGGTACTGACTGTGGGACCAGACAAG/G/JGATGTAGATTGTCACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTTCCCATTTACAAATAAGGAGACAAAAATTAGGAGATTAATAAATCATCAC TGTTTCAAAATAAGGAGTGTGAGGTTTGTCCC



WI-1795b	130 T C ---	---	GAAGCAACCAGAAAGTATCTTTATCCCCATCTAGATTATGTCTGGGTTCTCCAGACTCCTACGATTA AATTGTATGATGTGAACAACACTGATGAGGTACTTAGATCTCAGTGTCTTGCGAGAAAGAAAGTC/CJ GTCTACCAATTTTACCACAAATTCGTAGTACAATTTAAGTATCTCTTGTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGAGGATTT
WI-1795a	47 T C ---	---	GAAGCAACCAGAAAGTATCTTTATCCCCATCTAGATTATGTCTGGGTT/CJCTCCAGACTCCTACGA TTAAATTGTATGATGTGAACAACACTGATGAGGTACTTAGATCTCAGTGTCTTGCGAGAAAGAAAGTC GTCTACCAATTTTACCACAAATTCGTAGTACAATTTAAGTATCTCTTGTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGAGGATTT
WI-10616d	136 G A ---	---	CACACAATTTGCAAAACACTTCAAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCAGTCTCTCCATACGTAGGTCTGGTCTCCTATCACATTGCCA C/G/ATAGCCCTCCCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT ATGGATCATTCTCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616c	136 G A ---	---	CACACAATTTGCAAAACACTTCAAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCAGTCTCTCCATACGTAGGTCTGGTCTCCTATCACATTGCCA C/G/ATAGCCCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT ATGGATCATTCTCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616b	141 C T ---	---	CACACAATTTGCAAAACACTTCAAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCAGTCTCTCCATACGTAGGTCTGGTCTCCTATCACATTGCCA CGTAGC/C/CTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT ATGGATCATTCTCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-10616a	116 G C ---	---	CACACAATTTGCAAAACACTTCAAAAGTGAACGCCCGACATCATCAGCCCGTTAACGTCAGGCCATGT CCCACATAGAGAACGCTTTACTTCCAGTCTCTCCATACGTAGGTCTGGTCTCCTATCACATTG CCACGTAGCCCTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCT ATGGATCATTCTCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTGT
WI-1126c	52 G A ---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGCAAACTTCCAGTATCACTG/A/ATACTAATAAA AAACCCGTGAAGTCTGCTTGCATTTTCAAGATTCAATATATATCCAGATTGTTTCCAGCAAGAA AATTTTATTTCTCAAGATATAAAAAATAAATAATTTAATTTTCAAGTTCTCTCAAAAGGAATATGAAATT TGTTAAATGCAAAATCCAGCTGTAACITTTTGGACTTGTCTTTATTTCTT
WI-1126b	230 T C ---	---	CTCTTATTTCTCTGGGCACTGCTTTCTTTGGGGCAAACTTCCAGTATCACTGATACTAATAAAAA CCCTGTAAGTCTGCTTGCATTTTCAAGATTCAATATATATCCAGATTGTTTCCAGCAAGAAATTT TTATTTCTCAAGATATAAAAAATAAATAATTTAATTTTCAAGTTCTCTCAAAAGGAATATGAAATTTGTT AAATGCAAAATCCAGCTGTAACITTTT/CJGGACTTGTCTTTATTTCTT



WI-1126a	97 T C ---			C T C T A T T T C T C T G G C A C T G C T T T C T T T G G G G C A A A C T T C C A G T A T C A C T G A T A C T A A T A A A A C C C T G T A A G T C G C T T G C A T T T C A A G A T [ C ] C A A T A T A T C C A G A T T G T T T C C C A G C A A A G A A A A T T T A T T T C A A G A T A T A A A A A T A A A T A T T A A T T C A G T T C C T C A A A G G A A T A T G A A A T T T G T A A A T G C A A A T C C A G C T G T A A C T T T T T G G A C T T G T C T T T A T T C T T
WI-11183c	124 C T ---			T A G T G C T A A T T T T G G A A A G T T T G C T G A T T T T A A A A T C T T T T A A A C T T G A A A A T T T A G A G T A C A T A A A T A A A A T A A A G A C C A G A T A G G T A T T A A T T C A G A T G T A T T T T G C C C T T G T C A C T A A C A T T T T A T G A C A T A C A A A T G A C C A A A A T G A T G T T T T A T G A A G T G A G G A T A G A G T T T T A A A T A T T G G T A T G T G T G C T A G A G T T A G T A A T G G A A
WI-11183b	192 T C ---			T A G T G C T A A T T T T G G A A A G T T T G C T G A T T T T A A A A T C T T T T A A A C T T G A A A A T T T A G A G T A C A T A A A A T A A A A T A A A G A C C A G A T A G G T A T T A A T T C A G A T G T A T T T T G C C C T T G T C A C T A A C A T T T A T G A C A T A C A A A T G A C C A A A A T G A T G T T T T A T G A A G T G A G G A T A G A G T T T T A A A [ T / C ] A T T G G T A T G T G T G C T A G A G T T A G T A A T G G A A
WI-11183a	118 C T ---			T A G T G C T A A T T T T G G A A A G T T T G C T G A T T T T A A A A T C T T T T T A A A C T T G A A A A T T T A G A G T A C A T A A A A T A A A A T A A A G A C C A G A T A G G T A T T A A T T C A G A T G T A T T T T G C [ C ] C T T G T C A C T A A C A T T T A T G A C A T A C A A A T G A C C A A A A T G A T G T T T T A T G A A G T G A G G A T A G A G T T T T A A A T A T T G G T A T G T G T G C T A G A G T T A G T A A T G G A A
WI-10770b	174 G A ---			G C T T G G T T T G C T T T A G T C T T A T T G T C T C A G T C T T G A G T T C C C T T T C T G C T G G C C C T T T T G T A T T C A C C A T A C C T C T A T G C C T C G T C T C A G A C C A T T T C C T C T A T C T G G A G C G C T C T C C T T G T A C T T C T C C T G T T C A C C A A C C T C T T T T A T T C T C A G G A C A C T C A [ G / A ] T T C A C A T G C C A C T C T C G T G A C A C T G T C T C T T C A C A T C T T C T G T C C C C T T T C C C
WI-10770a	49 G T ---			G C T T G G T T T G C T T T A G T C T T A T T G T C T C A G T C T T G A G T T C C C T T T C T G [ C ] C C T G G C C C T T T T G T A T T T C A C C A T A C C T C T A T G C C T C G T C T C A G A C C A T T T C C T C T A T C T G G A G C G C T C T C C T T G T A C T T T C T C T G T T C A C C A A C C T C T T T T A T T C T C A G G A C A C T C A G T T C A C A T G C C A C T C T C G T G A C A C T G T C T C T T C A C A T C T T C T G T C C C C T T T C C C
WI-9667b	82 C T ---			G A T G A C A A C T T C T G C T G T G A C C C T T A G T C C T T G C T C A T G A C A C T T T C A A T C T C T G C C T T G T A T C A T G G T A T A C A C T G G A C A [ C ] T A G C C A C C T C C C C A G C A G G C T T A G A A C T C C A T G A G T A A G G A C C C T G T C T A A T G T C C G T T T C T C T T A T G T A T T A C A C A C A G T C A T A G G A T G G T A G T A C A A C T A A T G G A T C T T G G C T G T T A A A C C T T T T C T C T G T A C C A G T A C C T A A G T C C A A A C T T G C A T T C T
WI-9667a	68 G C ---			G A T G A C A A C T T C T G C T G T G A C C C T T A G T C C T T G C T C A T G A C A C T T T C A A T C T C T G C C T T G T A T C A T G [ C / C ] T A T A C T G G A C A C A G C C A C C T C C C C A G C A G G C T T A G A A C T C C A T G A G T A A G G A C C C T G T C T A A T G T C C C G T T T C T C C T T A T G T A T T A C A C A C A G T C A T A G G A T G G T A G T C A A C T A A T G G A T C T T G G C T G T T A A A C C T T T T C T C T G T A C C A G T A C C T A A G T C C A A A C T T G C A T T C T



WI-10400d	189 A G ---				ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTAAGATGGTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTAAATTT TCTTCCCTTACCTTACTCTCCCAACCAAAATACGTAAGTACCTATGTCAGTGCCATGTAG TTTTTGGTTCAATTTACTTGCAAAATATTCAAAGGCGTTAATGCATTATG
WI-10400c	166 A C ---				ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTAAGATGGTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTAAATTT TCTTCCCTTACCTTACTCTCCCAACCAAAATACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCAATTTACTTGCAAAATATTCAAAGGCGTTAATGCATTATG
WI-10400b	165 A G ---				ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTAAGATGGTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTAAATTT TCTTCCCTTACCTTACTCTCCCAACCAAAATACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCAATTTACTTGCAAAATATTCAAAGGCGTTAATGCATTATG
WI-10400a	46 T C ---				ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTCAGACATCT GCTGGTTAACTGTTAAGATGGTTAGCACACATGTAAGCACTTACTAACACAATATTTTATTCTA ATTTTCTTCCCTTACCTTACTCTCCCAACCAAAATACGTAAGTACCTATGTCATGCCATGT AGTTTTTGGTTCAATTTACTTGCAAAATATTCAAAGGCGTTAATGCATTATG
WI-10809b	78 C T ---				AAAGGGCTACAACTAAGGCCAAACCAATGAACGGTATAGGAGGGTAAATGCAAGGGGAGACCC CACCTCTACCA[C/T]TAGAAAGGGCATTTCAAGCACATTCATAGGGCTTCATATACTGGTTAG CAACAAATGGAATGTATTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCAGTGATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ---				AAAGGGCTACAACTAAGGCCAAACCAATGAAC[T/G]GGTATAAGGAGGGTAAATGCAAGGGGAGA CCCACTCTCACCACTTAGAAAGGGCATTTCAAGCACATTCATAGGGCTTCATATACTGGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCAGTGATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ---				CGAGCTTGGGATAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTGC CAATGAAATAGTGAATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATTGAT CATTTTATATGAAATAAAAGATCCTGCAATTTATGGTGTAGTCTGAGTCC
WI-7038b	140 A C ---				CGAGCTTGGGATAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTGC CAATGAAATAGTGAATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGA[A/C]GACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCTGCAATTTATGGTGTAGTCTGA



WI-7038a	31	G A	---	---	CGAGCTTGGGATAAAGCAAGGGGACCTTGGC[G/A]CTCTAGGTTCCCTGCCACATCCAGCTTGTG TCCAATGAATACTAGATGCTGGGCTGTCTCCCTTCCAGGAATGCTGGCCCCCAGCCCTGGCCA GACAAGAACTGTCAGGAAGGTCGGAGTCTGTAACACCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAATAAAGATCCTGCATTTATGGTGTAGTTCTGA
WI-3429b	64	G T	---	---	ATACGCTTTCTGTCTGCCACAGTGAACAGCACCCAGGTGGCCAGGGTCCGAGTCCACACA[G/T] CCCTCAGCCCCCTTCAGCTTGCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACCTCATGTGA CAAAAATACAGATCCAGTCTCCTCCTCTGGATTTGGATCTAGCAAGACCAGACGGTCCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T	---	---	ATACGCTTTCTGTCTGCCACAGTGAACAGCACCCAGGTGGCCAGGGTCCACACA[C/T]AG CCCTCAGCCCCCTTCAGCTTGCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACCTCATGTGA CAAAAATACAGATCCAGTCTCCTCCTCTGGATTTGGATCTAGCAAGACCAGACGGTCCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A	---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGATAAAGAGTGAGTGACGGTGACCT GTGAGCCCCATTCTCT[G/A]TGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATTG TTTTGGCAGGGGACACTCCTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786b	111	A T	---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAA[A/T]GGATAAAGAGTGAGTGACGGTGA CCTGTGAGCCCCATTCTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATTG TTTTGGCAGGGGACACTCCTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786a	106	A T	---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAA[A/T]GGATAAAGAGTGAGTGACGGTGA CCTGTGAGCCCCATTCTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATTG TTTTGGCAGGGGACACTCCTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6711b	226	G T	---	---	GGCTATTTGTAATGCTTGGTATTGACTCCAAAATTGAATAAGTATTGGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAACCTTCACTTCCAACTCACTGAAT TTCAATACCTCCATTATAATTCAATACATCATTCGAGAGAAAAGACACGGTGCCAACTGGGTT TGGTTGGTGCCTGCACACCCACA[G/T]TGGCAACTAAGTGAATCTCTAAA
WI-6711a	36	T C	---	---	GGCTATTTGTAATGCTTGGTATTGACTCCAAAAT[C/T]GAATAAGTATTGGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAACCTTCACTTCCAACTCACT GAATTCATATACCTCCATTATAATTCAATACATCATTCGAGAGAAAAGACACGGTGCCAACTG GGTTGGTGGTGGCTGCACACCCACAGTGGCACTAAGTGAATCTCTAAA



WI-10613b	172 A C ---			ATTGTATGCCAAAATCATAATACCCCTGCATTCTAGAAACATACAGTGTATAGAAATTTTGAGCCATA TGGTGAATAATTTAGAAGTATTATCTCTATATGTATATACAGTTTAAACATCAATGAATGTGATTT TTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTTG[A/C]GCCCTAGGAGGTTACTATAATTTAGA AAGGCTCTTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-10613a	44 G A ---			ATTGTATGCCAAAATCATAATACCCCTGCATTCTAGAAACATACA[G/A]GTGAATAGAAATTTTGAGCC ATATGGTGAATAATTTAGAAGTATTATCTCTATATGTATATACAGTTTAAACATCAATGAATGTG ATTTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTTGAGCCCTAGGAGGTTACTATAATTTAG AAAGGCTCTTACCTTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-7587c	133 A T ---			GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAAGATCTGTGCTTTTCCAAACAGTGACTACCCCTTGAAGC ACATCCCTCTCTGGATCTGAAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAA[A/ T]GGAATGAACCACTCCCTGCCATTCCCTATAAGATATCCCAAGACCCAGGCAATTTTGCCCTCT TTCCACATGCCCCCATATGCTGAGCCCAACTGCACCTGGGGCTGCCCTC
WI-7587b	81 G A ---			GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAAGATCTGTGCTTTTCCAAACAGTGACTACCCCTTGAAGC ACATCCCTCTCTGGATCTGAAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCCTATAAGATATCCCAAGACCCAGGCAATTTTGCCCTCTT TCCACATGCCCCCATATGCTGAGCCCAACTGCACCTGGGGCTGCCCTC
WI-7587a	28 C T ---			GCTCTAGTGGGAAACCTCAGGTAGTCTCCGAAGATCTGTGCTTTTCCAAACAGTGACTACCCCTTGA AGCACATCCCTCTGGATCTGAAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCCTATAAGATATCCCAAGACCCAGGCAATTTTGCCCTCTT TCCACATGCCCCCATATGCTGAGCCCAACTGCACCTGGGGCTGCCCTC
WI-10681b	103 T A ---			ATGACTCAGGTGACAAAAGAGCATGTCCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCAACC ACAGAAAAGCTAAAGACATCCTTTTAAAAAGCC[T/A]AAAGACAGCCATTTTAAATCCTAATTCG TAGTTTATGATTTTCTCAAAATTTCCCAACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAAAGGAGTGACGCTCTGTTAAAG
WI-10681a	41 A T ---			ATGACTCAGGTGACAAAAGAGCATGTCCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAAGACATCCTTTTAAAAAGCCCTAAAGACAGCCATTTTAAATCCTAATTCG TAGTTTATGATTTTCTCAAAATTTCCCAACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAAAGGAGTGACGCTCTGTTAAAG
WI-7222c	126 G T ---			GCCTCTCCTCAACTGTCCTGGACCCAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCTGTTCTCAAGTTGGGGATGGG[G/TAATAA AGGAGGGGGAATCCCTTGAAACAAGAACTGGGATAGTTATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGAATTTTGTGTAAGGTGTATTTCAAAGACTCGAATTCATTTT



WI-7222b	255 G A ---	---	---	GCCTCTCTCAACTGTCTCGACCCCAAGGCTAGGAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCAACCCTGTCTCAAGTTGGGGATGGGAATAAAGG AGGGGGAAATCCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGAAGTTGTATTTCAAAAGACTCGAATTCATTTCTCA
WI-7222a	126 G T ---	---	---	GCCTCTCTCAACTGTCTCGACCCCAAGGCTAGGAAGGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCAACCCTGTCTCAAGTTGGGGATGGG[G/T]AATAA AGAGGGGAATTCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGTTGTATTTCAAAGACTCGAATTCATTTT
WI-8054d	41 C A ---	---	---	AAAGATGACACTTAGAACTGGATCATTGGCCCTTTCTCTT[C/A]TTATCTCTCTCCAGTTCAAAATG CTTGCACTTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTCCCTGGCGGTACAGAGAAATCCTTGCCCTT
WI-8054c	237 G T ---	---	---	AAAGATGACACTTAGAACTGGATCATTGGCCCTTTCTCTTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCTTAGCACAA TCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCTTCC TGTCATAACGCCGCTTCCCTGGCGGTACAGA[G/T]AATCCTTGCCCTT
WI-8054b	148 T C ---	---	---	AAAGATGACACTTAGAACTGGATCATTGGCCCTTTCTCTTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCTTAGCACAA TCTCTTTGTAGT[C/T]TTAGCCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTCCCTGGCGGTACAGAGAAATCCTTGCCCTT
WI-8054a	131 C G ---	---	---	AAAGATGACACTTAGAACTGGATCATTGGCCCTTTCTCTTCTTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCTTAG[C/G]A CAATCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTCAACGCCGCTTCCCTGGCGGTACAGAGAAATCCTTGCCCTT
WI-10854b	152 G T ---	---	---	TTCCACAAAAACTTCCCTGGCCCGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTAATAA ATGTTTATATTTTACTTTAAAGCGGAAGTTGAAACACGAGACGATAGTTAACGCTCTGGTAAGTTTAT ACGGTGTGCGAGGCAACA[G/T]GGAGAGGTACGGGAATAGTTCTACTTCTGTTTATTTTCTTG TTTTAGACACAGGGTCTGCTGTGTG
WI-10854a	102 C T ---	---	---	TTCCACAAAAACTTCCCTGGCCCGGGTGACTAAGATGAGAAGTGGGAGAACTGGATAGTTAATAA ATGTTTATATTTTACTTTAAAGCGGAAGTTGAAACA[C/T]GAAGACGATAGTTAACGCTCTGGTAAGTT TATACGGTGTGCGAGGCAACAGGGAGAGGTACGGGAATAGTTCTACTTCTGTTTATTTTCTTG TTTTAGACACAGGGTCTGCTGTGTG



WI-9826b	127 G A ---	---	---	AATTTATATGTGAAGGGTTAGCAAACTATGCCCCACAGGCCCATTTCTAGCCATGCTATTTTGTG TGCTGATGGCTGTTTGGTGTGTCACGAGTTGAGCCATTGTGACAGAGGCTGTTAT[G/A]GCCTT CAAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTGCTGATTTCTAGATATTTAAA GGCAGAGAAATCAGAAGTGTGAA
WI-9826	125 A T ---	---	---	AATTTATATGTGAAGGGTTAGCAAACTATGCCCCACAGGCCCATTTCTAGCCATGCTATTTTGTG TGCTGATGGCTGTTTGGTGTGTCACGAGTTGAGCCATTGTGACAGAGGCTGTTAT[G/A]GGCCTTC AAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTGCTGATTTCTAGATATTTAAAAG GCAGAGAAGATCAGAAGTGTGAA
WI-15986	60 T G GTGGTTTTT	TTGTTTGTGT GAAATGT	TGACATTATAT AAACGTAAAA	CGGACACGTGTATATACAAATACAGATCGTATGGGTTTGTGTGGGTTTTTTTTT[G/G]TTAC ATTTCTTTTACGTTTATATATATGTCAGCATTTCAA
WI-8655	29 A G AG	AACTGCAAAAT AGGAAACCAG	CCACTGGGGC TCCC	TTCAAGTAACCTGCAATAGGAAACCAGAGIAGI[GGGAGCCCCAGGTGGGACAAATCATGGCTACCCC TCCCCAACAGAACAGGGGGAGGAGTGGCCCCCTACACCCTTTAT
WI-8170b	259 G A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACCTTTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAACTACTCTACCAAGATGCTGGTAAAGGTTAG CATTTGGTGGAGAGATTTACAAGGTTAAGATCATGTGTCATCAAAAGTGCAATCCTATCAATCAGAA ATAAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACACAAGA
WI-8170a	204 T A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACCTTTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAACTACTCTACCAAGATGCTGGTAAAGGTTAG CATTTGGTGGAGAGATTTACAAGGTTAAGATCATGTGTCATCAAAAGTGCAATCCTATCAATCAGAA A[T/A]AAAGGTAAAGGGCCCTCAAATGAAATCTACGGAAAAACATAACAC
WI-8172	136 C G GACA	CCTTTATTAAA ATTGTTTTCTT	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCTCTTAAGTCATCTTCCAATACTCCAGGTACATGGTGAAGAGTCACTGTTAAACACGAA ATCTAACCATTAACCAAGCTTTTAAATCCTTGGTAACTCCCTTTTAAATTTGTTTTCTTGACAT A[C/G]AGTACCTTTACAGGTATTACATTTCTCTCACCCGTTTACA
WI-8183	56 G A TGC	TGAAATAAAA ACAATTTCTGT	TGTGTTGAAAT CAACCTGC	AGCAGGGTTTGAATTTGATCCCTTATTTTACATGAAATAAAAACAATTTCTGTTGC[G/A]GCAGGTT TGATTTCAACACAGATTGAATCTGTAAAAACCAAGCTGTTTCTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCCCATGC
WI-14149	83 C T ---	---	---	GCTTTATTGGGATTGCAAGCGTTACAAGGTTAAAGACAAAAACCAAGCATGGGATTTGCCGGAAAT ATTAGCGTTAAAGGAG[C/T]TGAGTTGAGTCAAAACACGGG
WI-8712	44 G A G	CACAGGGAAG AGGTAGTGA	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAAACAGCACAGGGAAGAGGTAGTGGAG[G/A]GAGATGGTCAGGCTTCCTG TTCCTTAACAGCAGAGCCCCAGCAACCTAGAAAGCCCTCACCTAGCCTCTTAAT



WI-8827	22 C T	TCCCTGGGAG ACTATGG	GGGATTAGGAT TTTAGTGTCA C	GGTGCCCTGGGAGACTATGG[C/][AGTGAACACTAAAACTCTAATCGCCATGCATTGGAATTATT CCGACTATTACTTCTTTAGTCCCTCTTATCCACCCAGCTCTCT
WI-8833	51 A T	TCCTCCATGCC ATTCTCTG	CCCTCACACATT ATAGGGCA	CTCCGGCTCTTAAAGCTCTGTAGACTGTCTTCCATGCCATTCTCTG[A/T]TGCCCTTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACCTGCCCTGTATATAAAGGTCAGCTAIGT
WI-8377	63 A G	---	---	ATTTTTAGCCATGTTGGTAAAAGTTCAATTTTACGTACATGGGTAACACCCAGGCCCTTTCCCC[A/G]T TATATCCAGGTATGCTACAAAGTCTTTTAACTCTTATCAGAAGTTATTATTACTGTTCTTCCCTTAGAGAG GCTACCAGGCTAAAATTCACTTAGTTGGTTTGTCTAATGTCCTCAATTTTATCCTGAAGCTCGTG
WI-8850	21 A G	GGGACTTAAC CTTTGGCT	CAAAACAGCCA GGCAGG	GAGGGACTTAACCTTTGGCT[AG]CCTGCCCTGGCTTTGGCTCTGGCTTGTCTTTTGGTTCTT TCTCTTCTACTGGTCTTTCTTTGCTTTTGGCAGCCACCTATGCTGCTG
WI-8853	79 C T	CCCGGGCATTG AGGATA	AGTCTTCTGA GCTTCCAT	ACTTTTCTTGGCTGAGCAACCTCATCTCTTTAGCTCTGTTGATAACGCTGGTTAATCCCCGGG CAITGAGGATA[C/][ATGGAAGGCTCAGGAAGACTTCAITCTCAA
WI-8865b	52 A G	---	---	AGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCAATGGTCGAACA[A/G]JACAACATGCT TCGGACTTACCAGGGAGAGTCGAGCTTCCATATAAA
WI-8865a	42 T C A	CACAGACTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGGTACTGGAATCACAGGCACAGACTGAGGAAGACAGTCAIT[C/][GGTCGAACAACAACATGCT TCGGACTTACCAGGGAGAGTCGAGCTTCCATATAAA
WI-8895	32 A C	---	---	GTGCCAACAACCTGGACACCAACCAAGAA[AT]A/C]TCCCGTCTTTGAAATTTCCATTAAAGAGCA CAATGGGGTAATTATACCAGGATGCTCCATCGCTCTTTC
WI-8456	93 G C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGGGACTGATATTTGTGAAATATAATAAACTCTTTTCC AAGGCTCCCATGCTTGGATGTACA[G/C]TTATGTCAAGTTAATAAACAATTTCTAAGTGTCACTC TCAACTTCTGTATTCTTGGCATGGTCCAGTAACAGTTACACGGCAGACCCACAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCCGTCTGCTCAGTCAACCCAC
WI-8496b	157 A G	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAAATGGTAATGTTGTATCAGTGCATATTCTATGAAA ATTATATCTCAAGTAAGTACCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAGTCA AAGACACAATGCTGCCAATGCA[A/G]TTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT GTGGCCAAAGTGGGATAAACAGTAGCAGTGAC
WI-8496	41 G A	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAAATGGTAATGTTGTATCAGTGCATATTCTATGG AAAAATTCATATCTCAAGTAAGTACCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAG GTCAAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT TGTGGCCAAAGTGGGATAAACAGTAGCAGTGAC
WI-14153	28 A G	GTGCAGGAAG GCCAGC	AACGGCAGGA GGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGG[A/G]TCCCTCTCGCGTTGTACCCACATCCACAGAGCA GCCCTAGTCCAGGTGCAGCCACTGCCACCACGGCACACGGGAACAGGACCCATGCTGC



WI-12108	40	C T A T A	TGAAAAGGG TTAAACTCAA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGAAAAGGGTTAAACTCAAATATC[CT]GAAATACTTTTCATTATACCAGGT CAAGAAAATGCCACAGCCAGAAAATTTATTTTAA
WI-5989	29	G A C A C A G G C A	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCCTATGTA CG	CAGGCAAAACGTCACAAAAGGTCACAGGCA[G/A]CGTACATACGGTTCTGTTATACCCCATATATTAC CCCTTCATGTCTTAAAGAAGACATTTCTCTAGAGATTTTCATTTTAGTGATCTTTTAAAAAAAAT CTTGTTAACTTGCCTCCATCTTTTCTTGCGTGAGGACACC
WI-12201	61	C T C T C T C A T G	CCCACTGATCA OCTGCATG	CCGACCACATA CCTGGC	ATAGTCTTTTAGCCTTTTCTCGAGTGTTTATGTCGAAAGCCCACTGATCACCTGCGTATGCGCA GGTATGGTGGGCTGGTGATGGACGTGGTTTGCAGCCCTCCACTGCTCGATAAAAGGC
WI-12018	31	A T T C T G A C T T	GGCAGOCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTCAGGAGCCAGCTCTGACTT[CT]CTCTCTGTTTCTGTCATCTCTCCCCACATACCA ACTTCTCACCATGATGATTATACCAATAATACAGTTCTTATATGAGGGCTCTGGAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57	A G C C T C	TGGCCTCGCTG CCTC	AGGGATCAAA GAGAAAAGGC	TTTTCGTTTGTATATGATCCGAATGCTTGAGAAGAAACCCCTGGCTCGCTGCCCTC[A/G]GCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTGG AGCGG
WI-15407	92	A G T T	CATGCCCTTA AGGATTAAGT AGTT	TCCTTTCTCTTT TGGTAGTGTGG	AGCATGTAAGGAGCAGTTTTATTGATTGGTATATTCAGGTTTCTAACCCAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAAGTTTAA[G/CC]CACACTACCAAAAGAGAAAAAGATTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109	T C A A T T	GTTGAGTATT GTTCTGCTCAT	GGGAAGTCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAAAAATTATTCTGATACAACATGGTGCTAGACATGGCTACACITTTA TACTTTGTGCATTTAGTTGAGTATTGTTCTGCTCATAATT[CT]CCCAATATGTACCAGACCTTCCC
WI-12326	25	G A C A	GACAGACTTC AAAAGCAATT CA	AGGTTTGAAAA TATGTATTAAAG TACTTTGT	CTGACAGACTTCAAAAGCAATTAC[G/A]CTTCCAGAATACAAAGTACTTAATACATAATTTTCAAAC CTGTTTGCATTTCAAAACAAAGTTAGCGTTTGTGTAATCAAAATTTGATAACCCGACTAAAAAT
WI-12361	63	C T	---	---	TTAAATCCACACTGAAGATCTGGAGTATGGGGGATATAGGAATTCAGCATATGTATTAT[CT] TGAACATAATTTACAAAAGTGAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87	C T A T C A C A C C A	CAGACACAGC ATCACACCA	GACCTCCCGT GGGC	ATACTGGTTAATCCATGTCATGTAATGTAGTTTACAAAGGAAAGGACAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA[CT]AGGGCCACGGGAGGTGGGGAGACGACACTTTTCCCTGGG AAAGG
WI-11321	67	A G T T T T	GGGAGGAAAA TCCAATAAAT TTTT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTTCTGGTGAATCTTTTAAGCAGGGAGGAAAAATCCAAATAATTTTTTAA[ A/G]AAGGTTTAGCTATTTCCCAATGCTATTATTAATACAATTGAGGTTAGGACGTTAAGTCTTATCAGA CTGTGACTGGAGCCCCG
WI-11324	40	C G T G C C C C A	GGATAAATCA TGTCGCCA	ATCAAGCTTTG GGGCTCT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCA[CT]GAGAGCCCCAAAGCTTGATGACAT TCTGTAAAGTTACAAAAATGTATCTGAAGAAGTTATCTGTCTTGTC



WI-11352a	69 T C G	AGCAGCAG ATAGTGGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTCTGTTTTCCAGAAAGGAGAGAGAGTCATCTACATAAGCACAGCACATAGTGGAA AGT[C]GCTAAGTGCTCTACGAGAGGTGAGATCATATCCATAGAAAACAGCTCTCTTTACTTGCA CACTTA
WI-11371	84 C T G	CAGCTGGAG ATTCTGATTCA	GCCCCGCTGA GCAC	TTAGCCCATGCTGTCATTTGCCAATCACCTGTGAAACCTATGAAAACCTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTCAG[C]TGTGCTCAGGGGGGCTGGACATCCATGTTTGGGAAGAGTTGCGCGGGT GATTCGATGCGTATAT
WI-11385	75 T C G T T T T	ACAGAAGACT TTCATATTCTT	GATTCATTCT AGTCATGGTCA TATTTT	CTTAAAGCATATAGTTTGGCCTGATGGTGACACAGAGACTTTCATATTTCTGTTTTTAAAGTC TCTTCAGT[C]AGGAAAAAGCTACAGATTTAAAAAATATGACCATGACTAGATAAGATCAGC
WI-11388	88 C A AAGTTC	TGTTTGAAT ACACGTAAC	TGCCTTGATC CAAGTTAAAT T	TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAAATTAAAGAAATGAATGTTT AAATTACACGTAACTAAGTTC[C]A]TATAATTTAACTTGGATACAGGCAATTTGTTATGCTAAT
WI-11392	55 T G A T A A T A C	GGTTATGTT CTTGAACCTTA	GTACATTCAAG TGTTTTGTAAA AAG	TTCTATCATCCATTAAATGGGCAAGTTATGTTCTTGAACCTTTAATAAATAC[T]G]CTTTTTTACA AAACACGTGAATGACTTTTCTTGTGCAAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGT CATACTCTTCCCCAGA
WI-11396	52 A T T	TTTGTTTTG AAATGGTGT	AGCTATTTC ATATTCACCA TC	AAAGAATAAGATGGCATTGTTCAGTTAATTTTGTGTTTGAATGGTGTTTT[AT]GATGGGTGAATA TGAAAATAAGCTTACCTCATCCACTCTAAAGGTAGTTGTTGATTTTGAACCGTTGTCAAT
WI-11441	100 C A CAGC	TCCCCACCAAC TATTTG	TGCCAGGCGCT TATTTG	CTGTCAGCTTCCCCAACTAAACCGTGAGTTCAGATGCTGCGCAGCACGCTGCTGTTCTTCTGGTG TATTCCTACTGTAATCCCAACCAACAGC[C]A]CAAAATAAGGCCCTGGCACAAAGTAAGCTCTCC ATTTTGTAGAATGAAT
WI-11466	26 C T TTTATTTTGA	TGAGAAGCCA CTACAACTT	GTTTATTGTTA TAAAAATGAC CTACAACTT	ACTTTGAGAAGCCATTATTTTGCAG[C]TCTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTTT TATATAAGTTGTAGGTCAATTTTATAACAATAAACTTTCTATTATCTCTCACATACATTT CATGTATCCTG
WI-13364	35 A G ---	---	---	TTTTCTTTTGTGCTCTTTTTTTTAGTAGAAGC[A]G]GGAACAGTTGTCAATACTACCTTCTGTTGG TCCCCTGTTAGACAACATACCTTCTTTTGAATGTAAATGTCA
WI-11276	41 A G AGCAGAC	GGCAGOCAGG GCGGGTG	TGTACTGAGGA GCGGGTG	AGGCAACACTGCTTTATTAGCCGGGCGAGCCAGGAGCAGAC[A]G]CACCGGCTCCTCAGTACACATT CCCCACCCCTGCCCTCGGTGCTCCCACTCAGGGCTGGGCATGGAGGGGCGAGGTAGGTCTGGAA
WI-12210	76 A G A	ACTGGGAAAA CAACTATTGC	TGCTAGTTTGC ATATGTTTTCC	ATTGGAACAACATTAATAATTTGTCATCTCTACATATAGAAAAGCTGCTTTGAATAACTGGGAAAAACAA CTATTGCAT[A]G]GGAAAAACATATGCAAACTAGCATATTGTCTCTAGA
WI-14186b	88 A G ---	---	---	AATGGTCTGGTTTTATTGAGAAGCTGTTGGTCATTTGATGGAAAACACATACGGGTACAAAATTACA GGTGGTTTAGTTCAATTACATG[A]G]TACAAATCATTAGAGTCTTTACAAAGTCATTAGAGTCTTTGGAT TTT



WI-14186a	52 C T A	GGTCATTGAT GGAAAGACAC	AACTAAACCA CCTGTAATTTT GTAAC	AATGGTCTGGTTTATTGAGAAAGCTGTTGGTCATTTGATGGAAGACACATA[C/T]GGTACAAAATT ACAGGTGGTTTAGTTCAATACATGATACAAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66 A G	GAGAACACTT GTGGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTTTTTGGCTATAGGTGAGTGTCTAAACTTGAGCTTGCAAGAGAACACTTGTTGGGGCTT[A] GTTCAACATGGACTGATAGTCCACCCCCAGATTTCTAACTGGTAGGCTGGGGTG
WI-12345	37 C A	GTGGCAGGAA AAAGAGGAA	TTGCAGAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAGAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATTCTCT TTCCTGACCAGCTGGGCTTGCGCACTTTGTGAGATTGCAAAA
WI-13416	71 C A	AAATTTTGG AAGTTTTTCAG AAA	AGTGTATTAG TTCAATGAATA ATTCAA	GAAAAGGCTGTAATTTTATTTTCAAATTTTGGAAAGTTTTTTCAGAAAAAAATAAAATGACAAGAACAA CATA[C/A]AAATATTGAAATTTTCAATTGAACTATAACACTTAGCAGAGGAGGACTTTTGTGAT
WI-12310	46 G A	TTATCCCAAG TATAATTTTA AAAAGC	TGTTTAAATAT GTTTGGTCTT AAA	TTTGAAGAGATGCTGAATTTATCCCAAGTATAATTTTAAAAAGCT[G/A]TTTAGGACCCAAACATA TTTAAACATCTCTTACACATACAGAAATTTTCAGTTTACAAATATCCAGAAAGGCAATTTCTTAAGCAG T
WI-12086	72 C T	COGGGAAAC TTGGATT	GGAGTCTTGG GTCTTGG	GAACCGAGCTTTATTGGAGCAAAGAGTGTGGACACTGTTTACAAACAAACGTTTCCGGGAAAACTTG GATTTT[C/T]CCAAGACCCGAAGACTCTCCAGTTCTCACTGTTAGTAAGTCAATTTGGGGGCAGA ACAGGAACATGCCTTAGCT
WI-11549	102 T G	GGCATAAAGT TCATAATATTC TTTTATG	GGAAAGTCTGT ACAAATCCCC	ATGCTTTCACAGGTTGTATTTTGTAAAGAGTTTGTCTATCTATAATTTTATTTATTTTGGCATAAAGT TCATAATATTTCTTTTATGATCTTTTAAATATCTG[T/G]GGGGAATTTGTACAGACTTTCTCTC
WI-11585	79 T C	TGGGTTTGCAA AAACAAAA	CCATGCTTCAC TGATACTTC	TTAGAGGAAAGAAATAAAACACCGTAATGGGAAATCAGTTCCAGAGGTAGGAAGGAAAGCTGGGT TGCAAAAACAAAAA[T/C]GGAAGTATCAGTGAAGCATGGCCCTAGAAAGTCCAAGAGCAGGGGTAGAGT TT
WI-11604	68 G C	---	---	TTAGTTGGTTTCTCTGAAACITTTATGCTGTTTATTTTAAACATAGGATGTTCCAGTTACCAGCATTT G/CJAGAACTAGGGACTTTTCCATGAAATAATTAAGAGCTAAGGAATTTCTGACGCTCACCATTTTTC TTTGTTACTCTGCAGTT
WI-11614c	108 C A	---	---	CAAAATCAAAAAATTGAGGAGGCAAGAACAGAAAGTAAAAATCCAGAAAGACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCA[C/A]TATTAAAGTATTCGTCAGCTAC GGACTTCGT
WI-11614a	60 A G	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAC ATGOC	CAAAATCAAAAAATTGAGGAGGCAAGAACAGAAAGTAAAAATCCAGAAAGACTCAGCTGCTTG/GJGG CATGTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAACATATTAAGTATTTCGTCAGCTAC GGACTTCGT
WI-11626b	83 T C	---	---	TTGATTTTACTAAGGCTCTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATACTCAG ATATTTTAAAAATAAA[T/C]TACTTAATAATAAGAAATAGCCATACCACATTTGTTCCATTTGCTAC AAGAACAAATTGGCAATGA



WI-11626a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGCTTCCACTGGAACATGAAGGTAGIG/A/GATAAGGTGTACAGGATAATATACT CAGATATTTTTAAATAAATACTTAATAAAGAAATTAGCCATACCACATTTGTTCCATTTGCTAC AAGAACAATTTGGCAATGA
WI-11627	23	T C	CCTTTCCTCC ATTGTCCTC	CATTTGCAACC CATCTCAAG	ACCCCTTTCCTCCATTGCTCTC/T/CJTTCAGATGGGTGCAAAATGGAAGTAAAAAGCAAAAAGGG AGATGAGAATACTGATGCTTTTTTGCTGGCTTACTTCCATTGCGATGTCAAGTCCATCCATG
WI-11636	61	A G	GGACTTAAAA AGATCTGCTTA	AGAACTTGGT AAATATTTTAT	TCAGAAATGTTGCAAGCAAAATACTATTTGTAAAGGTGGACTTAAAAAGATCTGCTTATCCTA/GJTA TATCCACATAACTCTAGTGTACATAAAATATTTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTTTGGTA
WI-11537	119	C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAAGAATGAT T	GTACCAATTTCTTATGGTGGCAAAATAGCAAACTGTGAGTAACGAGGGCAGCTGAATAAATTTACAG TATACAATATTAGAGAAATATTATGTTGCAATTGCTCATCTTACTCTGACCA/T/C/GJATAATCATTTCTT TTTGCTGGGTCCAGGACC
WI-11654	37	G C	GCCAAAAGAC TATTCAGCAA	GGCTCTCCCG GACAGTT	AGTAGAATCATCAGTGCCAAAAGACTATTTCAGCAACTG/C/JAAACTGTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTGTTCATATACTCTACTCAGAGTTACACTCATATTTTCATATTTTT ATTTTGGGTGTTGGGT
WI-11656	28	G A	ATTGATTTTAG AAGGAACTGC	CAAGGCTTTGT CCTCAAGTAAA	ACCTGATTGATTTTAGAAGGAACTGCAA/G/JCTTTACTTGAGGACAAAGCCTTGCCTGCAGTTGTTT AAATGTCTGTAACCAATCAGATTCCAGCCCTGGAT
WI-11680	55	T C	...	...	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTCTCCCCCTTTT/CJTTCGATAAA GGCTGGGAAGGTGGTTTGGCCAGACCGTACATCTTTT
WI-11696	47	T C	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAACTT	GTCCAAGAACAAAGATACTTTGACATCTTTATCACAGCAGGGGACAG/T/CJAGGTTGGCTTCTCTA ATGCCCACTATCTGTGTTTTCAGAACTTTCCACTTCGCC
WI-11702	69	C T	GAATAATACT GAAATAACCA	AGAACAACTT AAGCAAATTAT	TTACATGTGGTCAATGGTGACATACTTTCAATAATTAAAAATCGAATAATAACTGAAATAACCCACAGC AG/C/TJTTTCAGTATAATTGCTTAAGTTGTTTCTAGAAAAACACTGCTAAATTTTTTGTCTGCAGA
WI-11706	60	C T	TGGCTGGAATT TTCTCTCTT	ATCACCAGAG AACAAATCCA	TGCTGATTCATCGCTTCTACCATCTGGCTGGAATTTTCTCTTCTGTACAATTTATTTGGC/C/JGGCTG GAATTTGTTCTTTGGTGATTTGTCCTTGTCTGCT
WI-11709	105	T A	AGAAGCTTGC TTTCAATTGTC	TCATTTCTCT AATTTACGGG A	AATATCATCTCATATCAGGCATGTTTATAAAAAATGAGAGATTATGTCCTTTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAGAGCTTGTCTTCAAGTTGCTA/GJTCCTCGTAAAAATTAGAAGAAATGAAT GGCCAGATGGATGGAATA
WI-11710	103	C A	GCACCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCAATCAACCTGTCCCGAGCTTTCCAGCACACAGCCAGCCACACTCTAGACACGCCCTTCAG TCCAGTCCATTTCTGGCACCTAGCCTCAGTCTTCA/C/AJCTCCTCCTCTCCACACTCCTTC



WI-11715b	123	C T	AGCTT	AGGTGGCTGC	TCCCACCTG TGGCT	AGAAATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACAGACAAAATGCATTACAACCTGTGGTGAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTC/TAGCCAC AGGATGGGACTGGGAAGA
WI-11715a	49	A C	AAA	AAA	A	AGAAATGGAGCTGTTGGGAGGGACATGCACACAATGTAAACAGACAAAATGCATTACAACCTGTGGTGAATGTGGCCACTATGAATCCCTATGTATAAGAGGAAAGAGGCTGGCTGCAGCTTCAGCCAC AGGATGGGACTGGGAAGA
WI-11727	43	G C	TCAACA	AAACAACCTT AAACAACCTA	CCTGTGGTTG TGTTGCAG	CTGGATTTCTATACCTAACAACTCTTAAACAACCTATCAACA/G/CJCTGCAACACAAACACAGGC AAATGAAACAGATGCCCCAGACAGACACCCACCATGGCACAC
WI-11728	16	C G	---	---	---	TTTATTTATCAAACTTC/GJCAATTCATTTTCAAAATGTAAAGTTATCATCAGTCCCATCCACTTT CTCCCATCTTCTATCTTTTCCGACCTACACTTTCTCTCCCTACAAACCCGGTTCCAAA
WI-11758	61	A G	TOGCTG	ATCTGTGGTTT	TGATTTGGCCT GTGGTCTA	TTTTTCTCTTTTATTAAGTCCGCTACTACTAAGAGGAGAACTGTGGTTTTCGCTG/A/GJTAG ACCACAGGGCCAATCAACACAGCTTCTTTGTAGAGAACATGGAGAGTGCACAGATCACCATCA
WI-11295	37	A G	AATATAA	GCCTCACAAA GTAATTTCTAA	AAAGTGCTCA TCTGTGAATC T	CCGGCTCACAAAGTATTTTCTAAATATAATTTGCT/A/GJTAGAGTTCACAGATGAGCACCTTTTCA CATTAGGTGATATGCAACAAATCACTATTGGCTCAGCAGGAACAGACTTTT
WI-11773	93	T C	---	---	---	AGCACATGATTTCTGCTGGAGTTTCTGTGAGCTCAGCAACAGAGTCAAGATTAAGAAAT ATTTATGGCTCTTTTTTCCCTTC/GJGTGATTGTTAATTAGGAGTCAAGGCCAAGTTATC
WI-11282	42	C G	GCAAGGAA	GGCTCAGAGA	AAAACTCAGA CTGTAAATTTT GTGTG	CATGACAACCTCTTTTATTAATGGCTCAGAGAGCAAGGAA/C/GJ/CACACAAAATTTACAGTCTGA GTTTTGCGGCGCAGAGACCCCTCTCCACCTTTTTCATGCTGTGTACACACACACTGTCCAAAGCCTC AGA
WI-11790	28	A G	AAACCTCTG	CCCAACTTACC	CGTAGGGGAG GCTAAGC	TAATTCACCCCAACTTACCAACCTCTGT/A/GJCTTAGCCTCGCCTACCATGTCTCAGAGCAC TTACATTAACTACAAATGGGCAAAATCATCTAACACAAAGC
WI-11879	61	C A	AGTATACA	TCATCTAATCT GTGAGGTATTT	GATAGTTGAAC CTCTTCACTTT ATAAAA	TTTTAATCCCAAAGCTTACAACCATCTTTTCACTAATCTGTGAGGTATTTAGTATACAG/C/AJAGT GATTTCTCTCTTTCTTTTATAAGTGAAGAGGTTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91	C T	AAGTTAAA	GTTTTTAATGT GGTATTAGAA	CAATTTTCAGA TTGCTATAGC AAAC	TTTACTAATTTCCATTTCTCCCTTTTATAGTTTTTAAATGTGGTATTAGAAAAGTTTAAATTACAT ATGTGGCTTATATTCTATTCTA/C/JTTGACAGCACAGTCTTCAAGTTTGTCTATAGACAATCTGA AAATGGGTTCTGAAC
WI-11906	52	A G	ATCTGAA	TGTTATAACAT CAAAGAAAGA	TTAATTTCTGC AGTTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTATAACATCAAGAAAGAAATCTGAAT/A/GJTAGGGAACTG CAGAAATTAACCTTCAGCTAATCTCAGAAATGCCAGATGAAGTAAGTAACCCCTTTACAG



WI-11909	78 A G	TTTGTTGGG TGTCAG	CCTCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAAGACAAATGGATTGTGGAGCATACCTGAAGACTATTCCTAAATGGCTATTTGTGTTG GGTGGTCAAG[A/G]CTATTACAGAAAATCTCAGAGGAGGACAAATGATAGTGCACACTGCAGCCAGCTCG GACTGGCTTGCAAGAGTC
WI-11806	60 T G	CATGAAGAGT GGGCAGTTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTAGCATCAATTTGCCCCAAGTTTGGCAGGCATGAAGAGTGGCAGTTCA[T/G]GTT TTATTAGTATATAAAATTTGGCTTTACAGGAAGCATTATGG
WI-11946	31 C A	---	---	CCCTAGTGAATACAACTTTGTCTGGAGAC[A/G]CCAGTAGTCTAAGAAAACCTCCTAGGCTGAG CTCTCTTGGGAATCTAAGATAAAGAACTGAGATCCTGGGAAGAAGGAA
WI-11965	65 T G	TGAAGATCAG ATCTCTGGTTT GATT	CAGCTGTGGTG AATGTTGAT	ACAAAAATTCACAAAGTACAACACTGCTTATTTCTTGCTTGAAGATCAGATCTCTGGTTTATTTAA[T/ G]ATCAACATTCCACCACAGCTGAAGGAAATTAACCTGAACCT
WI-11027	90 T A	TGCCCTACTAC GCTTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAACACTGCAGAAAGGGCAGGACAAAACAAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAAT[A/G]AATAAAAAATCTGTAAACACATTTCTCATTTCTCTACGA ATACCTTTCTTTTGATATTGCAATTTCTATGGCATACACAGAGGCACCTCTCAATGCCCTG
WI-11049	95 C T	---	---	TTCTGCTGAAGATCACAAAACAAATTTCAACCTCTGTGGTTCAAAATATTTAAGGATCTTGACCTTT GTGTTATTTCTGTTTCAACTAAGGA[C/T]AGACTTCAGAAAGGCATAGCTTCCCTTGTAAAGCTTTT AAACATCTTTTTCATTTGTAGGAAGGAACATTTTCAAAAGCCCCAA
WI-15488	69 C T	AAAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAACATGGTAGGAAAGTTCTCACTCTGCACATATAAAAGGACAGCCAGATATCA AC[C/T]GTTACAGAAATGAAATAAGATGGAAATTTTAAACAAATTG
WI-13654	49 A G	AACAGTTAAT GAAACACATC CGT	GGCTGGTGAAA TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAAACACATCCGTA[A/G]GTATGACATCATTT CACCAGCCAGCTACTTTCATGTGGCAGAAAAGGTAACCTTTTCCCATTTTACAGACAAAACCCAGT
WI-11070b	135 C T	---	---	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATATGGAAAAGGAGCTAGGACAAATCTTGCTT TCAAGTAAAATTGTGACTGAGCAGAAAATCAGCCAGCTATCTTGGGTGCAGAGAGGTACTCCAAGTA C[C/T]GTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAGGGAA
WI-11070a	110 G T	CAGAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATATGGAAAAGGAGCTAGGACAAATCTTGCTT TCAAGTAAAATTGTGACTGAGCAGAAAATCAGCCAGCTATCTTGGGTGCAGAGAGGTACTCCA GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAGGGAA
WI-12020	121 T C	---	---	AATCTTTTATATTTCCAGCTGTGAGACAGTATTTTGGGGCTGATGTTACCTCTAGCGGGGAAACC AGAGCCAGCTATTAAAGCAGCCAGAAAGCTACAGTAATTGAATACATGACCATTT[C/G]CTCTTTTAGC ACGTTCTTTGTTCTCTC



WI-11076b	142	G A ---			---	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGGCTGGCATGGCTTATCTTCTTTGGGAGGCCTCAGGAA ACTCTGAATTAATGGCAGTAGGCAAGGGGAGCAGGCATGTCACATACCCAGAGCAGGAGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-11076a	106	T C AGCA	AAGGGGAGC	TCCTGCTCTGG	GTATGTGAC	CATGGTTCTGCCAGCTTACAGGAAGCATGGTGGCTGGCATGGCTTATCTTCTTTGGGAGGCCTCAGGAA ACTCTGAATTAATGGCAGTAGGCAAGGGGAGCAGGCATGTCACATACCCAGAGCAGGAGAGA GAGAAAGAGAGGAAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-14263	49	T C GGCATATTCA	CGCAGAAAA	AATTAGTATGG	GACA	ACCTTTAAAGTTTCTCCCACTACTCCCGCAGAAAAAGGCATATTCAAT/CJTGTCCCATACTAATT TTTGAATAACCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA AATTATTGCTGAAATTAGGAAGGGAGCA/CJTGAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGAAGCAAGTACCATTTTCCAAAGTATAAACTCGTA
WI-14267	28	T C ---			---	GATTTGTTTATTCATTCTCGCTTTTCAATTTTGTCTTTTAAATAGAACA[G/A]CTTTGATTTTAGTA TATGACATCATCATGAAATTTTCTCTTACTTTTGTATTTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGAATGAGTTCA
WI-13892	50	G A TAGAAC			ATCAAG	ACCTCTTTCTGATGACACTTGTACCTGTAAAGGGTCTAGAGAGAAAGAGTAGTAGCTCTACTTTGC TACAATTCAGGATGCAGGGCATGAGAGGATTCCTCTCTC/GTCCAAAGGGAAGAGCTTTTGGC AATAATGGAAAGAGGAGTGAACAAAGTAATGAACAAACAGACCCAGATCAGAGGAAGAGATG GCTTTCTTGTTAATCTGGAGCA[G/C]ATTCAAGCAGCAAAATATTACTGAACACTTGCTATGTGCTG G
WI-13951b	88	G C ---			---	AATAATGGAAGAGGAGTGAACAAAGTAATGAACAAA[C/TA]GACCCCAAGATCAGAGGAAGAG ATGGCTTTCTTGTTAATTTCTGGAGCAGATTCAGCAGCAAAATATTACTGAACACTTGCTATGTGCTG G
WI-13951a	39	T C AAAAA	GGAGTGAACA AAGTAATGAA	TTCTCTGATC	TGGGTCT	GAGACCAAAAAAGGCTCTTGCCCAT[G/A]TATTCCTGCTCTCCCTGACTGACCCAGTGTCTT ACAATGAACATCCCTCAGCCCCCATGGCATGGTGCATCCCTTCTCTGGGATCTGTGAATATAACCA ACTGCTTGTCAATGGC
WI-13264	25	G A TTGCCAT	AAAAAGGCTC	GGAGGGAGAG	ACGGGAATA	TTATTTGTCATTAGCAAAAGGAAGTTAAATACTGATAGA[A/C]GATGCAAAATTTGTCTTTTCATGCA TTTGTGGAGCAAGTACTAATTGTTCACTGTCATTTCCCTCACAAGGAGTTGAGCCCCCTAGATGAC
WI-13960	39	A C TGATAGA	AGCAAAAGGA AGTTAAATAC	CATGAAAGGA CAAATTTGCAT	C	AACTCTTTATTGTTTAGCTAGCCCCAGTGACTTTATGCATCTTTAACCAGAACCCCTTCAG[C/T]AG AGCAAGTCTGAGCCAGAGGTTTATCACACTTTTGCTCTCAGGGTCCACCAGGAACCCAGGTCTTGGCT
WI-15843	62	C T CAG	ATCTTATAACC AAGAAGCCTT	CTCTGGCTCAG	ACTTGCTCT	



WI-13983	52 G A	TCTCTCCACT CCTTAAACCT	CAATACTCTCT TAGCCAGTGG	TTGTGATCTGATTTCCGAAACATAGAAATCTCTCTCCACTCCTTAAACCT[G/A]CCACTGGGCTAA GAGAGTATTGTACAGAATATGCACCTACTGACTTACAGAAATTAGAACATCCAGGCCACTCAGTGAGA
WI-13850	51 A G TT	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTA	CATGAATCTCAGGGTCACAGCTTTATTTTATAGATTTTAAACACAGCCAT[G/T]TACAAACATTGT CAGGGAACATTTACAAGATAAATAAGATGGACTTGCAGGTGTAAGGATTTACACTTCA
WI-15295	27 G C A	TGTCAGTTTGA ATGTATTCTG	TGAATAGTTGG CAAAGGAAAA	AGATGTCAGTTTGAATGTATTCTCTGAT[G/C]TTTCCCTTTGCCAACTATTCAATTATGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCAAGAAAAAGGCCCCGAAATATGAGTGAGACTCA
WI-14284	55 C T ---		---	ATTTCAAACAAATCCAGAACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAACA[C/T]TATGCCAT GCGGGAATAAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA
WI-14288	85 G C	CCGCTGCTATT CCCAGAT	GGTCTCTCTCC ACCAATCTT	ATGACCAGACCAGAGCCCTGTTCTATATGAAGACAAACAGGTGGCCATCTTGGTGGAGGGATA CCGCTGCTATTCCCAGAT[G/C]AAGATTGGTGAAGGAGACCATTGACAGATGACAAACGG
WI-13522	33 C T	TGATGTAGTTA CCCCACTAAT	CATAATATTG AAGTCAGTGGT	TTTATTTTGATGTAGTTACCCCACTAATACAAC[C/T]GAGAACCACTGACTTCAAATATTATGAGAG AAAATTACTCCAGGGAATTTTGAGAGAAGATAATA
WI-13529	42 T C	CACAAACATT TATTGAACAG	TCTATACACTT CTCACTCTCTT	AAATATGATTCCTATTCACAAACATTATTGAAACAGTTACCA[T/C]AAGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGCTCTGAGGGGTTTATAGTCTAACAGGGGAACAACCTCTC A
WI-13859	84 G A ---		---	TTATTTGTCAGAAATTTCCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAGTTTACTAC TTTGAAAAGGAAACTAT[G/A]JACAAACAAGTATATATTCAGGAAAGGACTCCTAGAACTTTGAGCA ACA
WI-13536	29 T C ---		---	TGAAAGGATACAGAAAAAACTCAGCGAAG[T/C]GAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCAGCTCCAGTTGCTCTCCAGTCCCTTACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52 G A ---		---	TTTATTGTTTGGTAGAAAAACAGGCTCTTTAACACTGAAATAACATCTCAC[G/A]AACTGTGCGCTC CTAGATTACAAAAAGTCAAAACCAATTTCTTTGACGCCGGCCCTTGAATCTGACATTCAAGTCA CGTAATAGAAACCAGAGCT
WI-13477b	61 A G ---		---	TTGGTTTTTAATACCTCTTGTGGATAAAAGGACATTGTTTTTCATTAGCTGTCTTCAA[A/G]GAC AGAGAAATAAGATAAAATACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32 A G AAGG	TTAATACCTCT TGTTGGATA	GAAGACAAGC TAATGAAAAA	TTGGTTTTTAATACCTCTTGTGGATAAAAGG[A/G]CATGTTTTTTCATTAGCTGTCTTCAAAGAC AGAGAAATAAGATAAAATACCTTAAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT



WI-14297	86	A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACITTTATTTAGCATGCAATGCAATTTATTTCTGGCAATAAAATTAATATGTGCAGTTATAAAAAAT GTTGGGTACTTTTCCAAAG[AT]AAAAATGTTTCTGAATGTGCACACTAGAAATATATGCAGAATCCTTT AAACAGTCGACT
WI-12229	89	T G A A A	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAAA	TCCATGTAAATATTTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTAAGAAATCAACA TGTGCACAAAAAGAGTAAAAAT[7]GJACCAAAAAATTAAGATTTTTTGGGACAAATTCACATGTTT AAAAAT
WI-13582	43	C A A	TGCAATCTAG AGACTGGGA	TCTGGGCAGTT AGATTCCA	AAGGTCGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[C/AT]GGAATCTAACTGCGCAGAG AAATCAAGACCGATGGTGTGAATCTGGGGCAGCTTCAAAATTTCTGCCTCTCTAAACATTTTCCAC CCAAITTTTTCATTATGGC
WI-13857	28	A G	---	---	TCTGAGTTGATAAAATGCTTTTCTGAAC[AG]TACATTTTAGGTATCTGGCACAATTAACCAAAATGT CTGCCCATTTTGTGTAGCTTTTACACAGTACAGATTTTCATTGATGTCGCTCCACATCTG
WI-15809	77	T G T G T A A A T G C C	TGGTTTTCTGT TGTAATGCC	TAAGTAGCTA ATTCAATGTTT GTAAA	GTTTTAAGTTCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTTCTGTT GTAAATGCC[7]GJTTACAACATTTGAATTAGCTACCTTAAGTATTTGAAGAGCTTCCATT
WI-15892	123	A T	---	---	TTAATCAGTCTGTGCAAGAAGAAACAGGACTTGATCAAGCTTCCAGCCCTCACCACCTCTATCAGCA TAGCAATTTTAAGGATCAGAGCTTTGTTTACATTTGTCTAAACCAAGAGAGGAA[AT]GGAAATCA ACTCCACAGATCAACATGT
WI-15801b	81	T G A A	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCITTTATTTCCAAAGTGGGAAGCGCATTTTTCATTGGCTTGAATGAGAAAGCTTCATACTCCACTTA GCTGCAGTAAATAC[7]GJGATCCCATCCACTCTCTCTCTTTTTTGACTGAAACTCTTCAAGAACT GCTGAATGTCCTCTCTC
WI-15801a	24	G A A A T G G G A A G C	TTTATTCCAAG AATGGGAAGC	TCATTCAAGCC AATGAAAATG	TCITTTATTTCCAAGTGGGAAGC[AG]CATTTTCAITGGCTTGAATGAGAAAGCTTCATACTCCACT CTAGCTGCAGTAACTATCTGCATCCCATCCACTCTCTCTTTTTTGACTGAAACTCTTCAAGAACT GCTGAATGTCCTCTCTC
WI-13763	59	T C G A G T G A T	GGCTGGACACT GCAAGTGAT	CCCACACCTGC CCCT	GCTCGTAATGAGACAGAACCTACAATCTGTTCACACTGGGCTGGACTGCAGTGAT[7]CJAGGG GCAGGTGTGGGCGAGGTGGGCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA
WI-13578	48	T A A C C	TCAATAAAGA GCAGAAAGAA	CAGTGTGAAG AACATCTTTT GTC	TTTTTTTTTGGTGAGTGTGCTTCAATAAAGAGCAGAAAGAAAACCT[7]AAGACAAAAAGATGTT CTTACACACTGAGCTTTACACAGTCAACCAACATTTGATATTTTCCCGAGGGCAAAAAAGA GAGCTTCCCAGAAACCTC
WI-13789	62	G A A G G G A G	TTGGATGGCTG	CAGTGGCTTC CTCTGTTT	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAAACTCAAGAATTTGGATGGCTGAGGGAG[7]A GAACAGAGGAAGCGCACTGGGCTGGGACTGAATATGGACAGTGGATGGTGGTCTCTCACTCTCTT GAGGTCCCT
WI-13594	66	G A A G C	TTTTTAACACA GATCACAAAA	CCTTTGGGCA GTACTTTT	AATAACAAGTTTAAAGTTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAAACACAGATCACAAAAAGC[7] G[AT]GCACAAAAAGTACTGGCGCAAGGACAAAAATTAATGCTAAGAAATTAGGCCAAACAGCTGC



WI-15625	40 C T ...	...		GTTCCTCCACCTACTCCCGCAGAAAAAGGCATATTCAA[C/T]TGCCCATACTAA TTTTGAATAA CCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA
WI-13367	84 C G A	CCACTGAA GACTCACCAG CCCT	TCCCCACCCCA CCCT	GTCTCATTCTTGCTAGGCTGTAATTTTCAGTTTAAACAAGTTTCTTATGTGATTGTGGCCACACT GAAAGACTCACCAGAA[C/G]AGGGTGGGTGGGAATACCTTAATCAATATTTGTGGAATTTACCCGAT GAAATCCAGTTATTCCT
WI-13600	26 G T	TTAATGAGCC AAGCATCCAT	CATATTGAAAA TTGTTACTAGA TGATGG	CTCACTTTAATGAGCCAGCATCCAT[G/T]CCATCATCTAGTAACAA TTTTCAATATGCACATTATAT TATACTGGAACAAGAAATACGGATTGTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCCTCT TGATTCCTTCTCTACCC
WI-13602	89 G T	TCCATTCTGGA GACAACACA	GCATACCTCAT GACAATATTTA ATATTAAT	GATAGGAAAAGAAGAAATGAAGTCAATAGTCTTTAGCAAGCCCAACTAGCTCAAGGAATAGACAGCC CTTTCCATTCTGGAGACAACACA[G/T]AAATCTATTAAATATTGTCATGAGGTATGCACCT GCOCA
WI-13650	76 A T	AAAGATTAC AATATTTCACT TTTAAAC	CAGGCTAGGAT ATGAAGAGTA GTTTT	GCATTAACATTTAAAAATCTGAGGGATATTGATGAGAACTATGATGAAAGATTACAAATATTTTAC TTTTAAAC[A/T]TAAAAACTACTCTTCATATCCTAGCCTGATGACTTAAAGTTACCGG
WI-14319	83 C T A	CAATTCAGG CACAAAGCTA	CCAAATCATCT ATATTGTTGCA TG	TGTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAATAGCAATT CAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAATT
WI-13528	80 A G AAAA	CAATACATT GCATTTTCCTA AAAA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAAACTGTAATCAATACATTTGCATTTTCCCTAAAA AAAGAAAGACATT[A/G]TTACAGAGAAAACCTGTGGTATCATGCAGGAAAAAGCAGAAAAAATTT
WI-13909c	93 A T ...		...	ACTTAACTGGCTTATCTCACGGTAATCTTCTGTATTTCCAGTGAAGTTTCATCTTCCCTCACACT CTCTTCAAACCTCGAATATCTTTT[C/A]TGAGATGTCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80 G A C	TCCTCACACT CTCTTCAAAC	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAACTGGCTTATCTCACGGTAATCTTCTGTATTTCCAGTGAAGTTTCATCTTCCCTCACACT CTCTTCAAACCT[C/G/A]AATATCTTTTCAGAGATGTCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86 C A ...		...	TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAAAACAAATTTAAAAAGGGACAGAAAAATTAAG AATCAAAACATCAATCTGGAC[C/A]ATGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-14323a	78 T C ACATCA	ACAGAAAAAT TAAGAATCAA ACATCA	GCCTTTTCAAG GTTCCCAT	TTTTTATTGAATTCCAAATGTAGCAAAATCATTAAAAACAAATTTAAAAAGGGACAGAAAAATTAAG AATCAAAACATCAIT[C/T]CTGGACCATTGGGAACCTTGAAAAGGCATGGCAGTGGAGACCAGTAACCTA
WI-15399b	104 G A AAA	AGATAATGAA ACATCTGCGA	GATGAGGTGAT TCCCACACTT	AAAATTGACAAATCAACTAGCTTGTCTTTTGTGCTGTTTGGGAAGACTACCATTTATTCAAAATTTATGT AATACACTCATCCAGATAATGAACATCTCGGAAA[A/G/A]AAGTGTGGGAATCACCTCATCTGTGC



WI-15389a	33	G A TC	AATCAACTAG CTTGCTTTTG	TTGAATAATG GTAGTCTTCCA AA	AAAAATTGACAAATCAACTAGCTTGCCTTTTGTGTC(G/A)JTGGGAAGACTACCAATTATTCAAATTTATT ATGTAATACACTCATCCAGATAATGAACATCTCGAAAGAAAGTGTTGGGAATCACCTCATCTGTCG
WI-15747	88	T C AGTGTT	TGCTTCATTTT AAACTAATTT	CATAATTCACC AAAAGTTTATA TAATTT	TGTAATCTGCTTACAGTCTTTGCAAAGACAGACATATGTTTTTGCATAAAGATATAAAATTCCTTCAT TTTAAACTAATTTAGTGTTC(C/J)TTAAATATATGAACTTTTTGGTGAATATGAACGTGTACCAAAAC C
WI-13752b	117	C T ---		---	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTAAAGTCTGGATATACCTGGCTTGCAC(C/Π)GGACACCTTTTACG GAGGGATTCGGACAAC
WI-13752a	106	T C AGTCTGGA	CCCTCTCGTTA AGTGTGTC	CCCTCCGTAAA AGGTGTCC	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTTCGTAAAGTCTGGATATAC(C/J)TGGCTTGCACCGGACACCTTTTACG GAGGGATTCGGACAAC
WI-14339	102	T G TTAC	CCCAATCAAA CAGTACATGA	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACCCCTTCACTGGGCTACAGGTAATTTCACTGGGATGGGAAG CAGATGAACCCACCAATCAACACAGTACATGATTAC(T/G)GCGTTTCCAGAAATCTGGATAC
WI-13744	115	C T AAACTGAA	TGGTGTCTGAAC AAACTGAA	AATCAGGAAA GATAAGCACAA GC	TGGATGGATGGATGAGGCCACCTGTGTTCACAAAACACGTAATGGAACCTTCATGCAGCTTTAGAT TTCCCTTGGCCAGCTAGGAGCTTGTGTATGGTGTCTGAACAAAACCTGA(C/J)GCTGTGCTTATCTTTC CTGATTTCT
WI-14061	68	C T ---		---	CCCTTGACTATATTGTTTTTCCAAAAATAGGACTATGTGTAGAAGAGAGCCCCCGTACATACCTTAT C(C/J)AACCATTTTCATCCACCATTGTAAAAATCTCATCTCTGGTCTGGATACTCAAAAACAGAT
WI-15719	69	A C CATTGAGC	ACCTTTTCATC CATTGAGC	TGACTACTGGC AAGAGTTTTAA ATT	TTACAGTTGGATTAACACTACACACTGAATATACTGAATTAACCTTTTCATCCATTTCAG C(A/C)AATTTAAACTCTTGCCCAAGTATCATGAACCTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106	T C AACTT	CTCTAAATCG ATACATCCAA	GAACTGATGCT TGCTGCTAACT	TAATCCATCAATCTAAATCACACATACATAGATCAAAACAGAAAGTACCACAGTATGCTTTATTTTGCA GGTATTAAATGGTCTCTAAATCGATACATCCAAAACCTTT(C/J)AGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27	G T CACA	ATTTTATTTCAC ATTAAACTTG	GTTCTTTTGATA TGTTGGCTTAGT TTT	GGATTTTATTACATTAAACTTGCACA(G/T)TAGCAAAAAAAATCAAAAACATAAAAACCTAAGCCACA TATCAAGAACAATATACAAATAGAGATTGAAATTTCTCAATAGCATTTGGAAGGTATTTCCATAAATA
WI-13785d	72	G A ---		---	TCAAACTGCACACTATAAAAGTGTCTTTAAATGCAGCAGCAGGAGATGTGAAGACACACAAATGAAC AAGTGC(G/AT)AGTGACACATAGCTGTCAACACAGTG
WI-13785c	56	A/C ---		---	TCAAACTGCACACTATAAAAGTGTCTTTAAATGCAGCAGCAGGAGATGTGAAGAC(A/C)CAAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACACAGTG



WI-13785b	40 C G ---	---	---	TCAAAGTGCACACTATAAAAGTGCCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAAATG AACAAAGTGCCTAGTGACACATAGCTGTCAACACAGTG
WI-13785a	27 T C TGCTT	AAAAGTGCAC ACTATAAAAG	TGTTGTGACAG CTATGTGTGAC T	TCAAAGTGCACACTATAAAAGTGCCTT[C/G]AAATGCAGCAGCAGGAGATGTGAAGACACAAAATG AACAAAGTGCCTAGTGACACATAGCTGTCAACACAGTG
WI-13793	88 C G ATAGG	GGATTTTACAT TCAGCCTAGAT	GGGCAGGAGGA TTTGTTACT	AGAAACCAAGTATATCATAGGCAATAAAATAGTTTTACCCCATTTGATACACATAAAGGGATTT TACATTCAGCCTAGATATAGG[C/G]AGTAACAAATCCTCTGCCATAAATCTATGACTTG
WI-13794	52 A G TTTCTTTCTC	TTCTCACCCCT TTTCTTTCTC	AGAATGGGCTC TTAACCTTGT	TAGTCTCTACAATTCCTTCAATCCATTTTCTCTCACCCCTTTTCTTCTC[A/G]TACAAGGTTAAGA GCCCATCTCTCAACAAACAAAACACATAGAGCAAT
WI-15729	35 A G GTGTAGACTGC	CTTTGAACCAT GTGTAGACTGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[A/G]GGCACCTTTAGAAAGAAAGCTGAGACTGAA AAGTCTGTCTGACITCCAAAGGAAGGTAAAGTCCCTGTTTGAGCCCGGGCCCTGCTCATTTGA
WI-13424	66 G A C	TGAGGTTTTTC ACCTATTCTT	TTTTCTCCCC AGGGTCTA	GTCTTTGACAAAGTCTCCCAACTGGTTTGAGATTTTCCCTCTGAGGTTTTTACCCTATTCTTC[G/A] TGAACCCCTGGGAGAAAACACATGTGTAAAGTGGCTCAGGACATGAGGAGCCGCTTACACAAGAT GCTGGCTAAGGGGCTTC
WI-14065	29 T C AATT	TCTTATAAAA GGTCAGAGGC	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGGTCAGAGGCAATTT[C/G]AGATCCCAGATTACAGTTGTCTCATAAAAAGAT TCAACTTCAAGTAGCACAAATTTCTGTCTGCTTTTAACTCTGAACATTTCTTGAAGCACGAA
WI-13446	22 G C TCACTCATCA	GCCATGTTCTT TCACTCATCA	AAGGGAATCA AAATCAGAAG G	TGCCATGTTCTTCACTCATCA[G/C]CCTCTGATTTTGATTCCTTTCTGCTCTGTAATTTTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTTGAATTTCTGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCCTAATT
WI-13725	56 A C TGGGTGOC	TGAGCACATA TGGGTGOC	OCTGCTGTCTC GGGC	TCACACAAAGGCATTTGGAAATGTCACCTTACACATGGTGAGCACATATGGGTGCC[A/C]GCCCGAG ACAGCAGGATAAGTTTCACAAAACCTTGACCAGGCAGGTTAGAAGCAAGGCATGGTTTCAAGGATG
WI-15702d	107 T C ---	---	---	CAAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAAAT[C/G]ACTAATGGGTCTTTTGAACAAATAGTTT TGA
WI-15702c	101 T C ---	---	---	CAAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAAAT[C/G]ACTAATGGGTCTTTTGAACAAATAGTTT TGA
WI-15702b	90 C T ---	---	---	CAAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAAAT[C/G]ACTAATGGGTCTTTTGAACAAATAGTTT TGA



WI-15702a	48 G C A A A G	A A C A A A A T A A A G G C T T T C A A	C C T C A C C C C T T T A C C C C	C A A T G T T T T A T G A A G A G A C T C C G A C A A A A T A A A G G C T T C A A A A A G [G/C] G G G T A A A G G G T G A G G A A A G C A T G T G A G A G A A A C T G T A A C C C T G T A A C A A T A C T A A T A G G T T C T T T G A A C A A A T A G T T T T G A
WI-13831b	113 T C ---		---	T T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A A G G A G A T T C A C A T A C T T C C A C T G T A C C T C G G G T A A G T T T C C T C T C T G T A G A T [G/C] G T C C A T G T T A C A G T C A A C T A T A A A A C A T G G C T C A
WI-13831a	56 G C ---		---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A A [G/C] G A G A T T C A C A T A C T T C C A C T G T A C C T C G G G T A A G T T T T C C T C T C T G T A G A T G T C C A T G T T A C A G T C A A C T A T A A A A C A T G G C T C A
WI-13806	62 G A ---		---	T G A T T G A G C T T A G A A G G A A G T C A T G T T G A A A T C A G A G A G G C C A A A A C T A G G C C T C A G G T [G/A] C C C A T T A A G C A T G C T G T G A A T G C A A A G G A A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
WI-14372	86 A G ---		---	C A C A T T T C A G C A A A A A A T C G A G G T G C A A A C A C A G G G T T A T T T C A C A T T A A T A T A A C T G G A T T T T T T G C A A A T A A A T A G G A [A/G] T T C T C T T T A A A T A C C A T C T C C T C A C T T C A T G G C C A G T
WI-14373	95 A G ---		---	A G G C T G T T T T T G A G G C C T G A G G C C C C A A C A T G A C A C G T A A G A C T G T A A C C A T G T C A T G T G A G T T A T G A G C T A G G A A C C C T G G A C G A A A C C A [A/G] C A C A T A T A C A A T C A T C T C C A C C T C C C A A C G C C T T T A C T T T C A C A G C C T C T G C A
WI-14078	61 C T G C A A G A	A A A G A A G T A A A T T A G G A A G A	T G T G T C A T G T C T C T T A C T G C	A G A A A C C G A G A A C T C A A A G A A C C A C A C A T G T G T A T C A A A G A A G T A A A T T A G G A A G A G C A A G A [C/T] G C A G T A A G A G A C A T G C A C A C A A A T C G A A A C A A G G G C A T G G A G A A G G A C T T T A G A T G G T C A C G
WI-14083	47 C T A C A C T	A G A C T T G A G A G C T T A A A A C A	G C C T A C T G G A C C T C T A A A C T A C T G A	T T G C T A C A T A A C A C A T T A C T C C A G A C T T G A G A G C T T A A A A C A A C A C T [C/T] A T T T G T T A T T T C A C A G C T C A G T A G T T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T G C T T A A G G T C T T A C A A G G C C A A
WI-14085	31 A G A G A A A A	C A T T T A T T T C A T G T G T A A G A	C A G T C A T G T T C A C G T G C T A G T T	T G C A T T T A T T T C A T G T G T A A G A G A A A A A C [A/G] T A A C T A G C A C G T G A A C A T G A C T G C A T G G A T A C A C G G C T C A G C A C G A G G C T A A A G T C A G A A G T G A G T G A A A A C A A A A T A G C A T G T T G A T T T A A G T G A A A T A A C A G A A C A G G A G G C C T T
WI-12169	121 G C T T G C T T	A A T A A A A C T T C C T A T T T C T T	G G G T T C T G A G G T G A A A G A A A A A	G T C A A A A G G T T G G C A A A T T T T A T T T C C A C T T A T C A A G A A C T T A C A A A A T A T T T T G T T C A T T C T A A A T T T T C A C C T T A T T G C T A A G T T A T A A A A T A A A A C T C C T A T T T C T T T T G C T T [G/C] T T T T T C T T T C A C C T C A G A A C C C C C T T A
WI-15705	50 A G A T C	G G A G G G A G A T T T T A G A C T G A	A G C T G T A G T C G T C A A A T A C T C T A G A A	T T G T T T T A T T T G G G A G A A T A A G A G G A G G G A G A T T T A G A C T G A A T C [A/G] T T C T A G A G A T T T G A C G A C T A C A G C T C C T C T C T T T T G T A C T A C G A G A C C C T G C T T A T A G C C C C A A C A G A A A T C C T C A T C T G C G G T T G C C A G A C A G



WI-14379	102	C T	CAOC	GGGTTATGTCA	TCATTAAACA	ATCATCTGTTT TGAGGTTGACA	TTTAIGCTGTTGTTTCTACTGGTGGTCTCGCTCACTAATATCCAATCCTAGTATGATTTCTTT TACTTGTGCTATTAAACAGGTTATGTCACACC[C/T]GTCAACCTCAAAACAGATGATACT TAAATAAAACAAAGCAGAAA[C/A]CCCACTTAAACAGAGGACACTGCAGAGGCTTATGTACA ACACGTGTCOCGCGAGGCTGGCGCAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22	C A	---	---	CGCAGAGCTG CTGTATTTAAA	---	ACCGCAGAGCTGCTGTATTTAAA[A/G]ACAAGCGTCTGGATCTCTGCAGGGGCTGGGACCAGCTGC AGTGGGGGCTCCGGCACTGCTCTCTCCAGGACTCTTCCACCCACCCC
WI-15937	24	A G A	A A A	AACTGAAAC GTATTTCTCC	GCAGAGATCCA GACGCTTGT	GGCCTTTAAGT TTCTACGGTG	TGAAACTGAAACGTAATTTCTCTCCA[A/C]ACACCGTAGAACTTAAAGGCCGCAAAAGACTCACACCC ACCACCTAGCGGGGCAAAAAGGAAGTTTCAGGTGATACAAGATGTCTGCCATCACACCTGAAGGAT GGTT
WI-15944	24	A C A	A A A	---	---	---	ATGTTTATGATCAATTCACCAATACAGTACAGGGAAGGTGAAATGAGTAAGAAAAAATCAT ATTTAAGTCCCGTTAACACTAAGCC[A/G]TATTATTCAAAATGTGTTTCAAAATCTCAGCCAGAT CACCAAAGCTCAGTCACTAC
WI-14124	92	A G	---	---	---	---	GACAAAAGGCGAGTTTCTGTAGTCCAGCAGGGCCAGAGAGTTATCAGAACGGTGGTTTGACCT GCATAGATTTTTCAGCACTA[C/T]GTGGCCATGCCATTCTGTAAAGTAAATTAATGAACA
WI-14125	88	C T	C A T	GGTTGACCTG CATAGATTTT	GGATGGGATG GCCAC	---	GTTTATTTCTCACAGTCTGGAGGTTAGAAGTCTGAGATGAGGATATCACCAGCATGGTTAGGTTCT GGTAGGAGCTCTCTGGCTTACAGCTGGCTGCTTCTCACCATGTCTTCACAT[G/A]GCCCAAAAGAGAC AGAACAGCTCTCTGGT
WI-14136	120	G A	A T G	ATGCTTCAACA TGTTGGCACCA	CAGTATGTACA GTGACATAACA	---	TTGTTGTTGGCACCAGAAAAGCT[C/T]ATGTTCTATGTTATGTCACTGTACATACTGTAAACAAGACT GCAATTAATATTGTTTCTTATGATTTGTTTCAATG
WI-14138	23	C T	G A A A A G C T	TCCTTCAGTAG TAGTATATTCA	GCTCATTCTT TTAGTGCTAAG	---	GGCAGGTTTATTCATAATTTTCAAACTTGAAGCAACCAAGATGCTCTCAGTAGTATATTTCA GACAATC[G/A]AATATTACTTAGCACTAAAAGAAATGAGCTATCAAGTCAATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-13551	74	G A	G A C A A T C	---	TAATATT	---	TTTTTAAGAGTGCCTTCACATCAATTTATTTGATTGCACACAAAACTTTTTAACCTC[T/G]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCCCAGTGCCTTTTGAGATAGAGCCCTTCTTCAGAAATCA CCTCCG
WI-15953b	59	C T	---	---	---	---	TTTTTAAGAGTGCCTTCACATCAATTTATTTGATTGCACACAAAACTTTTTAACCTCCGTCAA AACACAACAAGAACAGATGAATAAGGAAGCCCCAGTGCCTTTTGAGATAGAGCCCTTCTTCAGAAATCA CCTCCG
WI-15953a	26	T G A T	A	TTTTAAGAGTG TCCTTCACATC	TCATCTGTTCT TGTTGTTTTG	A	TTTTTAAGAGTGCCTTCACATCAATTTATTTGATTGCACACAAAACTTTTTAACCTCCGTCAA AACACAACAAGAACAGATGAATAAGGAAGCCCCAGTGCCTTTTGAGATAGAGCCCTTCTTCAGAAATCA CCTCCG







WI-16002	59 T C	GATAACATAA AATGATCATG AGAAATTC	GCATCTCTC TTTGACTTTT	CCAACATTTTAAACCTATGACTGGTCAATGATAACATAAAATGATCATGAGAAATTTCA[T/C]GTTA AAAGTCAAAGAGGAGATGGCTAATGCATGCTGGCT
WI-15361b	101 A G A	CCCACTTGAAC TCAAGTCATC	AACTAAAC CTTTGTGCCTA AAA	GTGGAATTTTAAAGCCATCAAAATTTCTTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCCACTTGAAGTCAAGTCATCA[A/G]TTTAGGCACAAAGGTTTAGTTTCTCGG GAAATCAAGTTTAAACCA
WI-14759	73 T C	GC GTT GACTT GTGCGG	TCCACACTGC CCCC	TGAGTTACAACAATGAGCAACAAGTTAGAAAAATTTGGTTTATTCAAACCTCCTAGCGTTTGACTT GTGCGG[T/C]GTACTCAAATGGGGGCGAGTGTGGACGGGGAGGATTGCAACCAGAGTTTCATACTG CAA
WI-12535	50 A T	CTAGGAGGGTT GAGGTGTAGA TAT	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTATTCAGGTGGTGACTAGGAGGGTTGAGGTGTAGATAT[A/T]CTTCTCTCTCTC GTGGAGCCTTACTGAAGACAGGATCGCCGTTCTTGTTTATCAGCTGAGAAAGGCGAGTCTCGCCATC TTAAAGACCTGCCCTCC
WI-13805a	112 G A	AAAGGCACAC GGGGAA	CTCAGCCTGCC TTGACC	TTCCATTCAATTATGCTTGGCTTTACCAATTTTATAGCTATTGGGAGGCGAGGAAATTTTGGC CCCAGAAACCATGAGATTTGGGTGAGAAAAAGGCACACGCGGAA[G/A]GGTCAAGGCGAGGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18 T C	---	---	ACACAATATAATTCCTAT[T/C]CGAGTGATTAAACCTATTGTTGTTTAGAACCAACAAAACTAC AAGAAAAACATTTTCAAAACCTTTTTTTTCAGGCTGA
WI-14808	52 T A	ACCCACCACA CTACCCGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAAACACACTTTAAGCAAAACAGTTAAAAAGTACCCACCACACTACCCTGT[T/A]AAAATCTTAAC ATTGTGATGCCTCTGCATCAATTTTAGAAAAACAAGAAACACACAACCTGAAGGCCCATGTA
WI-14816	29 A T	---	---	AGTTAAAAAAATCGAGTCAGCATTTAT[T/A]AAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCTGAAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTC
WI-12542c	71 G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCCATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70 G T	---	---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCCATCCATGTGAGGGCTCTAGATC AT[G/T]GTAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45 C T	GCTATTAGGC AACTGAACA TTTAAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGT[C/T]ATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57 C T	GGATACAGCA GTAAAGAATA CAAAAA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATCTTAGAAAACTGGGATACAGCAGTAAGAATACAAAAATCCTGC[C/T]CTTATA GAGCATACATCTAGAGGTGGGAAAGAGGCAATAAATA



WI-14836	28 T C ---			---	TC TT TGGAGGATAGAGGACAGAGTGTTC/GTTGATTTTTCGTTTCGGTTTCAGTTGGTTGTCATT GGTTTTGTTTTTGTCTAATTTTGGCCACCCCTATAAAAAGCAGTGCCACCCAGAGGCAG
WI-14856	60 A T A A	TGGTGACACG GAAATACTT	TTTGTTTGCTA CTTTTACAAA CTTT		ACATTTCCCTTATGATAGCAACAACATAATATGATGGTGGTACACGGAATACTTAAT[AT]TAA AGTTTGTAAGTAGCAACAATAATGAGTATATACTATAAGTGATAGAGGATGATATGAAAAA GGCTATAAAAAGCTCCAAA
WI-14863	61 G A ---			---	ATGGCAATTTACTTTATAGCAATGAACAATATTTGTCAAAGGGCAAAATATTTTGTCTG/GAAG TTAATAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACATATTATTGATTGCCACT ACCTGGC
WI-14867	46 T C A	GACATTCCAA GGCTCTCTAAC	TGGGGCTGCAG ACACTC		TTTTAATTAAACGTAAAAAGGCAGGACATTCGAAGGCTCTCTAACA[TC]GAGTGTCTGCAGCCCCA TTCGCTTTGAGATGTGAATGTGTAAACCCAGGGTGA
WI-14733	98 G A A	CCAAATTGAC AGATATTCTGC	GATGAGGTCAG GCCATTTATT		ACGGAGTCGTCCTGATGTATCTTGTCAAAAATGTTTGGCTGATTCTAATCATGAAGAACAATT AGAAAAATCCAAATTGACAGATATTCTGCA[G/A]AATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAAAAACACAAAA
WI-14898b	79 A C ---			---	TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT[TC]GAGTGCCACTAAGGAAA ACTTTCCTCAT[TC]AAGCTGCTGCTGTGCACGTTGCTGGGCTTTGCTAACCCCTGGTGTGCATCT GCCTGTGTTCTGCTCT
WI-14898a	50 A C CA	CATGTACAGG AAGAGTTGCTC	AAGTTTCCCTT AGTGGCACCT		TTTTGTACCTATTCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT[TC]GAGTGCCACTAAGG AAAACCTTCTCATAAAGCTGCTGCTGTGCACGTTGCTGGGCTTTGCTAACCCCTGGTGTGCATC TGCTGTGTTCTGCTCT
WI-14907	48 G A GGACTCTGAC	GGCACACATT CCAATACATT	TCTGCTGCAAG GGGAAT		TGGTATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC[G/A]ATTCCTTTCAGCAG ACATTTGTGAAGCTGCTGGTGGGCACACCCATCAATCAGTGAATCCTGCTGACAGAGGGGCCACATG CAGCATGCTCACGTTG
WI-14911	52 G A C	CAGTCTCTGGT	CAAACCAGGA AAGGACCTT		CTAGAATCTGGGAAGTCCAAGCTCAGTGCACCAATACATTCACTTCTGCTGTC[G/A]AAGGTCCTTTTC CTGGTTTGCAGACAGATACCTTGTCTATCCTCACATGGCAGAGAAAGAGAGGAAGTAATCT
WI-14913	88 C A ---			---	CTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCTGGGACCAGCCAAATTC TAGTGATAGTAGAGGACTCA[TC]CCTGCACGTGCACCTTTCATATACAGATCAACCAATCCAAAAC CTACACCTCCAAACACCT
WI-14914	66 G C A	CTGGACACAG TTTTCTCTAGC	CAAGCCCAGGA CAATAAATTC		ATTTCCCTTGATTGGCTGTGTAAGCCTGTGAAGTCATGCACATCTGGACACAGTTTTTCTCTAGCA[G/ C]GAATTTATTGCTCTGGGCTTGATGGCTTTCACAGC
WI-14926	49 T C ---			---	GTTTATTTTCAAAATGACACATCCACAGATTGAAATGGGCACCTTAGCGAA[TC]ACTTTGTGGACCACA AGACTTGTCTGAGAACATGTTCAAAGACAGTTTTTCAAAATAAAAATTTTCTTAATCAGGTCCA



WI-16083	89	C T	ATGTTTAAACA CAAACATATC AAGGAT	TGAAAAAGATT CCAGCC	GCATCTTTATTACCACAGAACTCAITTTATGTCCTTAATCATGTTTAAATATATAAAGCATGTT TAACACAAATATCAAGGAT[C/T]GGGCTGGAATCTTTCCATTCTATAGAAAAAGCACTAACCATC CATTAAAGCAG
WI-14930	55	C T	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTTCTGTGTTCTGGAAACAGCTCTCCTTTCCACAGGAGGAGTCCCTCATGGAT[C/T]GCGGGTATTG GTTGGTTGTGGTGATTGGGGAGCACAGGGAGAGCAA
WI-14946	47	T C	---	---	TCAACTGAAGGTGTCAAAGTGGTCTATTTGCCCCCAGACATAACA[C/T]CTCTAAATCATCCTCTA GATCAGGGAGTCATAAGGACCATTAAGGCTCATACACACAGTACTTTATGAAAGGATT
WI-15987b	80	A G	---	---	ACATTAAACAGCACAAATTAAGGGTCCCAACGAGGTTGGTAGTGCCTCCACTATGTGAGGACAC TAAGAAAGATGGT[C/A/G]CTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-15987a	32	C T	CACAAATTAAA GGGGTCCAA	GGAAGGCACTA CCAACTC	ACATTAAACAGCACAAATTAAGGGGTCCCA[C/T]GAGGTTGGTAGTGCTTCCACTATGTGAGGA CACTAAGAAGATGGTCACTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	56	T C	AGGAAACTG CTAAGTTGTCA G	GATGATCTTAC ATCAGTTGTG GA	GAATAAAGTTCTTATTGCCGTTCTTCAGGGAACAGGGAACTGCTAACTTGTGAG[C/T]TCCAACA ACTGATGTAAGATCATCTCTGACCATAGCGAACCTGTAAAGGCTTGCTGTTCCCTCCAGCTGA
WI-16100	52	A G	CAAAAAGCTA TTTTCTACAC TTGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTTCTACACTTGAC[C/A/G]GTAATATACTG TTTTCTGACATTCCTGTTATCACTCTCTGAAATC
WI-14958	83	A G	AATAATTTAT CTCTTCTTTT CAAGGG	AATGCATTCA TTGGTTTT	GTGATTGATCTGTAATATTGGGATTATTTTCAACTCTAAATTCOAAGATGAAATTAATTTATCT CTTCTTTTCAAGGG[C/A/G]AAAAACCCAAATGAATGCATTTTTCAGTTTCTCCAGGCCCTTTGAACTGC AGCAGAAAAATTCAGGA
WI-14976	35	C T	GTTGATTTGCT TCGTTCAAAG	TCAAACTAAAT CTTCCATTCTA AGC	TATTTTTTAATTGGTTGATTTGCTTCTGTTCAAAG[C/T]GCTTAGAATGGAAGATTAGTTTGAGGAG GGCAGGTTTGGGGTAGGCTCAGCGGGCATAGTGGCCACAAGAGATGCCCATCTCACACCTGGAG ACGTCCATGAGCACCTCG
WI-14981	31	G T	TCAGTGGTGT TATTGGATTT T	CACCTCTGACA TAATACTTAGC ATAAA	TAATTGATTCAGTGGTGTATTGGATTTT[G/T]TTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAAGAAAAAAGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80	C T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCTC	TGATTACATTTTTTAAATCATGCCTACCAGCCCATCTAAGCCAAATTCAAACACCACTCTGCATTA AATGAAGCTGCAG[C/T]AGGAAAGCTGAGCACATAGCACCCTGATCGGAAAGAAACGTA
WI-15002	72	T A	---	---	AAATCTCTTCTTTCACACACAGATGAACCTTTAATAAATTACAAATGCACCTGAAATGCTTCTTGA TTTCC[C/T]ATTCAGTTTAGGCTCAAAATGGGCTCTCCTCAAGGCTGGACCTCAAAAGGCCAGTT
WI-15000	90	G A	GACAGAAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTTTGAAGGTTATAGAAATTAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAGTA[G/A]TGAAGTTTGTGCAGAACTAGAAAAACAAAAATCCACCT



WI-12323	68	G A	CACAATACCTT CATGTACCTAT	CACTGGACATA TTCCCTACCTG	ATTTTGTGATGTTGGTTAAATCTTAICTCTTTTTTATACAAATACCTTCATGTACCTATGAAATAA G/AJACAGGTAGGGAATATGTCCAGTGCACAAACAGAGGACTCACACCTGTGTCATAGACAGCACC
WI-14683	91	A T	AAGGACGAT TAGTATCTAA	GGCATGTCCCA GTGTTTTT	CATAAGTTGCATTATTACACGTCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAACAA[A/T]CAAAAAAACACTGGGACATGCCCCCTGAATTGCCAAGT TGGAGTTGCTAAGAATCTAC
WI-13470	100	C A T	CCTGCCCTTAT ATTGGAATTTTC	GGGAGACCATG GGTCTCT	ATTTTGTGTTTATTAGCACCTGAAATTTAGGCAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAAATTTCCCTGCCCTTATATTGGAATTTCTA[C/A]JAGAGACCCCATGGTCTCCCAAGTGAGGAAGCC AGGGCACTCAGCCCTTC
WI-14712	38	T A CA	TGAATGCTTCC AAGTACAAAT	TGAAAGTATGT TGTATATGGTA	TTTGGTGCTACTTTGTGAATGCTTCCAAAGTACAAATCA[T/A]CTCACAATACCATATACAACATACT TTCAATCACAACCTCAAAATATAAAATAAACCTACAAAATCACATTGC
WI-13712	40	A C TCTATTG	TTACTTTGTT GTCAATTTTAT	CCATAAGGTCT CACACTTTTCT	TGGATACCCCTTTTACTTTGTGTCAATTTTATTCTATTG[A/C]JATTATAAGAAAAAGTGTGAGACCTT ATGGCTTCTGCTTATTGGCAATATGCAATATAATATTGTGTGTTTAAATTTATGCAT
WI-16163	35	C T A	TCTGGTGATGC AATTGAAATA	GCTGCCAATTA CAATTAACCTTAC	TCTAAGATTTTACTCTGGTGATGCAATGAAATAA[C/T]ATTGTAAAGTTAATGTAATTTGGCAGCATT GCCCAAAGTTTAAAGAGGACTATTCTTTTAAACAAAGACAGTGTGACATTTATTTCAGGT
WI-13453	88	T A TC	AATGCACAAA ATCTTGCTCT	TCAGATTTTTA CATCTCTTCT	TTTTTTTATTGCATTTGAGTGCCTTTATTATATTGGGAATTGCAGTGATATTAAACATTTGTACAAAT GCACAAAATCTTGCTCTCTCT[Q/T]JTGCTAGAAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACCTCATTGTCCAT
WI-16167	58	T C GATTTTT	CGCACTCTAA ATTAGAGATA	TGCTCGTGGTG AATAAGATG	CGGATATAATTATGTACCCGCACTCTAAATTAGAGATAGATTTTTTCTGATATACATTT[C]CATCTT ATTCACCAGAGCACACCCACACGACAGTAGAACAGTTCACACCTGATAAAATTGCACAAGATG
WI-14482	17	G A ---	---	---	GCAGAACCAATTAATAA[G/A]AATCTGCAAGTTTTCCCAAGAAACTCTGGAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGAGAAATAAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81	T C ---	---	---	TGTAGTTCTTCAAAGACATGTTGGCAGATAGCCAGGCCATCTATGTGTATTCCAGTATCATGTAC GCACTAAAAAAAT[C]GTGTGCTTGTCTGCTGTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97	A C CCGAGATCGC	TGAAGATTAA CCCGAGATCGC	AATTGTGTGCA TTTTGAAGAGA	ATCTGGTATTGTGTATCCCAACAAGTATACAGAACTCTCTATAAAACCAACCCCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTCCG[C/CT]CTCTTCAAAATGCACACAAATTAAGACG
WI-15012	59	G T ATGT	GCAGCAAGAT TACATCAGTA	CTCCAAATAGC CTAGAGTATAG	CATGGCAGCAAGATTACATCAGTAATGTAAATAATAATACAGCTTTTTTTCATTGAAGCTTTT[G/T]TACCTT TACTATACTCTAGGCTATTGGAGTGTCCCCAC



WI-15100	74	G A ---					TC TTATT CACAGCC AAGAAAATACCCAAATATTTCCAAATAAAGCAAAAAATTTGGAACAGACTGGA GTGAGAAC[G/A]GGTCCACCACCAAGCCCTCAAGACAAGATGGACACGGCAGCTGTTCTGGGGT GCATTTCTAGTGGACTTTAT
						GTCCACATGTT	TGGTACAGAATGTTTAATTACAGCAGGCGAGTGATCCAGTTAAATAAAATTAATAAACCTTTATTTT CCCAATATAAAATTAATAATTAATAA[A/T]GTCTTAAAGAAAATATAACATGGTGACAGCTTT
WI-14492	92	A T AATTACT				TAAGAC	TC TTAAATTTTATCGGAATCCAGGACACAAAGAAAACACCCAAAAACCATGGAGACAGAAG ACGAGACACAACCTCTCCCACT[C/G]CCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-12002c	89	T C ---				---	TC TTAAATTTTATCGGAATCCAGGACACAAAGAAAACACCCAAAAACCATGGAGACAGAAG AC[G/A]AGACACAACCTCTCCCACTGCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-12002b	68	G A ---				---	TC TTAAATTTTATCGGAATCCAGGACACAA[G/G]AAGAAAACACCCAAAAACCATGGAGACAG AAGACGAGACACAACCTCTCCCACTGCCTCCCTGCTCTAGAGTGGGACAAAAGTGGGGGTGAGAC AG
WI-12002a	30	C G GGACACAA				TGGTTTTGGG TGTTTTCTT	TTTTCATTTATTTTCCAGAAAAGAAATCACATTTTCAGTAACAACCTTACATATAGAAATTAACCTTTG TTCTGGAATGGGAGCCCTAGTTGCAGTA[C/T]GTGTCATAATAATAATTAATTCAGGATTTTG TGAAATAGGTGATTGGGA
WI-15116	96	C T GTTGCAATA				CCTGAATATGC AATTATTTAT ATGACA	GCAAAAGCAAAGTATGGAGGCCCTAAAGGAATGGGA[C/T]GTGTTGGTGGCTTGATACTTGGT GCTTGTTGATGGAGCAAGAGCTCTCCTGGTCCATGCAGGGGCGTCACATATTTTAAGTGCACATAAT TTGGCAAACCTGTCATTC
WI-12578	37	C T AATGGGA				TCAAGCGACCA CCAACAC	ATTTACGTTGGCCAAAGATCTCCCTTATGTTGGCATTGCA[G/G]AGACACTGCACCTATCTGAGGTTA GAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATTAACCATTTCCCTAA
WI-15153	40	A G GCATTGCA				T	CCTTTGCTCTGAACTGGGACCAGGATGTGAAATAATTTTGAATCTGATGCAGGTCGAGGTATGGC TTTGAATCAAAATGGG[C/T]GACCTTTTCCCTGTTGGTGGAAAACTCTGTGAGGGTTTGGCA
WI-15215	84	G C TCAATGGG				CCAACAGGGGA AAAAGTCA	AGGAAAGAGTGGTAAAGCAAGCGCATCTTGGATGGATGATTATGTTCCAGGACACTTGAGGAC CTAGAAAGCAAAC[C/T]GGAGTGATTATGCCAATCAAAATGCAAGGTTGGAGATATGCTAAAA
WI-15225	80	C T C				TTTGATTGGCA TAATCACTCC	AAATTTGCTAGTGCAAAATGGACCCAGAAATGGAGGGCTATGTAACACACA[G/A]ATATGCACACCCAC AGCCATGTCAGTGTACAGATCCTCTTGTGCAATTCAGCTTTCTTAAAAACACATCAAGGCTGCA
WI-15152	51	G A ---				---	TGACTGTATACCAAAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAATTTACAACTCACTGGGGAAGAAACAGACATGCAAAACACGAGATAAAACACAAT
WI-15123	55	C T TAGGATG				TTGCTTAAGGG CAACAGAC	



WI-15182	49 C A	GCACAACCCAG GGCAAAATA	GCATGGGTTAA TCCAGCA	GAGACTGCCCTGTGACACAACCTAGCTAGCTGCACAACAGGGCAAAATG/AJTGCTGGATTAAACCC ATGCTAATGGGTTACCTTTATTTAGTAATCATGGGTCCTCATAGCATGGTCCAGATCCG
WI-15198	38 T C	GGGCOCTGGC ACTATG	ACTTATCCGTC AGCAGAGTAG	GTGGACCTCTACAAGTACCATGGGCCCTTGGCAGTATG/CJCTACTCTGCCTGACGGATAAGTTGGC ATATGGTTCCAGATTGCTGTCTACACAGTCCAGTTCCCTAGAGACTAGTCCGACTCTCTT
WI-12601	42 T C	TGAT	GTGTAGTCTT ACATGCTTAGC TAGAC	TCAAGTGGTAATAGCAATTTATTGAGTATCTTGCTTTGATT/CJGTCTACGTAAAGCATGTAAGACT ACAACATTACGACCCCATCTCTTCAAGAGGGAAGTGTGTTATTATGGAAAAACATTTTGTCAATTCAGAT T
WI-14510	104 A T A A	TGGCAAAATA TGCATAACAA	TTGAAAATGGT TAAACTGGCA	ATGTTGAGAGTAATAATGCCCTACATATTTAGTGTAGTACACCCCCAGATATTTTTGGGGAGAAGAG TTGTTTGCCTTTTGTGGCAAAATATGCATAACAAAAT/AJTGCCAGTTTAAACCATTTTCAAGAGT
WI-15239	57 T C A	CATTTGCAAT AAACACCATC	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAAAGATTGTGCATTTTGAATAAACACCCATCAT/CICCTGAG TCCACAGATAAGGTCCCGGAGAGGGGCTTCCCTCTCTCGTGGTTGACGTTCCAGCGAGT
WI-12634	52 T C AGT	GCATCATATG AACTGTCTAGC	GGACAAATTGT AAACATAGCT AATAGC	ATGAGTTTATAAACTGGAGACAGCCGCATCATATGAACGTGTAGCAGTATT/CJGCTATTAGCTA TGTTTACAATTTGTCTGAAGGGTCTAGATGTGTACACCCCCAGAAAGTGGTATCTCTGA
WI-15249	34 T C A A	GGGCTTGACAC AAAGTTCTAA	GGAAAGCCAG AGATTTTAAAC AA	TTTGCTTGAAGGGCTTGACACAAAGTTCTAACTTT/CJTTGTTAAAAATCTCTGGCTTTCTCTGGCTGG TGAGGAGGCACAGGCTGGGTTCTTCAGGTATCCACTGTGTGCCCCGATCTGTTCCTCCACTCCCCAG CCACATTTCTGGCTCT
WI-12159	28 C T GCAAATGC	AAGACACCGT GCAAATGC	CCCTCTCCTCA GTGCACCTT	CTGTCCGGGGAAGACACCCGTGCAAAATGC/CJAAAGTGCACGTGAGGAGAGGGGAGGCTGTGACTC CCAAAACCTCGAATATTTTATGAATCTAAGAGTCCAGACGCAGTTTCATCCACGGAGATCTGC
WI-12648	41 A G TAAGGATGC	CCTAGTGGCAT TAAGGATGC	TTGCTACTAAA AGTGGACATCC T	TCCCCAGATTGTATGGAATGCCCTAGTGGCATTAAAGGATGC/A/GJTAGGATGTCCACTTTTAGTAGC AACCGATGTTAATCACTACTCCATGTTAGTGGCTTTACTTGGATTATCTCACITTAACCAACCA
WI-12684	64 G T ACAGCTGTGC	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTCAGTAACCCATGCTGTAACAGCTGTGC/G/ TJCCATTTAGGCTTTGTTGTTCCATTTAGAGAGCACAGGAGGAAATTTAGCATAATCTT
WI-15260	75 G A GA	AAAGGATGAA GCTAATCATG	TCCTCCAGGG AGCTTGC	TTTATAAGCTGAATGAAAGAGGTCGACACAGCGGACACTGTCAATAGTGAACAAAGGATGAAGCT AATCATGGA/G/AJGCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGAAATTA TCCCTG
WI-15325	39 T C GAGGC	CATGTGGCTGG GAGGC	CCTTCCACCAT GATTGTGA	AAGGTTTAATGGACTCACAGTTCCATGTGGCTGGGAGGCT/CJTCACAATCATGGTGAAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGATGAGAGC
WI-13936	123 C T C	AGTTGGCATTC AATAGCCTAT	TGAAACTCCCA CATGGAGTT	TATTTGAGTATTTTCATCCATGGGCTTCTCACTCCCTATACATTTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTTCAGAACCTATGACCTGTATCTTTCAGTTGGCATTCAATAGCCTATC/CJTAACCTCCATGT GGGAGTTTCAATAATA



WI-14528	62	T G	TTTAACTTTT TCTGGATGGTA TAAAT	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTAAATATATTTTAACTTTTCTGGATGGTATAAATTT/GJTT GAATTATAAATTTTAAATTTTATAAAGTGCTAATCGAGACATCACTGGGTATAATTGA
WI-15347	74	C T	GACTTCAAAG GAAAAGAACA AATTT	TCACTCCCCCA AGTCTTGG	TATTTCTTTCGGTTTCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAAGGAAAAAGA ACAAATTTCTCAAAGACTTGGGGAGTGAAGGCAGAGCCTGGTGACATGGACGAGGTCTGCAGA CG
WI-14546	95	C A	CCAATTTCTAG TGATAGTAGA GGACTCA	AAGTGCACGT GCAGG	GTATTTCTGATGCTTTGACATCTGGGGCATTGCTGTCTAGAGAGACTACTTCTCTGGGACCAGC CAATTTCTAGTAGTAGAGGACTCA/C/AJCTGCACGTGCACCTTTTATATACAGATCA
WI-15353	37	G A	---	---	TTTATGGCTGTCTCTGTAATACAATGTGGTGAACAC[G/A]TCTTAATTCAGGACATCTTCCACCTTG TTTGGCTTCCAGTTGTACTGCAAGACAGTGTGAGGCACATAGGCTGATTAAATCAGTGG
WI-14580	100	G A	CATCCCATCT GTCITGCA	CCGACCAAGAT CCTCC	AGAAATTTTCTTTTTAACAGGACAAGTAACAGATTACATCAAACTTCAGAACTTCTCAAATAC CTAGTTATTATACACATCCCCTCTGTCTGCA[G/A]GGAGGGATCTTGGTCGGCTTAACA
WI-8540	73	T C	GGCTGCATTT GGCTTA	GGCTTCTTTT TCAGGCAC	CCAGCTGGAGGTGGAATAAATGGGGCAACCACAGAAAAAACACACAGCTACACACAGGCCTGCATT TGGCTTAT/CJGTGCTGAAAGAAAGGGCCGACCCTTTGATAAAGAAIGTCT
WI-8039b	97	T C	---	---	AAGTAGAACACAATAGAAATGGCTCAAAATATCAGAATGCATACGCACATCACGAGTAAATACTG TTTGGTAAACCTGTTTTCAGTTAAATATGTAT/CJGTGCTGGTGCATGTATGATTAAATATCCTTCT TACCACAGTCAACCCTAAAGAACCAAGCTTAGGACTAGGGACACAAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGTTGAGATGATGATTTTAAATGCCGACGCCGACACCCACA
WI-8039a	87	T C	---	---	AAGTAGAACACAATAGAAATGGCTCAAAATATCAGAATGCATACGCACATCACGAGTAAATACTG TTTGGTAAACCTGTTTTCAGTTAAATATGTATGTGCTGGTGCATGTATGATTAAATATCCTTCT TACCACAGTCAACCCTAAAGAACCAAGCTTAGGACTAGGGACACAAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGTTGAGATGATGATTTTAAATGCCGACGCCGACACCCACA
WI-8044	107	C A	---	---	CACAACATTCAGAAGTTTCTGCAATGTGCTTCTCTGTATGTCTAAAAGATTTGAGCTTTGACTAT ACGATTTCCACACTGAACGCATTCAAGGTTTCTCC[C/A]AGTATGGATTCTCTGATGATTAAATA AGCCCCGAATCTGGCTAAAGGCTTCCACATTCAGACATTTGTAAGGTTTTTCTCCAGTGTGGAC TCTCTGGTGTGCACAAGAAATGGAACCTCGGCTGAATGCTTTCCACACT
WI-8550	32	G A	GGGAACATCA ATGCAACAAG	TTTGGGCTTG AGTTTACAAAT T	CTTACTACATGGGAACATCAATGCAACAAGT[G/A]JAATTTGTAAACTCAAGCCACAACTTAGTTA ATAATCATGGTTAAGGGACATTGCCAAAGAGCAACTGATGCCCTCAGTGAA
WI-8057	87	T A	---	---	TATTAGATAAAACCCCTTTGTTCCGATTTCAGGATGTTTAAATTTGCTCTCTTTAACTCTGTGACTTTT CCTGGTTCAAAGGACAGT[A]GATGGACAGCAGCAGAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGTAAGGCACCTCTGTGGCTCACAACCTGCCCTCTCAGAGGGTGTGCTTCCAGCCCTTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGTGTTGAAGCAGCCAGATGGTAAGG



[illegible]



WI-6375	28 A G A A	GGTTATTGCA TATGGAAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTTATTGCATATGGAATCAATAG[A/G]TATCTTTTACAAAAAAGGTTAGAATAAAGATCTC ACATTTGTAAGGCACATATGAACATTTTATAGCAAGCACAAGGGCAGTGAGACATCAACAA TTGTGCTCAACAGATGAATTCATAACCTTTGTTTCTGATAAGACAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTTA[A/T]A/GCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T A ---		---	TTGTGCTCAACAGATGAATTCATAACCTTTGTTTCTGATAAGACAATTCAAACATACAAATCAAT TACAAC[A/T]ATGTGCTTATCAGCTCCCTCCACCCCTATATTTATGCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A T ---		---	CTAATATAATCTGGGCACATGGATCCAAGAGAGATTTGCAGCAGATTTTCATTATAGTTACTTAA CAGCTAAATAATAAGGGTGTAATTAACCTTACTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[G/T]ATCAACCTCCCTAAGCATCTGTCTGTCTCG CAGC
WI-6523	165 G T GCTG	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGAAACAGGAAGATGGGC TCTGGAGTCCAAACAGGATGTGGAGTCCCTGGTAGTTCTCTCTTTTACACAACTTTCCCTGAGA ACTGTCCAGTCAGGTGGACCTTCACAACAACACGAAACAGTAAACTCTGAGAGAAAAC[C/G]CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195 C G ---		---	ATTGTAATTAATAATTACATGGGCCTATTTATTAAAGGACATTTGTGTAATGTTCCACTTTGTTTAAA [C/T]AATTACAACATGTGGCTTAAATAATGTACAGATCAATGTACAAGTTTGAAAAATGGCG
WI-6558b	68 C T ---		---	ATTGTAATTAATAATTACATGGGCCTATTTATTAAAGGACATTTGTAATGTTCCACTTTGTTT AAACAAATTACAACATGTGGCTTAAATAATGTACAGATCAATGTACAAGTTTGAAAAATGGCG
WI-6558a	42 G C ---		---	AACCAACAAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAA AGTTGTGCTA[T/C]AGCAATGGATGCTGTGTCAGAACATACTGCCAATAAATTTAAGAAAAAGGA ACTCAATGAAGTTACTGTTATATAAAACAGGAGCTCACAGCAGGATGTAAAGATTAATGGAAGAT ATCGTGAGGCCAAAAAC
WI-6629	75 T C GTCATA	TCTTTTCAGAG AATAAAAGTT	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTAAATCAATCAATCAAACTCCAGCTGTTCTCTGCTTT TTACTTAGCAAGGAAAACTTTAGTGAATGCTACTTGACAAGAGAAAAAGTCATTTCTCAAGCACA T/C]ACCCAACTTGAAGGTGATTGAACCCAAAATAATGGGTGGGAAACACCAATGAGGTGGAGGA ATGAGAAAGATGTGTGGCCAAAGCTATCTGTTATATTTGATGTTGCCAAT
WI-6644	134 T C ---		---	TGCTAAACACCACCATTTAATAGGAGAGTACTAGGAAAAAATCAACAAACACAGCATGTGAAACAGT TGGGCACGGTGGTAAAGGGCACAGACTCTGGGCCACAGC[C/T]GGCTAATACACTGCAATATTTTA TGTTAGCAAAATTAGCTGGTCTGTGTAATAACCAAGAGCGGTATCTGG
WI-6690b	106 C T AGCCACAGC	CAGACTCTGG	TGCAAGTGTAT TAGCC	



WI-6690a	28	T C	AAACACACC ATTATTAAGG AGAG	GCTGTGTTGG TAGTTTTCT	TGCTAAACACCACCATTTATTAAAGGAGAGTC/JACTAGGAAAACTACCAACACAGCATGTGAAAC AGTTGGGCACGGTAAAGGGACAGACTCTGGAGCCACAGCGGCTAATACACTGCAATATTTTA TGTTAGCAATTATAGCTGGTCGTGTATACCAAGAGAGCGGTATCTGG
WI-6770	53	A G	CAACCCCAA AACATCACA	GCTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTAAATGACACAGATCTTCCCAAAGTAATCCAAACCCCAACATCACA/JGJAATTATTCTAT ACTATTATACACTCCAAAAGCAAAATACTTCAACTGCAATCC
WI-6686	151	A G A	GCAATCTTCCA AAAACAAAGA	CCTTGTAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAGGTTTCAGCAAAATCAGCTAGCACTAATCTTGACCAAAATGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTTTAATTAGATGAAATTCACATTTAAACACATGGTAACCTCCAAGCATTTCT TCCAAAACAAAGAAT/JGJAACATTGGAATAGTCACTACTACAAAGGAC
WI-6761	32	C A G	GATCTAACAG CTGCAGAATG	AAAAGCTGGG AAGGAAGAAG	CCTGAGAGGAGATCTAACAGCTGCAGAAATGGC/JA/CTTCTTCCCTCCAGCTTTTGTGAACAAAAC AATTCTCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGTTGTTCAAGTACAAGGTCTC
WI-6844	225	T C	---	---	TAAATACTGCCAACTAGCATTACGTCCACTCTTGCAATCAATTAACAAAGGGTATTTCCCTCCTTG GTATTTCAAATGATGCATTATACAATAAACGAAAGTTAGAACTTAAATGCACCCTGATTAAATTATG TAAACTGGTAATTTGTTTTAAAGAGCATAATAATTGGTTCCTTCTTCATAAAATGGAATTTTAA TATTCTCTGATAGTCTTGAGGTT/JCJATCATTATGAGTAGTGCAAAAGTGTG
WI-6824	112	A G	---	---	CGGTTTGTACACTTTAATGGGTTTTTTTTAAGGGATTTTTTCAGGCTTGTGCAACATCAAA ACAAAAGGTACTGAGTACTCCACAGGGTACAGAGTGTGCCAA/JG/CACCTTAGAAAAATTACAT GACCGGAGAAAATGCGCTCTTGCTCTTGAAGAGCTTACAGTCTAGGATTTGACAACCTCACAGT CTTAGGAACTGGGCAAGTAAGGCAAAATCTTCATCCCTAGAGCTATTGTG
WI-6889	139	T C AATTC	GAAAAATGAG ATGCAGTTAA	TCACTTTGTGG CTTTTAATTAT TCT	GTACAAAAAGCTGAGAAAGAGCCAACTGGAAGTGTCAAGAAACATTTCTGATAGGTACGGACAA AAGAGCTCCTTCAATCAAGAGGATTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTCT/JC/JAGATAATTAAGCCACAAAGTGAAACTGTTGTTCTGGGGCCCTATGTTGTAGATT CTCT
WI-6911	216	T C	---	---	TCCCAGCTCATATTTATTGGGCACAGAGTGGGCACCTCAAATATCTGATGAACITTGATGAACGTAA AAGAGGTCTCCTTAAACAAGATATCATCTCCGGAAGAGAGAAAGTCCCAACCATATAAAATGTATGAT CAAGTCCCAGAAAACCTTGCCCTCCCAAGGAATGTGTTCTTAATTTGGTTTCAAGCACACTGGTTCC CACTTTTACCACCTT/JC/JCATGACATTGGACAATAGTACTACTCTTTTCTAC
WI-9413	112	G C	---	---	GCCAGTCTCTAGTAAGTCTCTAGGGACATGACCAGACCAGAGCCCTGTTCTATATGAAGACAAAAC AGGTGGCCATACCTTGGGTGGAGGATACCGCTGCTATTTCCAGATG/JC/JAAGATTTGGTGAAGGAG ACCATGACAGATGACAAAACGGAACAGTTTCTCAAAAACAGAGGTATGA
WI-9557	74	C T	---	---	AAAAGCTTTAAAAAAAAGTGGTGTCTATCTTTAGAAACACTTTTACGAAGATCAAGTAGCCCCAGCT ACAGCCTC/JTGGTGCACTTAACCCCTCTCTCTTTT



WI-9617	37 G T ---				TGCTCTTTTATTTACAGTTTCACACACACGCCGTG/G/TTGGCAGACTACCAAGTGCCTCCGAG CGCCACGCTTGGCCGGAAGTCTCATTTCTGTTCTGCTCTATGGACTGATTGAATTTGGATGGCCAG CTCCAGAAATGTTCCACGTGGGGCACTCTGTGGCAGAGAGGCTGAGCCCTTGCCACACTGGCACCA AAGAGGTTGCACGATGCAGCTTGCACTGGGTCCAAAGCCGGGTGCTGTG
WI-9657	121 T G ---				AATGCTGGAGAAAACATCAACATTGAGTTGACATTTGTTTGTGAAGTATAGCTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAAGCCAGATTCTCAAAATAAAGT/GJATAATTCIT TGATTAATAAATGTTTATAAATGTTTATGAAGCTCATTACATTATCTTTTAAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTTCATAATTAAATGCTTTTGATATAGATTGAGG
WI-13119b	114 G C GCTGGGA	CCTCCCAAGTA	AAAAATTAAC	CAGGTGTGGTG T	CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTG/CJACACCCACACCTGGTTAA TTTTTTAATTTTTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAAACAAACCAACTAAC
WI-13119a	51 C G ---				CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT/C/GJACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCCACACCTGGTTA ATTTTTTAATTTTTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAAACAAACCAACTAA C
WI-13112	71 C T AGCTTTT	TCATAAAGAC TACAGACTTA	TTAGAAATTTT GTGTATTATAT GGAAAAAG	--- TTAGAAATTTT GTGTATTATAT GGAAAAAG	ACAGGAATCTGAAAGTTACCAAGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTTTC/TCTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAGAAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACIATGGCAAAAATATTTTATTAATTGAGGGAATAGGCCAAT TT
WI-12988	36 C A CTCAGTACAA	TGGTACGTGCT CTACTGATGCT	CAAGTGTACA CTACTGATGCT	CAAGTGTACA CTACTGATGCT	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA/CJAAACAGCATCAGTAGTGACACTTTGAT AAAAAGGAATTTTAGCTTAGTAGAAAAAGAAAGCCCAAGGTCAGAAGTATAATGAATATGTACAT CTTTATGGAAACTGTTTGTGTGACCACATCTTTATCTTCCCTGTGGATGAGATGTGCACACACAAGT AAA
WI-13020a	108 G A CTTT	CTAATAGTGG AACCCTGAGA	CATTATTAAAC CCCTTTCAGA	CATTATTAAAC CCCTTTCAGA	TGCTATTTCATGACAGACACGTGAGACAATAATCTTATTTTACAGATGGAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGGAAACCCTGAGACTTTTGA/JATCTGCAAGGGGTTTAAATAAT GCAAATATCACATATAATTTCCATTTTAAACACCATAATTAAGTTTCCATTTTCTTAAAGAAAATGA TAAAAATGTTTCCCCAATAT
WI-12837	87 A G AAGTCCA	CCATATACAT ATATCAAGGT	GCCATAGGAA ATGCTGTTTTT	GCCATAGGAA ATGCTGTTTTT	TGTATAAAAAATCCAACTTGTTCACAAGTACATATGTCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAGTCCA/JAGJTACAAAAAACACAGCATTTCTCTATGGCCAGTGTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAAAATGAGATTGCACACTAAGGCAGGATGAGGCAGAAAGCA AGTTGTGTTCCA



L42611b	50 GC ---			GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTCTCTCAGGTTGCCTGTCGCTCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCAGTCTCTCTGCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTACATCATATGTTATTCACCA CTGGAGCTTCACCTTTGTTAC
L42611	34 TC ---			GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTCTCTCAGGTTGCCTGTCGCTCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCTCAGTCTCTCTGCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTACATCATATGTTATTCACCA CTGGAGCTTCACCTTTGTTAC
WI-1172b	179 C T A	TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG	TGAACGTGTGGTTAAACCTAGGCAATTGGTTAAATCAATTTAAAAACAGGCCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCAGTATGTTCTTGAATACCATTTTCTGCTTTC AAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAG[C/T]CTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17 C A ---			TGAACGTGTGGTTAAAC[C/A]TAGGCAATTGGTTAAATCAATTTAAAAACAGGCCCTAGAAACA GTGACCACACCTCAAGCAATGATTATCCCTAGCAGTATGTTCTTGAATACCATTTTCTGCT TTCAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCCTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35 G C A	GCAGATTGGA AGTGTGAAAA	CACTTACATTT CTGAATATTTA GACTCTTT	AGAGGCAGATTGGAAGTGTGAAAAAATGAAAGAA[G/C]AAGAAAAAAGAGTCTAAATATTCAG AAATGTAGTGTGCTGCCCTCAACTGTTCTTTACCCACITTAATCTGCAATTTTGAAGAACTAGATTGAAT TCCTTTGCAAAACCCCTTGCAATCATGGATACCCGAGTTAAACCGTTAATTAAGAGACATTAACATGG CCTGGTG
WI-1231b	141 G A ---			TCCATGGTTTGGTTGCTACTGACTTTTGTAGCTTACTGCCCACTATGCATTGGAACTCCCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTCTTTATTTCTCTCTTTCAATTTCTT TCAC[G/A]TTATTCCTCACCCTGAACGCCCTTCTTCCCTCGTAGTGACATTTTAAATCCACTTTAC ACATTCGGACC
WI-1231a	126 T C A	GGCTCTTTATT CTCCTTCCTTC	CGTTCAGGGTG AGGGAATAA	TCCATGGTTTGGTTGCTACTGACTTTTGTAGCTTACTGCCCACTATGCATTGGAACTCCCATATTC CAACTAAGCAGGAGTGTTCACAATAAACAACATAGGCTCTTTATTTCTCTCTTTCAIT[C]TAATTTT CTTTCAGTTATTCCTCACCCTGAACGCCCTTCTTCCCTCGTAGTGACATTTTAAATCCACTTTACA CATTCGGACC
WI-472	114 G C ACAGAAAAAG	ACATACATAT CCATTATACA	GACCTTTCCTT TCCAGCCC	GAAGGCAGGACTGTGTTTGGAGGACAAAAAGTAAATCTTTTATATCTTTTATTTTAAATTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACAACAGAAAAAG[G/C]GGGCTGAAAAAGAAAG GTCAAGTGAGATTCAGATATCTTAAATGCAAGGCTGACAAATTTGGCTTGATT



WI-478	46 C T	GCATGTCTGTG TTACTCTATTT TGITC	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGTCTGTGTACTCTATTTTGTTCCTAGCCACCTGTGGCATTTG CAAAATATGATAATCTCTGCCACCATACTGCTTTAAACACAAATAGAAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTTAATAATCAAAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAACCAAC ACTGCCCA
WI-533	29 T C	ATCAGAGCAG AGTACCTTTCT AACT	CCTTCCAACCT CTACACAATCT T	AGCCATCACAGCAGAGTACCTTTTCTAACTTTCJATAAGATTGTGTAGAGTTGGAAAGGAGGACAGGA CTGTCTGTGGTATAATGACCCTGTGTCCAGTTAATCCA
WI-601b	112 T A	---	---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGCGAACAGAGAGGTTTCTATTGACTCCTAACTGAGTACTTAACTGAGTACTCAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74 C T	---	---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGCTTGAACAGAGAGGTTTCTATTGACTCCTAACTGAGTACTCAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107 A G	CTCCTTCACAA CCTCACCA	CTTCCCGGTAA GCCAAGT	AACAAAACAGACACACCTCGGCTTCTCTCACCAGTCCACATGGTGCCAAACAATCCACATTCT ACATCTCCCACTGGCTGCTCTTCAACACCTACCAAGTCTTACCTGGCTTACCGGGAAGCATATAA GCCAAAGCATTTAGTCTTTTATTGCAACATGGTCTGGCTGCAATAC
WI-919	36 G A C	ACTGCTTGTCT GTTGATTTAAT C	TTATCTAATC CCACATGACAG C	ACTCACTGCTTGTGTTGATTAAATCAACCTAGCGTGAAGTGTGCTGATTTGAATAAAATA AACACAAAATGAAACACACACGATTGCTAACAAAGCAGATCTTTTCAAGGCACACGTAAGAT AATAACTTCAA
WI-991	37 A T	---	---	TGCATTCATTATGCACCAATAATAACTTCTGTACATATJCATTTATTTTATTATTCACAAAAT TATGAGTGAGGGATGATTGTTATCCCTATTTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCAAAGTCACAAAGTTAGTGACAGAGCCGGGATTCGAATCCATCAACTTGAATCCAGAGAAAAT GTTCTGCATCACTGTACAACTGACTCTCTTTTCTCCTTTGAAACAAGGC
WI-1011	70 G C	CAGTATCTGA AGTTTTGTCT CCA	AGGAACACCTA CAAAATGACTT CT	CTTCTGACCTGTTTGCAGTGGATCTGTTTGAAGGCTCTGCTCAGTATCTGAAGTTTGTCTCC A/GCJAGAAAGTCATTTGTAGGTGTTCTGGCGTTTGTCTACGTTTCCATTTCTCTAATACACTGC CGTCTTAAGGGAGGCTTGCAGAGCATTTATCAGATGGCTGTTTGTCTGCTGACTGAAG
WI-5381	178 A T	---	---	TTATGAGAAAGGTCATGAGTTTACAGATCTCAAGGAAGAAAGGCCCTAGAGATGACACCAGAA ATGAGAGTGGCTTGTCTCATGAAATGGACAGCATGTTTCAAGCAGAGGGAACAGCATGGAGAGA AAAATCATACTCTATCCACGTGCAGAACTGGCAATTTAGTTTGTATJTTTACTAAACACAAATGT TTAACTTGGGGTCCACAAACAGGATATGTTGGCAATGGTATTCTGTGATG
WI-5791b	76 G A	---	---	CTATGTATTCATCTAGCAAAAGGAGACTATTTGGATAAGTTTCAAAAGATGAGAACAGGTCTTA GAACCTCAGTGAJATCGAAAGGAGTTTCTATCTAGTCCATAGACCTATCTCACTACCCCAAGGTA AAAAATAAATAAAAGTAAAGAACTTACATCAGATTGTGCTTCTTATTTGCCACCCCTGTTGT TAGGAA



WI-5791a	44	C G ---				CTATGATTCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTTC/G/ACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCAAAAGGTA AAAAATAAAATAAAGTAAAGAACTTACATCAGATTGTGCAATTTCTTATTTTGGCCACCCTGTTGT TAGGAA
WI-5406c	120	C T ---				CACTCTGCTGTTGTCCATGGTGGCCACAGACTCTTCCAGAAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/C/TTATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGGAAGAGGAGGAAAGGAAAGGAAAGGAGAGGCAAA GG
WI-5406b	118	C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT		CACTCTGCTGTTGTCCATGGTGGCCACAGACTCTTCCAGAAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/C/TTATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGGAAGAGGAGGAAAGGAAAGGAAAGGAGAGGCAAA GG
WI-5406a	42	A G ---				CACTCTGCTGTTGTCCATGGTGGCCACAGACTCTTCCAGAAAG/G/GGCCACTTCCACAGATGCAACAG GOCCTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCTTATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGGAAGAGGAGGAAAGGAAAGGAAAGGAGAGGCAAA GG
WI-5798	48	G C TG	TTATTCTCCC TTGTTTCTTT	ACTGTTAGAAA ACCAGTATTTT TCAAT		CCATTCTCTTCTCCCTCCCTCTCCCTTTATCTCCCTGTTTCTTTG/G/C/ATTGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACTATGTTATAACATGCATAGTTCTATATGGGTATCA
WI-5415	54	T A TTT	TCCTCATGAAT TCATCTTTTCAG	GGACTAATTC TGATCCGATCT		CCTGCTAATAATAATTAAGCACGATTTGCTCTCATGAATTCATCTTTCAGTTT/T/A/JTAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTATCGAAATTGGA
WI-5437	41	C T G	TCCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAATATG GTTTAAG		TGTTTTAACCCAGGCAGACCTCCAGAGAAAAATCCAAAGAG/C/T/CTTAAACCATATTTTGTTTAA GAACTCCTGTGCCAACCACTCTTGATGTGAGTGAC
WI-5481b	131	A G CTGCAGTCG	TGTCATTATG CTGCAGTCG	TTACTTCCAGG CTCCAAGTATT		AAGCCAAATTCACATTAGTTGATGAATTTGAATTTTACAGTATCTAATGCATGGGCATCTGTTTCAAC TCTCTGTTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTGTCAATTTATGCTGCAGTCG/A/G/A ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTTCACAATTA
WI-5481a	29	G A AATTT	CCAAATTCAC ATTAGTTGATG	CCCATGCAATTA GATACTGTAAA ATT		AAGCCAAATTCACATTAGTTGATGAATTTG/A/AAATTTACAGTATCTAATGCATGGGCATCTGTTTTC AACTCTCTGTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTGTCAATTTATGCTGCAGTCGAA ATACTGGAGCCTGGAAGTAAAGACTTGGCTATTTTTCACAATTA
WI-5492	38	T C ---				TCATGAGTCTTTCTTCAAGAGATGCTGTTAAAGTCCCA/T/C/CAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCAA



WI-5826	134	T C ---		---	TATTTTTTTTTTCTCAATCCTGGAGCACACCACCTGCTCTTCTATTTCATGCTTCACATTTATTTTTT TTTCACCTTAGTTAAATGCTTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATTCTTTAGT[C] TTTCAAAATTAATGCCACCATAGAAATAATTTCTAACCAACCAGCCAAACAGCCTCACTCTTCCTT CCTGGTGCACTTACTCTTTACAC
WI-5546	40	C T A	CCCAATACTTT TTCAGGTGAA	CCTGTATTTTA GCAACATGGG	CCTATAACCCAACTATTTTCAGGTGAAAAAGGGAAAA[C]TACCCATGTTTGTCTAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGTGTAAATCTGATGTGGGAATAT TAGAAATTAAGCGAGAGAGGCA
WI-5552	97	C T	GGCACAGCCT TTTTAGAGT	TGCACAAATTG OCCAGG	TGTTTGTCTGCACCTCCCAACAAGTGGTCAATGAGCCTCAAGGGTTTGATTGAGCGGGTATGGGT GGGGCTATCGGCACCAGCCTTTTAGAGT[C]TCTGGGCAATTTGTGCACTAGTGTGAGA
WI-5836b	161	C T ---		---	TAAGTTGATTTAAACACTCTGTGCCCTCAATTTTCTCACCTATAAATAAGATAATAGTATCTAAAA AAAAGAGAGAGAAATTAAGTGGATAGACATGAATACTCTGATGATACGTGTTGTATCCCTGAA TCCTGCAATATACACATGATTCAATGAT[C]TJCCATTTTGAATAATTAGCTTTTGAATGTTTTTCCA ATG
WI-5573	58	C T	GTTCATAAGG AGGTGGGA	TGAACAGTTGG AGAGTAATGTG TC	TCGGGTATTAGGATGCGTTCAACCCTCGATGATGGCGTTTATAAGGAGGTGGGGA[C]TGACAC ATTACTCTCCAACGTGTTTCATCAGAACACTTCAACAGCG
WI-5850b	134	G A ---		---	CAGGACCTTGGAGCCTTGGCTTTGCTCTTCCCTCCACCCCTCACTCTTCTCTGCCCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCCCTCTATGCACGCGTCTATCTCTATATGGGCAATATCCAATGTCCCATTC[G/A] TTTTGGCAATTTCCCTGTATATCAACAGAGAGAGAGGGTGG
WI-5850a	92	C T ---		---	CAGGACCTTGGAGCCTTGGCTTTGCTCTTCCACCCCTCACTCTTCTCTGCCCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCCCTCTATGCA[C]TJGGCTCTATCTTCTATATGGGCAATATCCAATGTCCCATTCG TTTTGGCAATTTCCCTGTATATCAACAGAGAGAGAGGGTGG
WI-5612b	125	A T TTC	CTATTAAATGA GCATCGTGTCA	TTCTCTTGAGA AACCTAAAAC ACTG	TGCCCTGATTGACACATAGTTATCTGACAGTAATCATCTAACATCAACATCACAATATCTTTCTGCCTG TCACACTAATTTGCAAGCATTCAAATTGATTGACTATTAAATGAGCATCGTGTCAATTC[A]TJGAGTGT TTAGGTTTCTCAAGAGAAATTATGCTGTCTTCTCTGTAACCTCAAGTA
WI-5612a	44	T A ---		---	TGCCCTGATTGACACATAGTTATCTGACAGTAATCATCTAACATTCACAAATATCTTATTCTGC CTGTACACTAATTTGCAAGCATTCAAATTGATTGACTATTAAATGAGCATCGTGTCAATTCACAGTGT TTAGGTTTCTCAAGAGAAATTATGCTGTCTTCTCTGTAACCTCAAGTA
WI-5636	26	A C CCGCAATAA	GCCAAATTTAT CGCAATAA	CATCGAGGACT TTGGGA	TGAGAGCCAAATTTATCCGCAATAA[A]CJTTCCTCCAAAGTCTCGATGGAGGCATTTTCAGAATCGGG GCAGGGGAGGCAAGGTGAGACAGATGTGAAGAAC



WI-5865c	103 C G ---			TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTTAAGAACTCTTTTTTTCATTTATGCATTC ACTGACTCACTCACTTGCTCTATCAAAAATTAA[C/G]AAATAATTAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCTTCA GAGAAGACAGACAACTAAATAAATCCAGG
WI-5865b	99 T A ---			TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTTAAGAACTCTTTTTTTCATTTATGCATTC ACTGACTCACTCACTTGCTCTATCAAAAATT[A/AA]CAAAATAATTAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCTTCA GAGAAGACAGACAACTAAATAAATCCAGG
WI-5865	165 T A ---			TTAGAAACCTCCATTTATTCTGCCATGGTACATCTTTTTAAGAACTCTTTTTTTCATTTATGCATTC ACTGACTCACTCACTTGCTCTATCAAAAATTAAACAAATATTAATATTTTATTTACAGAGGAACTC AGAAGCCAGAAAAAATGACCAAGACACAGT[A/CC]AGTCTCCATCTTCAAAAGGTCACAGTCTTTC AGAGAAGACAGACAACTAAATAAATCCAGG
WI-5874	76 T G ACAGAAAA	CATAGCATGG ATAATATTAT	CCTAGTAAGTT TCAGTCATTTG ATATGT	CTCAGACATTCATTTTCATTTAGTTGTTAAATTTTGTGATTTTCATAGCATGGATAATATACAGAA AAAAAATTT[G/T]ACATATCAAAATGACTGAACTTACTAGGTAGCAATTTGTTTGTCAATTTGCT CATGGAGCCGACGTTTCAGCTCTCAGTTTTCCTATC[A/T]TTTTTTCATAATTTACTCTCTTTTCTGTC ACAATGTTCTGCTCTGCTATTTTCAACTCTCATTTGCTGATGGATGGTAGTCATAAAATATGGGTGATTC AGAAAAATAAGTAAATG
WI-5752	36 A T TTTTCCATC			TTAGCAGAAACAACAACAAAAATGTCACAACACTGCAGTAAAGAAGTGTTCCTCCGATAAAAT[C/G]C CATTAGGTATTAGATAAGCATCCCATAAAACATTTGTTGAAAACGAAGCCGAGTTTTCGATTACACACA GTTGCTGTTTAACTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCCACGAAA CATTGTTGAAAACGAAGCCACGTTTTCGATTACACACAGTTAGTGTCTGTT
WI-5760b	61 C G ---			TTAGCAGAAACAACAACAAAAATGTCACAACACTGCAGTAAAGAAGTGTTCCTCCGATAAATACCCAT TAGGTATTAGATAAGCATCCCATAAAACATTTGTTGAAAACGAAGCCGAGTTTTCGATTACACACAGTT GTCTGTTTAACTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGC[G/A]TCCCACGAA ACATTGTTGAAAACGAAGCCACGTTTTCGATTACACACAGTTAGTGTCTGTT
WI-5760	187 G A ---			AAATATCTGGCCTTTTCTCTTAGGAGGAGATTCTCACCATGGGAATCTTG[A/G]TGCAAGTTAGAT CCCACCTCACTATTGAGAAGCTAAAAGGTAAAGACTACTCATTTCTCAGTCTTCTTCTGCTG
WI-5944	52 A G GGAATCTTG	TTCTCACCATG GGAATCTTG	GGGTGGGATCT AACTTGCA	GAGTTAATGAATCCTGTTCCCTCTCTAAAACCTCTGTTCCCCCACTTCACATTTCAGCAGATATT CTTTCATGGGTTATTTTGCCCAAGTCATGAGGAGATGCATTAATTTGATCATTTTCAAGAGTGTGAG TAATGCTTGGT[A/C]TGTGCTGTGCCGTATCTGCTCCAATCACCCATTCACACTTTATTTCCCTATTAT GCTGAATGAACGGTTATATACAG
WI-5967b	148 C T ---			



WI-5967	165 C T ---					GAGTTTAAATGAATCCTGTTCCCTCCTCTAAACCTCCTGTTCCCTCAACTTCACATTCAGCAGATATT CTTTCAATGGGTTATTTTGGCCAAAGTCATGAGGAGATGCGATGTAATTTGTGATCATTTTCAAGAGTGTGAG TAATGCTTGGTACTTGTCTGTGCGCGTATC/TGTGCTCCAATCACCGATCCACATTTATTTCTCTATTAT GCTGAATGAAACGGTTATATTACAG
WI-6093	53 G C ---					GGGTAAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGCTTTGGGCCA/GCjGTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTTCCAACTGTGCACTGAGCCCATTTGTAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACTTTCAGCAAACTTGATTGACGGTGAC ACACCATGCTTCGAGAAGGAATGAGG
WI-6141	80 T C AGTACTT	CTTCTTAATTA AGCATCTACA			TGAAAACCCCA GAACAGTG	GACTGTCTCAAGAAAAAAAATTGAAAATTGAATAATTAAAGCACCTTCTTAATTAAGCAT CTACAAGGTACTTAT/CjCACTGTTCTGGGGTTTCAATCCTCTTCACCTTTTAGACTTCAGGAAAT CAGAAAAATGCATGAAAACAGGATTGTTACATGCAGAGAAAATAGGGGAGATAAAAATTTGTCTTTT CTC
WI-6450	45 T G TGTACA	CCAAAGACTT ATTCTATATCT			TTGTTTGAAT GTGTGGTACTT CT	ATAGGACAGTTTTTCTTCCAATGACTTATCTATATCTTGTACAT/GJAGAAGTACCACACATTTCA AACAAAGAGCCAGGCTATGCCAGGGTGGGATTATTTTCACGGTCACTGTAATATGCAATGTAAGACTA TTTTACTGGCCTCTTTTATGTCATAAAACAGGTATTTGGTCTATTTCAACAAACATGTGTCAATACAG
WI-6461	88 C T ---					CAGTTGTCATGTCCTCTGGTACTAGAAATATAGTCTTTATAGAAATATGTGTTTGAATAAAGCCACA AATATTCTATAAAACAACA/CjTAAGGAACGAGGCTCAAAAGTGAACAAACCGCCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAAATATAATCCGTGACCTCTTA
WI-7466c	141 G A TTTGTCTGG	TTTTCACAGTC			AGTGCATGCC AATTTATAAT	GAACTATCCTTTAGTGGTCCACATTTTCTATTCTGATTCTTTGGTCACACAGGACTTTCTGGGCT ATGAAATAGTCT/CjATTCAAGTGAAGTATATCATAAAGACATGCAAAAACCTTTTCACAGTCTT TGCTCTGGGAATATCTCACAAAATTAATTAATAATTTGGCATGCGACTTTCTGATTAGCCTGACAGGA TTGTCTCTTT
WI-7466b	80 T C GTC	GACTTTCTGGG CTATGAAATA			TGCTTTTTATG ATAACTAGTTC ACTGAA	TGCTTTTTAAAAATAACAATGACCACCCTGACACCATAGTCTGTCTCCATTGCCACGTCTTCTC AGTAGAATAAGACAGGGACTTTGCTGGCTGCTATCT/CjATTCTCCTTCAGAAGAGCACTTGGCCCT CATAGGCATTCATAGATATTGTTGAATGAATGTGCTTTTTCATATTGATTCTCTACATTTGATACA TTCTCAGGAGGGACATTTGGCCTAT
WI-9814	104 C A ---					CCCTTAACAAGAAAACTTGACTTCTCTCAACTCAAAATACCTTCTCTAATAATTTA/GJAGTAACCA AAATATCTCTCAAAATAAATTAATCTTTTAATTAGAAAGAACACAGTGTAGAGGTAGTACATTCA CCAAC
WI-9720b	55 A G ---					



WI-9720a	47 A G ---	---	---	CCCTAACAAAGAAACCTTGACTTCCTCAACTCAAAATACCCCTCTCT[AG]ATAATTTAAGTAACCA AAATATTCCTTCAAATAAATAATCTTTAATTAGAAGAAGCAACAGTGTAGAGGTAGTACATTCA CCACC
WI-9825	123 A T ---	---	---	CACGCTCTAAGGCAGGATGTGGCTTATGAGATACCTTTGCATTGTCTGCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTCATGTGCAGATGAAGGCTCAGGGTCT[AT]JAGGATTAG TAAGATCTCTTTCTAAAGACAGGAGAGATTATTACAAGAAGAACTCACCCAGGGTTAGTTTGCATT TAAGAAITGCCAGCTTTTGCCTGCATCATCTTGAACATTAAATCCCATG
WI-9748	74 C G ---	---	---	CCACTCAGTAAATCAATTTGTAGCACCTTATTCTAAAGATTCTAAATTTTTATATGTTTACCCCTTT GTCATT[C/G]TCAGACCAAGTACATGTTTTCACACAGCCATCTTCTTTCTGGAATCTTTCAGAAT TACAGTTATGATGTCCTTTTATATCCCCA
WI-9943	91 T C ---	---	---	TGAGGCTATGATTGCAGATTTGTAGTACTAATCTTATTAGCAATTTCAATGTTGTGGGCACGTGT CGTTGTGTTTATATCCATCTCT[C/J]ATTTTAAATTTCTACTGAGCAGAAAAAATGTATACATT AACCTTTGCTCCCTATTGTACCTTTTAATATTGCATTTCACACCTTCTCTTTTGTCTATTAGGGA
WI-9891	39 T C ---	---	---	AGGGCCCTTCACAGATCCGTGAGCTCAACACTGCCTCTT[C/J]AGTGAGCCTGTGAACACCCCAAGAC GGCTGGTCATCAGTGCATCCTCTCTCTTTCCGGACAACATCTTTTAAAGAAAAAAGAGTGT CTTTGAATGTATCCATTTATCCCAATAATCTTGTTTTAAATAATCTTATTAGGCCAAATCCCAAT GTGCTGAAATATCTGCCAAGCATGTCTTCTACACAAAAGGGATTGCAAA
WI-9897b	84 C T ---	---	---	CTCAGAAATTATCAGATCTTCCCAAAATGTCATGATCTTGTCTCAACATCCTATTTTTCCTCAAAC ATTTATCTAGCCTGT[C/J]AAGTCAATCCAGTGAGGCTGTTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83 A T ---	---	---	CTCAGAAATTATCAGATCTTCCCAAAATGTCATGATCTTGTCTCAACATCCTATTTTTCCTCAAAC ATTTATCTAGCCTGT[C/J]AAGTCAATCCAGTGAGGCTGTTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9935b	115 C A ---	---	---	AGATAACCCCTGGAAAACCTAGAAGAAATTAATAACGTGTTGCACACCTCACAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGTGCTTGACTGGCAGGGGAGTTGAGACA[C/A]JAGCCAAAGAAAAGCC TGATATTAGAGGCACITGCAATTA
WI-9935a	42 C T ---	---	---	AGATAACCCCTGGAAAACCTAGAAGAAATTAATAACGTGTTGCA[C/J]ACCTCACCAAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGACTGGCAGGGGAGTTGAGACAAGCAAGCAAGAAAGCC TGATATTAGAGGCACITGCAATTA
WI-9983	146 C T ---	---	---	CCGTGTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCCCTCCCAATTCCTTTGCTTGA TTCCCAACCCCAAGGTTCTCACCCTAATCTGATCAATCTGACTAGGTCATGGCTGTCAGGTTAA AGCATTATGA[C/J]AGACACAAAGACAAAGAGGTTAAAGTTGCTGTCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACCTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG



WI-10019	139	A T A T C T	T G A T G T A A T G C T A T G T A G C A A	T T G A T T A C T G T G C T T A G G G A	A T A T C A G T G G G T T G A G T A T A C A G C A A T C T A T T T T G T T A T T A T T A T G T G T G C T A T A A A T C A A T G G T T C T A A C A T T C A A A T A A G A T C T T T T G C T T C T G C T C A G A T G C T T T C A A T G A T G A T A A T G C T A T G T A G C A A A T C T A T A T T C C C C T A A G C A C A G T A A T C A A G G C C T T C T A C C C C A
WI-10020b	122	T A T T T	G C G A G A A A A G A A A T C A T G A C	G A C T G T T A A T T T A T T T A A T C A T T A G T C T G G	T T T A C T T C A T T G C A T C T T G A C T C G T A T T A A A T A A A T T A T T A C T G G C T C T G A A A A G A A T T T A G G C A T G C A T A G A A A T A G C A G T G T T T T A T T G G C G A G A A A A G A A A T C A T G A C T T T T T A A A A A A T A C C A G A C T A A T G A T T A A A T A A A T T A A C A G T C C T A G G G T T C C G A A G T G C C T A A A G C A C G T A G T A G C C C T C C T T A G A
WI-10020a	39	T C A T A A A T T	T G C A T C T T G A C T C G T A T T A A	A A A T T C T T T T C A G A G C C A G T T A A C	T T T A C T T C A T T G C A T C T T G A C T C G T A T T A A A T A A A T T A T T C T G T T A A C T G G C T C T G A A A A G A A T T T A G G C A T G C A T A G A A A T A G C A G T G T T T T A T T G G C G A G A A A A G A A A T C A T G A C T T T T T A A A A A T A C C A G A C T A A T G A T T A A A T A A A T T A A C A G T C C T A G G G T T C C G A A G T G C C T A A A G C A C G T A G T A G C C C T C C T T A G A
WI-10064b	170	C T T T A C A T G	C C T T T A G A T A T A T T G T A T T G T	A C C T T T C T G A A G C C A G A T T T C	T C T G A G T C T T C T G A G A C A C T T G C C A T G G T C A A G G T A G C A G G A T C A G G A A G G C A T T A T A A T A A A T A T A A T T T G C A G A G C A T C T C T C C T A T G C A C C A G A T A T T G G G T G A C A C T C T G T T T A T C C A G T A T C C C T A C T C C T T A G A T A T A T T G T G A T T G T T T A C A T G C T G A A A T C T G G C T T C A G A A A G G T T A G G T G T T T
WI-10064a	54	C A C A G G G A A G G	G T A G C A G G A T C A G G G A A G G	G A G A T G C T C T G C A A A T T A T T T A T T A T	T C T G A G T C T T C T G A G A C A C T T G C C A T G G T C A A G G T A G C A G G A T C A G G A A G G C A A T T A T A A T A A A T A T A A T T G C A G A G C A T C T C T C C T A T G C A C C A G A T A T T G T G T G A C A C T C T G T T T A A T C C A G T A T C C C T A C T C C T T T A G A T A T A T T G T G A T T G T T T A C A T G C G A A A T C T G G C T T C A G A A A G G T T A G G T G T T T
WI-10289	29	T C C A A C T C T T	T C T C T G T C C C T C C A A C T C T T	A T T C T T G T T G T A T T G A A T G G A A T T A A	C C A G G A T T C T C C T G T C C C C A A A C T C T T A T T C T T A A T T C C A T T C A A T A C A A C A A G A A T T T A T A G A A T A T G C A C C A C A T G C C A C A A A G A C A C C C T T A T A T T A G T
WI-1319	40	A T A T T C T T T	T G G C A C T T A G A A C A T A G T T T	G C C A C A C A C C C C T A T G G T	A A G A A A A T C C T T G T G G C A C T T A G A A C A T A G T T A T T C T T T A T T A C C A T A G G G G T G T G G C T T A T C T T T T A C C T G G C A T G G C T T A G G T C C T G T T A T A A T T G G T A T C T T T T G C C A C A A A G A G T C T G T T C T G A C A G T C T T A T G A T C T A T T T A A C A T T A A C A C T G G T C A G A T G T G T T T A A A A C T T G T T G A A C C T G C A G C
WI-10316	104	T C C T C T T	C T G T T G A T T T C T A C C T C T A T T	G C T T T G G A A T G T A T C C A A A A G T T T	A G C A A C G T G T A C A A C T A G T G A G G T G T A A A T C A G A A G C A T C T A T A T T A T T A C C A G T C A C C A C C C T G G A C T A T A G T C T G T T G A T T T C T A C C T C T A T C T C T T A T T C T T A T T C T T A A A C T T T T G G A T A C A T T C C A A A G C A T C A T G G T C A C T T C C A G T A T G A A A G G A T G T T A A A A G C C C A G C
WI-2572	61	C T ---	---	---	A G T G A G T T G T G C A C A A T T T T G G A G A C A T T C T G T G A C C C C A A C T T A A A A C A C T T C T C C C A C A C T C T A C A A G T T A A C A C T T C A G T A C C A G G T G A T G A T T G A G C A G A



WI-10368	31 C T	TGAAGCAACC AGGCTTGT	CAAGATATTAT ATTTATCTCT AAGAGGG	GAGAACTGCCTGAAGCAACCAGGCTTGTTC[CTACCCCTCTTAGAGAAATAATAATATCTT GAGATAGGAGGAGCAGCCTGAGGACAGCTGGGTTTGTTCACCCACTGGAAAGCAGAAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTGCTGCTAACTATATGACCCCTGATGGATTGCCTTTTCAGGG T
WI-10391	32 A G	CTGCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAGTT GA	CTCCCGTTCTCTGTCTCAGGTATGACTCCCA[GTCAACTCTTGACTCTCTAACTCCCATCTCGGTG CTGTCTCCAGGGGACGCTGACACAGCCTTTTGTCTGTGTGACAAACAGAACTTGCAGAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146 A C	GTTACCCAGA GTCTTCTAATA GCAA	TGCCGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCTGACTTACGCGGTGCTCAATAAATATTTCTTTTTCATATT TTCCAATTAATACTAGAAATTTTACCAACAGAAATTTTAAACATTTTAAAGTTACCCAGAGTCTT CTAATAGCA[ATC]AGCTACTGGAAGCGGCAAGAAATTTAACCT
WI-10567b	82 A C	GGGTGCTCAAT AAATATTATT CTTT	AAAATTCTGTT GGTGAAAATTC TAG	AGCGATGAAATTTATATGTTATGCTGACTTACGCGGTGCTCAATAAATATTTCTTTTTCATATT TTCCAATTAATA[ATC]TAGAAATTTTACCAACAGAAATTTTAAACATTTTAAAGTTACCCAGAG TCTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCT
WI-10567a	60 T C	CAAACCTCAA ATTGCTTTAAG TACTTTA	AAATCCTCAA GTCAAGGTCTT C	CGTTGGGAATTTCTATCTACCTAAATTTATGCGTGAATTAATAATATACATTTTAAACAACTCAA TTGCTTTAAGTACTTTA[CTG]GAGACCTTGACTGTGGATTTTGTGATTTTCTTTTATTTTAAATA AAACATGCATATTTAAGTTGTGCAAGATGACTTATATGTTAATATCTGATATCAGCATCCCTT TATGTAAT
WI-11153b	84 C G	GGGAATTTTC TATCTCACCTA AATTAIG	GCAATTTGAAG TTTGTTAAAT GTAT	CGTTGGGAATTTCTATCTACCTAAATTTATG[AT]GTGATTAATAATATACATTTTAAACAACTTC AAATGCTTTAAGTACTTTACGAAGACCTTGACTGTGGATTTTGTGATTTTCTTTTCTTAAATA AAACATGCATATTTAAGTTGTGCAAGATGACTTATATGTTAATATCTGATATCAGCATCCCTT TATGTAAT
WI-11153a	33 C A	CACAAATGTA ACAAGAAATG ATCC	CCATGGCTGTA GTCCAGT	GTTGTGAAACTCCAGTATCATTTCCCTCAAACCGCTTAAATCACAATCAGCTTTTCTTCTGTA GAGCTCAAACCTCAGTCTGAATGAAATTTGCTGCACAAATGTAACAAGAAATGATCCTA[TC]ACTGGG ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58 C T	CAAGTGAATT ATGACCAAAA TGAGA	TGCTCTTTCA TTTGAGGTTTT T	TGACTCAAAGGAAACACACAAAAAGTTTACCAGTGAATTAAGACCAAAATGAGA[CT]AAAT TTGTTAAAAAAAACCTCAAAATGAAGAGACAAATATAGTTCAAGATTCAAGTTCAATTTGT ACCTACAAAATAGGGATAGTCATGGTGTGGGAGACTTTCTTTCTTTTCTTTTGTG[CTCTTA GAATCCATTTTGTCTTTTGGCCAGCATTCCTCTCCCCATATTTTAAGGAGAGAAATCACTTTTCT CTGTTGATGATCACAGGTTCTGCTCTTCCCAATCCAGAGGAGGACTATTCACCCCATGGGTCAT AGAGAGGATTAACAGGGGTGATGCTGCAATGGGAATATTGAAAACC
WI-10656	59 T G	---	---	---



WI-11169b	154 T G	TTAACCAAGA GTTTTTCATTC TTTTT	CTAACTTAAAA ATCCTCATTC AAATATAA	CAGCATAGAGGCTGTAGTACCTTGAGTTAGATTTCTCTATCGAGAAAGCAATAAGTGAAGTAA CTGACTTGAAAAAATAATTTAAGCCTAAAGTAGTGCTTTTAAACCAAGAGTTTTTCATCTTTTT TTTAAAAAAGAGCAGACAT/GJTTATCATGTGTTCTGATAATTTTTTATATTTTGAATGAGGATT TTTAAAGTTAGCAT
WI-11169a	95 A G	AATAAGTGAA AGTAACTGAC TTGAAAAA	AAACTCTTGGT TAAAAAGCAC TACCT	CAGCATAGAGGCTGTAGTACCTTGAGTTAGATTTCTCTATCGAGAAAGCAATAAGTGAAGTAA CTGACTTGAAAAAATAATTTAAGCCT/GJAAAGTAGTGCTTTTAAACCAAGAGTTTTTCATCTTT TTTTTTAAAAAAGAGCAGACATTTATCATGTGTTCTGATAATTTTTTATATTTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25 A G	---	---	CAAGTGCTTGGACCTGGATAGGTG/GJACCGGCTGAAGGTTGGACAGTTGTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTATATAGATCTTGTTCTTTTGGGTTTACCACAGGGTCACTAAAG AGAGATGGGAGACAGTCTCAATCTTGCTAAATAATCCAAAAATAGCCATGGGTTGGACAAAAATAC AAGTTAGTGCTCTCTAATTTAATGGGCA
WI-10686	133 C T	TGCCCCGTGTC AAGG	CAATCTCTAAA TTCATGTGTAG ACACA	AATAACCTGTGGCACATAAGGCAATACTGAGCCCCATACAGAGTGTTTTATGTTAATATTGAAA AAAGTCAAGAGAACAAAGATGATATAGTTCTGCTAGAAATCTTGAATCTGATGCCCTGTCCAAGG C/TJTGCTACACATGAATTTAGAGATTGAATGAAAATGCAAAATTCAGAAAAGG
WI-11175	77 T A	AAATGATTCCT TCTGCTCAAAG A	CTGTTCTCACA TCTTTTTGAA AA	GGTAGGATGATCTAGAATGCCACTTTACAGCCACTGAAATATATGCTCCCAATGATCTTTCTG CTCAAAGAGT/AJTTTTTTTAAAGTTATCTACTTATTTATTTCTGCTTTTCAAAAAGAAATGTGAGA ACAGTACAAAATGTGTTTCAGTATAGCAAAATTAATAATTAATAAGTAAGAAAAAGAGCCAAAT TGGGC
WI-10694	144 A G	TGCAATGCTT TATGAGTTTC TGAATTCATCC AGAAAAACAG C	GGCATTTTGTA AAGGAGGAAA TCTCTTTTCTC TCTTGTGTCA TTC	TAGAGAGGCTTTTCAGTTTCAGGGTGGAGGGTGGTGGAGGATTCACCTCTTAGAAGCACTGGC TATGTACAGAAAGATAAACTCTGAGAGAACTCAGTTCTAAAGTTTCAGTCTTTGCAAAATGCTTTA TGAGTTTTC/GJTTTCTCCTTTACAAAATGCCATCAATTCCTCAAGGAAAAAAAAGGCTTTCT T
WI-2716	23 T C	TGCAATGCTT TATGAGTTTC TGAATTCATCC AGAAAAACAG C	GGCATTTTGTA AAGGAGGAAA TCTCTTTTCTC TCTTGTGTCA TTC	GTGAATTCATCCAGAAAAACAGCT/CJGAATGACAACAAGAGAGAGAAAGATAAAGGTTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGTCCAGTGCATGGAGCAGTG
WI-10719	115 T C	TGACTCTCAAG GCCATTCTAG AGCC	GCACTGCCAGC AGCC	CAGGCCCAACTCTGTCAATTAAGTGTTTTAGAACAGACACCTCAGTCACACAAAGTTCTCTGTGTATGT GCCACCATAAACAGTTACTGGAGGATGACTCTCAAGGCCATCTAG/CJGGCTGCTGGCAGTGCTTT TTCAGCCTGCTGCCATAACTAA
WI-10721	40 A G	TGGCTCTGCTA CTTGCCA	GAACTCCAC ATAAATAAT CTCA	CAACCAATTCAGATTTAATTTTGGCTCTGCTACTTGCCAA/GJATGAGATTTATTTATGTGGGAGTT TCTGAAGATCCCATGGTAAATAGTATCTCTCCCTGCTTAGGTTTGAAGAAAGTTGAA



WI-11204b	88 T C ---			GCACACGAAATTGATTAAATATTGGCTGACTTTGAGGAGGAGAGACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAAAGCTTTACACCTTTTCACCTTTTAAAGTAAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAAATTATTTCAGAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAGGG TGAAAAGAAA	TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATTGATTAAATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAAAGCTTTAAACCTTTTAAAGTAAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATGGGAAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAAATTATTTCAGAAG GCAACATC
WI-10732	80 C A ATTGGTTCACT	GCTGTGCTTC ATTGGTTCACT	AAGAACAAATG CATAACAGAA CTTTAA	ACATGTAATTCCTTTAGTGTGAGCTTCCCTACCCCCAAGAATATCCCTGGTTTATTGCTGTGCTTC ATTGGTTCACTTCATTAAGTCTCTGTTATGCAATGTTCTTGAAGTCCACATAGGTGTTAATCATTTCCA CACCACTCTGTTTAACTGTC
WI-11206	127 A T ACTC	GGTTGTGTTTT CTGTATGTACA	GAGTGACAATC CTAATGGTTGG	TAGTCTTTCTTTGTACGAGTGTACATAAAGAATTACCACCTCTGTACATTTTGTAAAAAGATAGCACAG AGAGAAAGCATACAGGGCACAGCACAAACATGAGGTTGTGTTTCTGTATGTACAACTC[AT]CCAA CCATTAGGATTGTCACCTCATATATAGACAGAATTCAGTGGTGGTGAATTTGAATTCACACACATGGA ATAAGTCTA
WI-11215	68 C T ---			GAAAAAAGTTTAAATTGGATTGCTTAGTTTGTCTTAAATTTGACCTACTTTCAGATTATTTTAGT [C/T]ATTTTCTATAATATTTCTTGTAAAGTATGATTTCTATAAATTAGGAAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATCTTTATCCAAAGCCCCATCCACCATGT TTT
WI-11219b	89 G A AGAGAAA	GAGAGAATAT TCCAAAAAGT	GGTCTCTAAT TTTTCTACACT TTCT	ATGAAAAATGCATTAGAAGAAATTGGAGGATAAAATTTGAGAGAATATTCAAAAAGTAGAGAAAA GAGACAAAAGAGATGAAAAATAGGA[G]AAGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAAAACATCTC
WI-11219a	18 G A ---			ATGAAAAATGCATTAGAAG[G]AATTTGGAGGATAAAATTTGAGAGAATATTCAAAAAGTAGAGAA AAAGAGACAAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAAAATCTC
WI-11222b	136 G A GGCTGG	CATACCCTGC AGTTGTGA		AGCCACAGTGGAAATCATTTACACTACCGAAATCAGCAAAATGCTAAAAATTTGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCCACTGTTGAACATTTGTTAAACATTTACCAGCATACCCTGCGGCTG G[G]ATCACAACCTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTTGCTTTTCACAGGCTACTGG AAAGCC



WI-11222a	25	C T A	GCCACAGTGG AATCATTAC	TTTTAGCATTT GCTGATTCG	AGCCACAGTGAATCATTTACACTA/C/TJCGAAATCAGCAAAATGCTAAAAATGGGCTTTGGATTTT TGTTTTTTGTTTTTCCATAGACCCACCGTTGAACATTTGTTAAACATTTACCAGCATACCAGCTGCGG CTGGGTACAACTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTCGTTTTCACAGGCTACTGGA AAGCC
WI-10775	39	C T	TTTATGCCATA TTAATTCAATTA	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTTGTTTTATGCCATATTAATTACATTACACTC/C/TJACATCATATTTTCTTAGCAAAATACA TCTAGACACCTGGCACTAGTAAGGATATTCCTGGCAGCATATCATTTGTTATCATTAGACATTGCA GGAACCAACATATGGATGGATAAATGTGTGTTTAAAGGCAAGCAATTA
WI-11226	165	A C ---	CACTC	---	TTGCATGCATTTATACGAAAGGAATTAATAATATCTTCCCTTATAGTTGAATTTTAAAGTAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATTAAGAAAAATGTCAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA/CJGACATAGTTGCTAAGGATATTTCCACAAATTAT TTCAATGA
WI-10778	62	A G	GCAAGGGAGG AACA TTTACA	CTGGTGACATC AGAGATGGAC	CAGTGGCTGGCTACTGACAAAAACGTAAACATCGTGGCAGGTGGCAAGGGAGGAACATTTACAG/CJG TCCATCTCTGATGTCAOCAGCGGGCCAGGAGGTTGATCTGGAG
WI-10789	21	C T	GGGACACACT GCTCTAGAC	TTGAGGGACCC TGGA	TGGGACACACTGCTCTAGAC/CJ/TJCCCAGGTCCCTCAAGGTGGGTGAGAGGCCCTACTGCCCT GCCCTGGGGACGACAGGACATCAGGGCTTAGTCTCTCTGGGACAGTGAAGGGCCACCACC
WI-10810	58	C T	CATCTTCATGG GCAGGAATT	CAAAACCTAAG AAACACAGAA ATG	ACAGAAAAATGCCTAGGTCTTGTAGCAAGAGAGAAAGCATCTTCATGGCGAGGAATTC/TJCATTT CTGTGTTCTTAGGGTTGTGGCTGGGCATCAGTTCAACTCAGCCCTGTCCCTGATCCAGCAACATT TCCGTAACCTACCCCTCTAGAAAGTCATGCAAGAGAGAAATGATGA
WI-10828	23	T C ---	---	---	GGACCAACAGAAATTACTTGGCAT/CJAGGGTTTCTTAAACTATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACTTCTAAAGGCTATAATATTTGGATACATTAGGCTCATTATGAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
WI-10832	91	G C	CATTAATCTGC AGGCTCTCC	CCTAACTGCAG GTGACTTAGAA A	TATGCCCTCCCAACGAGCCATCCACGCTGCTCTTAGCACAAAAAATAAGATACATCATCTGAATG GGCACATTAATCTGCAGGCTCTC/CJ/TJTTCTAAGTCACTGCAGTTAGGTCTGCAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGAGGAGGAGATGAGAGAAGGGCTGCTCCGTGAAATAC TAGTTGGG
WI-10834	96	C T	AGAATTAAC GTTCAAAAAGT	TGGCCCTATAA AATTGGTATTA AG	GATTTGAGTATTACAAAATTTGCCAAAAGACCATTAAACAAGATTTAATAGTTAAAGCCAAAACATA AAGAAATTAACGTTCAAAAGTGTGTTAAT/CJ/TJCTTAATACCAATTTTATAGGCCACCATTAACTT CTGAAGAAAAGGTGAGCATATGCAACTAAATTTCTAAAGTCCAGT
WI-2287	24	T C ---	---	---	GGATGATGTTCTGTGGTCCCTTTA/CJ/AAAGCCTCTTGATCCCCAAATGTGTAATTTATTTATCT TGGTATTTCTCGCTTACCCATAGTCACCTGTCAAGTGTCCACCCCT



WI-2296	81 A	G A	TGTTACTTTGA TTCITTTGCTCT	GCAATCACAC AGCTAACTGG	TGGAGGGTTAGAAATGCAGGTGGCATCCTAGAAAGGCTCAGGCTTTAGAATAAGTTGTTACTTTGA TTCITTTGCTCTGAC[A/G]CCAGTTAGCTGTGATTTGCAGAAAGTTACATTTGTTTGTG
WI-2300	77 G	T C	GGCACAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTTTCCTCGAAATTTCTTTATTTAGCGGGGCGAGGTGGTAGGCACAGAAGC CAGTCATAC[G/T]TGCTTTAAATTTGACCCCAACCATTAAGAAATAGCATTCA
WI-2371	55 G	T C	GTCITGTTCTT CCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGGAAGGCTGGTCTTCTTCCAGCTTCT[G/T]GTGGTGGCT GTCAATCTTTGACATTTCTTGTCTTGACGCTGTATAATTCCAATCCTTGCCTCCAGCTTTACATGATGT TCTCTCCGTGTGCTGTG
WI-2395	122 A	C	GAACATATTT GTAGAAAAAT	TCACCTTTCTA TTTATTCTGAA TTCA	GGGGGCACAATTTAGCTACAGTGCATATTTAAAGATAACATAGAAATATCATATAACTTGGTTTAC TGAAATCTGAAAACTTAGGATGAGTGAACATATTTGTAGAAAAATTTACTATCCAA[A/C]CTGAATTC AGAATAAATAGAAAGGTGAATCATCTTATATCATTTAAAGAAAGCTAAATTTATTAGTAACAATCTTTA CATTTACACAAACCCA
WI-2437c	192 G	A ---		---	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTG[G/A]GCTGTG GTGCCAAGGACGCAATTATG
WI-2437b	179 G	A ---		---	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGAC[G/A]AACATCACAGTGGGCTGTG GTGCCAAGGACGCAATTATG
WI-2437a	128 G	A ---		---	CACCAGCCACCACCCCTACAACCTCCTGTGGGGAGTCTGGCTTTGATTATTTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACCTTTCTAAATAATAGACACCAAAAAATCCCAAT[G/A]CTC TAAATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCAATTATG
WI-2440	71 G	A	GCAACCTACT GACAAATTTAA TTTTAGTT	AACAACCTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTTCTCCTTAGACCCCTCCAGAAAAATATGCAACCTACTGACAAATTTAATTTTA GTTG[G/A]GTGAGACCAATAGCAGAGTTGTTACCTGCAGAACT
WI-1356	123 T	C	TGTTTAGGAA ATAATGACAA GAAAAA	TGGTTACAACCT GTACCAAACAT G	CTGTAACCTACACACATCCTCCTGTAACTCTAGGTTACTTTGTAATACAAAACACAATGTAAATGCT ACATAAATAATTGTACATCTATATTGTTTAGGAATAATGACAAAGAAAAAGCCCT[C/G]TACAT GTTTGGTACAGTTGTAACCCAGCCATTTTCCCCCAATATTTCAATCCACAGTTGGTTTAATCCACAG AAACCACGAATG
WI-2886	46 C	A	CAGAGTCTGG GGGAGAAGA	TGCGCATGCTT TATCTCGTT	ACAGTTAAGAAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGGAGAAG[A/C]AACGAGATAAAGCATG GCAAGACCACCGCTGAAGTATCCAGGGTGTGTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAAGGTGTGACAGAAACAGAGGAGCGTT



WI-2906b	77 T A ---				CCTGAACACCTGGAGCACTCCCTCCCTGGACACCTTCATTCTTCTGCTGGAACCTTTCCTGGAATGCTC TTTCCCTCT/AJGAGCTTTGCTTGGCTTACTTTTCTTTTCTTTAGGTTTCAGCTTCAAAGTGACCT CCTTAGAGTTGGTTGCTGACCAACAAA
WI-2906a	50 A C TCTTGCTGG	GACACCTTCAT		AGACCAATCCA GGCAAAAGT	CCTGAACACCTGGAGCACTCCCTCCCTGGACACCTTCATTCTTCTGCTGG[A/C]JACTTTGCTGGAAT GCTCTTTCCCTCTGAGCTTTGCTTGGCTTACTTTTCTTTTCTTTAGGTTTCAGCTTCAAAGTGACCT CCTTAGAGTTGGTTGCTGACCAACAAA
WI-1736	175 C T ---				TACTCCTCATTCTCATGTCCCTAGACGTACTCAGATTCCATGCCCTGAAACATTATTTCCCTAAAT TAGATTTCCACCCCGCAGCACTATTTACACAGAAACAGCATGGAGCAGTTTGGAGTCTGGCTCTTAGA GAACTTACTTAAGGACAGTGGTTTCCATCTGCTTCCAC/C/JAGAGATCTAGGGTGCTTTTGGAAACC ACCTTGG
WI-1851	136 G A GTGTTAAGTA	GCATTGAATT AACTATAGAT		CACTAGCAATG TTAAACTGAAG TTG	AATACCCACGTCCTAACACCATCACACTGATCATCAATCAGGTTTTAACATATTAATCTGGGAGG ACACAAACATTTAGACCATAGCATTTGAATTAACATATAGATGTGTTAAGTAATTATTAACATGGTA CA[G/A]JACAACCTTCAGTTTAACATTGCTAGTGATTCCATGTGGATACCATGACCTTCTTACATCATG TGA
WI-3000	62 G A AGAGACCCC	CCCAAAACAC		GCCTACTATAGG ATTGACTAAGA CTCA	CTGATGTTTGGGAAGCACTGTCTTACATCTCTAAATGTACGACCCCAAAACACAGAGACCCCG[A/JT GAGTCTTAGTCAATCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGTCATAGTAGACACT
WI-1754	177 G A TAGTC	TTTTCTCCCTT CTTAAAGAGA		AAAGTCGAATT GCCTCTGG	ATGGATCTGCTCAATTATAGTCCAGATAAACAGCCCTTCTCCCGCCACCCCGGATTATTTTACT TAAGGGTTTAGCAATTCACTGACAAAGAGTTAGGTTTCAACATTGACCCCTCATAAAGTGATTTT TTCTCTTTCTGTTTTGTTTTCTCCCTCTTAAAGAGATAGTC[G/A]JCCAGAGGCAATTGCACTTTCTGT AGCCACAAGATT
WI-3167	37 T A TAGATTG	AAATTCAACC ACAGATCTAT		TGTGATAGTTT TGAGATGGTG	ACAACACAGCAAAATTCACACAGATCTATTAGATTCT/AJACCCCATCTCAAACTATCACATCAA AGAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
WI-3208	140 G A AGATAAAGA	GTGGAGTGGGC		TCACTCAAACCT AGGGCTTGG	CAAGCACACATTCAGGCAGTGGGCAGGTAGGGAAGGTGGGCAACTTGGCGACGAGAGAGGGAAG AAGTTCAGACCGTTGGGTAGGATAAGTGGATCCAAACCCCTTTGTAGGGCAGGTGGTGGAGTGGGAG ATAAAGA[G/A]JCCAAGCCCTAGTTTGGTGACACTGTGGGGATTCAAG
WI-1775	47 C T TTTTCTCTG	CCTGCATGGTC		AGTTGAGATTT ATGACAAATGAT GTAAA	ACTCCACCAACAGTTTTGTGAGCCAAACCCCTGCATGGTCTTTTCTCTG[C/T]TTTACATCATTTGTCATA AATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55 G A ACAT	AGCATATTCA TTGATTTCCCT		GAGGACTTAAA AAGGAGCATTT G	CTGCCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTCATTGATTTTCTTACAT[G/A]CAAATGCTC CTTTTTAAGTCCCTCAACCTTTTAAAGCGGAAGTTGAGACATGCACAAAATAGATTTCTCTTAGGA



WI-3416	33 C T	CCAAGTTGTA GCATTCAGAA	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCTCCTCAAGTTGTAGCATTTCAGAGTCTCTCTTAGAGGTAGTTGTGCTCGTCTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTGTACCTCTCCAAACAAGTGTACCAACAGGATTGTTAAG GAAATGTCAATGCTTGTACCTCTGACGCACACAATAATTAATCCATTGCCTAAAAAGACCAGG TCCTATTCCTACAACAACAGAAATTTAAACAAATGAAAAATCAGCTACTCTCTTAGGCCCATCAGAG AATCTGGAAGTCATGGGAAAAATGATGCCATGTAAATGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGACACAATCCCACTTCCAGAGCCATCATCTGTAAGAC CATGCTAGGTAGATCTGATCATGAAGTTGAACAAACTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTCCCTAAATTTAGCACAGTATTTAATGAGGTGGT[G/AT]GGGAGAAAAATTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474b	109 G A	---	---	CATGCTAGGTAGATCTGATCATGAAGTTGAACAAACTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTCCCTAAATTTAGCAC[G/AT]GATTTTAAATGAGTGGTGGGAGAAAAATTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90 A G	AGTCAGTTTCC CTAATTTTAGC AC	CAACCATCAAT TTTCTCCCA	TCTGGATGTC[CT]TGAGGACAGGGTCACCCAC TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTGCCTGTTTCCAGAGTCTGATTATCCATGCCCCCTG ATAGTTCTGTGAGCCACCTAAACTCGTTTCTGCTTAAGTTATCCAGAGGTGTTTCTAACCTGGATA TAAACATCT[G/CT]ATGGAAGGCTGCACTGGATGAGGTCACAAA TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCTGCCTGTTTCCAGAGTCTGATTATCCATGCCCCCTG ATAGTTCTGTG/GAGCCACCTAAACTCGTTTCTGCTTAAGTTATCCAGAGGTGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACTGGATGAGGTCACAAA TAAATCATGCTTATTTTCAAGGTAATCCACTCACAATAGGCAATTTGATGTGATCTCTTTCTGTAA GAAAAGCTCTCATGCTCTTCTGAACCTTCTACTTACTGTGCTGTTATGATGCACCT[G/CT]CCTTTTGG ATAGATGGTTGATAGGAGATGGTTGTTAAAGACACAATTTACCTGTGTTTCAGGCAGAAAAATAG ACTCTCTGTGTGTAATCACTGAATGAGTTCCTGCTTATGCTTAC AAAGCGATGTTGAGATACCACTCCATGAAAAAGTAAAAACACACACACAAAAATATGACATAAAA TIA/CJAAAAACTACTATAGTTTATGAAAAATGACTTCCAAAAATTCAGAGAAAAAGTCACCTTAAACAGG ATTCTCAATTCATCCAGAACTCTCTGTCATCTTAACTTTGACTGCACAG
WI-3678	125 G T	---	---	TCTAAATGTGAAACCAAAGATCTGACACGACCTAACTGCCAGTCTCAGTTATGATCAATGA AAAACT/CJACACCGTTCAATGAAAAACAATGATTGGTGAGCCATGTCCTTATTTAATGAAAA GATCTTGGGCAATTAACCT
WI-3687	67 A C	CCTCAGTTATG TATCAAAATGA	GGCTCACCAAT CATTTGTTTT	---
WI-3735	72 T C	AAAAC	---	---



WI-1819	51	C T	---			GAAAAAGCAGGAAGCCAGGACGACAAACCTTTTGAAGAGTCTTTACAGAC/C/TTCGTGGATCCG AATTTTAGTGTGATTGGCAGGCAATGCGGGGTAACTGTTCCAGTGTTTAACTTGCACAGAATTGC CAGATTAGCGATTGTTGACTTGTCCAATTAATGAATGTGGAAAAAAGGGTGGTAACTGTT AAGCTGCTGCAATGTTTAGACAGAGGGTGGGGTGGGAGGTGGAATACC
WI-3746	116	G A	---			GGCCTATTACATGACACTGGGCCAAGATCTTGCTCCCTTTCTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCAGGAAGATGGTTGCTTTCATCATCTCTGCTCTG[C/A]GCCCCAGGATAAAGCA GGCA
				TAAGATAACC		AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTGACAA/T/CJCGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAGACACTGTGACACAGAGATTGTTACTTTGAACAAGACACAGT CATTAAAGTGAGAAAGCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
WI-3867	49	T C	CAA	ATCCG		
					TGACCAATGTC	
WI-3898	25	A C	G	CTCTOC		CAATGACCAATGTCTTTAGAAGCAG[A/C]GGAGAGGACACCGACGAGACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGCGAGCCACAAAGGTGAGGAAGCAAGGGTGTGCGCCACT
						GGACCATTTGCCCTCAGAAGTACATTCAAGCCCTGGACGGTGTCTCCTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCTGAACTCGGCTTCTCACCTGACAAAGTG[A/G]TATCATGTGCTACACTGC AGTGTATAATGCTGCAT
WI-3901	114	A G	---	---		CTGAGGAGATTGATGCTACTTTACCTGAGGAACCTTTTATACCTCCCTGAGTTTGTTCCTTGCAA GACATTGCTGATTCTCTCAAGACTCACAGC/C/ACCATCCTTCATGCTTCTAGACCTATAACTAG ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAAGGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-3914	99	C T	GC	TGAAGGATGG		
				AACAGCAATA		CCACTCCCAGGCCAAGAGCGTCTATGAATCAT[G/A]CATTTGTTCCTGTTATTGCTGTTACACAGAT GGCAACTCTTGCAAAGGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC
WI-4019	33	G A	A	ATG		
				TGAGTTCCCTAT		TAATTACATTGCTCTGTTTGTGCAATTTATGCTTCTCTTATGTAAACACAATCACCACATTGAGG TCCTTAGTCATTGCATG[A/T]GTATAACAATATTGTCACCTTAATAGGAACCTCAAGCATAGTTATGTT ACATTTATTGCTAACAGCAG
WI-4091	84	A T	GTCATTGCATG	ATTGTT		TCCTCTTCTGTAATAGGAAGTCTGATTAGATGCCCTTTGAGGTTAGGTGGCTTCTAAGATGGTAATT ATCTGTCCCAAGTTTGTTCCTATAATTTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAA ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATGATACT
WI-4160	117	A G	CAACAGAA	AGCC		
					GGTGAGAGTC	
WI-4168	32	A G	AAATA	GAATTCAGA		CGTTGCTGGTGAGAGTCAAATTGATACAAACA[A/G]TCTGAAAATCTGTTTGGCAATCTATTAAAGG CAAATATATACCAGCAGTGTGGCTAGCAATTTCACTGCTGGGCATTACCTAACATAAATGAT







WI-5204	54 C T ---		---	TAGATTTTGATTGATGACAATAGGGAAGCCCTTTGTTAAATGGGTTTGAAGAA[C/T]GAAGAAAA TGGAAGGGGAAGAATTGACAGAAACCAAGAGAGTGTGAGGGGCAGCAAATCCCAGTTGACTGGA ATATAGAGTGATGTCAGGGTTG
WI-5215	70 A G C T C A A A A A	GGACCTTAAT ATTTAACAGA	AGATAATTTG TAAAGATAGTT TTGCG	TTTTCCCTTATTTATTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTTAACAGACTCAAAAA TAT[A/G]GCGAAACTATCTTACAAAATTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT GTAGTCAAGGTTTAAAGGCCAAATGAAGTTGACTAAAGACAAAT
WI-4448	112 T G A T A T A A	TTGTATCAAA GAGATGGGT	AATTAAGAA ATCTTTACATG GTTCTTT	CCCTGAAATGCTTTGCTTCTCCTCAACTCTCTAGGGAACCTTTTCCATGTCAGGTGAAGGTTTGA AGAGTACTTTTAATTAACCTTGATCAAGAGATGGGTATATAA[T/G]AAAGAACCATGTAAAGATTT CTTTAATTAGTGAATTTTCATCAGGGCTCTTCCACTGTCTATCAGTAA
WI-4456	49 C T T A T A G T T C C	AGTTGAATTA TTCAGAAAT	TTTCTGTTAT GCATGAACTTG	ACACATTTTCATTTGCTTTAAGTTGAATTATTCAGAAAAATTATAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAAACACCAGGTGGGCAATTGATTGAATTGT
WI-4461	49 A G C C T T C	TCACTGTTATT TTAAAAATTAT	TTGACCTTTC ACCAATTTCA	CTGAAACTAATGAGGTGCTAAATCACTGTTATTTTAAAAATTATCCTTCC[A/G]TGAAATTTGGTGAAA GGTCAAAAGAATGAATTCACCTTTTAGAATTTCTGGAATTTTATTTGGGATGATAATGCAATGGGC
WI-4465b	75 G A ---		---	CTACTGGATTTTACTTTGCTCAAGCCAGACAACACGAAAAGT[A/G]TATAAGAAAAACAGTTAGTAAT TCACCTTT[G/A]ATTCTCTCTACCTCAGGGGAATC
WI-4465a	41 A G A C A C G A A A G T	AAGCAGACA ACACGAAAGT	GGTGAAGATT ACTAACTGTTT TCTTT	CTACTGGATTTTACTTTGCTCAAGCCAGACAACACGAAAAGT[A/G]TATAAGAAAAACAGTTAGTAAT CTTTCACCTTTGATTTCTCTCTACCTCAGGGGAATC
WI-1949b	160 T C T A A T C	GAGTGAATAA ATGAATGCCA	TGAGAGGTGGG GACAAAAA	GGGTTAGGACCTCGAGATCTTTAGGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGT[G/C]AAGGCTGCTGACATGGTCATGGCTGAATATATGTTGAAGAAAT GGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCCCCACCTCTCACACCTTTTCCCTGG CACA
WI-1949a	86 T G A T G C T G A G T	CAGTGGTGAG ATGCTCTGAGT	CCATGTCAGCA GCCTTG	GGGTTAGGACCTCGAGATCTTTAGGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGT[G/C]AAGGCTGCTGACATGGTCATGGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCCCCACCTCTCACACCTTTTCCCTGG CACA
WI-4529	64 T C A A G A T G	CCAAGTAAGT CTATCATTCTG	TTCTAAAAATA ACACTTCCTGA AAAA	TGAGAGAGTTTTGGATTATTCATCCTCTGCAACACTCCAAGTAAGTCTATCATCTGAAGATG[T/C] GAGTTCTCTTTTATATCCTATGATTATTTTTCAGGAAGTGTTATTTTGAATATAAACTCCTGGGT CCCATCCAGGCTAGGGTCAATGGCATCCATCCATGGGTGCTGGACAAGATGGGCCCTAGGATCATTTT



WI-4540	110 A	G	GCACATGTGG CATCC	GACAATGCAGC CATGCA	AGCTTTTCCTTTCTTAAAAATTGGTGCCATAGTAGTGGCTTCTGTGTGCATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTGCAATAAGCACCATGTGGCATCC/GJTGATGGCTGCATTGTCCAGTC AAATGAGACAACCTTCCCTAT
WI-4582	226 T	C	---	---	AGCAAGCATCTGGCAAGCCTCGGTGACCAGAACATTAATTCACCAACACCACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTCAGGCCAGTTTAACTTATTCCTGTACACA AATAACTTTATGGGAGACAGCATTTGTAATTCAAATCAATAAATGACTCGGTTTGGCTGTACAAGCAT AAACAGAAGCGCTTGCAAAATATGGTT/CJCTCCTTGCTAGAAACCATTTGAT
WI-1965	105 G	C	AG	GCCATTGAGG AAGTGTTAA	CAAAGGTTAGTTTAACTTGGGGGCAACACAAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGCCATTGAGGAAGTGTAAAG/GCJAGAGAGATGACCCCATCCATTCTCTGG GCTTCTTATATGACACCATACTATCCACACAGATGTGGAGTCATTTATTTGGTTGGTGTATGACAGT CATGG
WI-5248b	99 C	T	TTG	AGAAAAAGAG AAGAAAGGAA AAA	TGTTTAAAAACCATAACAGTTTGTGCTGCTACGTTGTTAGAGCAACCCAGAAAAATTAACGCGCTAC CATTTTTCACGTGTTTCTATTGACCGTACTTG/CJTGCTTTGCTTTTTTCCCTTCTTCTCTTTTCTG CCCTCTTTTAACTATT
WI-5248a	38 G	C	CTACGTGTT	TTTTAATTTT TGGGGTGCT	TGTTTAAAAACCATAACAGTTTGTGCTGCTACGTTTGTGCTGCTGCTGCTTTTTTCCCTTCTTCTTTTCTG TACCATTTTTCACGTGTTTCTATTGACCGTACTTGCTCTTTGCTTTTTTCCCTTCTTCTTTTCTG CCCTCTTTTAACTATT
WI-4596	69 T	A	AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTTCTCGGTGACATTACTCTGTTGACTTTGCTCTGAAGCAGAAAGCACTGTGA C/T/AJCATTTAGGGCCATCTCCTGCCTGAAGCCTGCCTACAGCAATTTGTAAACATATGGCATTGGG ACATATCTCTGAGCCCATCAACTATTTGACACAGATTCTCCTTTTAAACA
WI-5252	119 A	C	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAAGAGTCTTGGGAAAGGATTTGTGATGATCATTG AATCTGTTTAAATACAGAAATTAATACTGAATACCTGTGTGAATCATTGCTTTT/A/CJTACCATGTACA TATTATATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61 A	G	CT	TAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAGGAAAAATGATAACCCAGGACTGTTGTTCAAGCAATGCTAGAAAAATATGCCTA/GJ/C CAAGTAGACAACCTTAAGCACCTAAGGCAGAAATGAAAGTTTCTCTCTTGTCATTAGTCCCTCTATTCA ATTACCAATTTATCGGGGTAATTAACACTGGAAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT TACAGCTTTTGTCTATGCT
WI-5257	77 C	A	GCAAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACAGATGGGGCAAAATTAAGCATATGAAAAATACCAAGTGTGGCAGAGGCATG AAGCAAAAGAGG/C/AJCTTTTCATCTGCCCTTGGTGGGTTTTTCAGTAACCTGCAACATGTCTTTGCCTCC CGGATGAAAAGATACCCCTTCTATGACTCAGCAATCCACTCCTAGGTATGCACCCCTAAACATGGGTG GCAAAAT
WI-4649	50 C	T	TTCCGAATG	TGTACTAGGTG TACTTACAAGA AATCATC	TCACTGTTTAGAAATTTCTTCTCTCAGTGAGACCATTCTTTCCGAATG/CJTGATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAAATTAACAAGTACTTGCTACCTGAATTTGTATTTTTTAA AAAATCCTCCCAATATTG



WI-4650	148	A G	GCACAAAGAA AGTATAAGTT G	CTGAAGTGTTA AACTGGATTGG G	AACTGTGGGATGTTATGTTGTTATTTTCTGGAGAGTCAGTTACTCTCACTAGATCATAAAGGG GACTTGGGAACCAAAAGTATCTCAAGACATTTTAACTCTAGAAGCACAAGAAAGTATAAGTTGTCTC TTATATTGCTTTTAA/GTCCAAATCCAGTTTAAACACTTCAGTAACGTT
WI-4677	82	T C A A A	TCCAAAAGTG ATTAGGTGAA CTT	TTCAACAGTG TCATTATTCAA CTT	AATTGAGATTTGAACATACGTGACATTTTGGAAAAATTTGCCAAAAAGTGATTAGGTGAAAAAAT GAGTTGAAATAAATGT/CJAAGTTGAATAATGACACTGTTGAAAAATGATGAATCTGCTTTCAATTCA CATGGAAGGAGACTAGAACACAGCAGGTTTATAGGGGAATACTCAT
WI-4698	135	C G ---		---	ATGATGTCTATCATGAGGAATCTGTAGAAAAATTTTACCTGGCAATTTGATTCAAATAAAGTTTGCC TCACCTGGGAAACTGCTTATCTTGATGTGACGTGACATTTCTTTCTTTTGACGGAAAGAAACTTCAA C/GTTTCGAGAAGGCTTAGATTATATCGCTGAAGCCCATCTG
WI-4722	88	G A	TGCATATGG AACACCACAC G	AATATGGAATC TGCATTCAGTT G	CTTCCCATTTCTGCCAGTTAGATGACTGCTCTCCACCAGCCTAGAAAAAGATGGGAGATTATTTC TGCATATGGAACACCACAC/GA/JCAACTGAATGCAGATTCATATTGAATACCTGGGAAATCAGTGA AAG
WI-2020	145	C A ---		---	GCCACAGTAAAGAGGAAAAATGGAGCCATGTAACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGGTCAGTAAATCAGTTTGTGATGTTGAGATTTGAGAAACGTAATTTAGTAAACCATGGG TCAACTATGAT/CJA/JCCAAAACAGCAGTGTGTCTAAAAAATATGATAGTTTCTCTCCTGTCCACC GCAATGAAAAGGAGTT
WI-2028	176	T C C C T G C T C A T C	TGTTACGTT C CCTGTCTCAT C GAA	GGTTGGAAACT CAAATTACCTA GAA	GACTACAGCGCACAGACAGGCAATTTGTGTGGCTTGCACAGGTGTTGGTTTTGTGTTTAAGTTAGATT TGAATCCTTTAAAGAAAGAAAGTGGCTCTTCACTTACTACAGACCTCATCTCCTGGTCTCTTG CACCCAGTCCACTTCACCTGTTTACGTTCCCTGTCTCATCT/CJTTCAGGTAATTTGAGTTTCCAACC TGTTGG
WI-2033	183	T C A	GGGTGCTAGA ACTAATCCCTC A	CAGTGGTTCCA CGTTCTCC	ATGTGATGAGCTCCACATTCGCAGATTCACCAACTATGGATAGAAAAATATAGTATTCCTCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAAATTTTCCAAAGTTATACAGGACCAGTGTGGAAATTT AGCATTCTGGGTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCAT/CJGGAGAACGTTGGAACC ACTGATATACCAAT
WI-4745	131	T C ---		---	TTATGGATACATGTTTCTGTGGAGGACAAAGATTGAAGCAAAAGGACAAAGGAGATCAACTGGG TAGAATAACTCATCGATCCACACAGGCTCCTCCACCATTCTCCATCCTACTTCTACTCTGAT/CJ AGGCAGACTTATATGAAAAAAGGGA
WI-2034	150	T C C C A A G G A C	CCACAGTGCA AGAGTGCAGGT CC	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGCTTTCAGAGTCCCTGGTACTGACAGAGAAGGCTTTGAGGACCATTGTGGCGCCAAGA CCTCCTTCTCGGTTTCAAGTGAAGAGCAGATGAATCTTCTTCTACAGCAGCTGAGACTTCAACCA CAGTGCACCAAGGACT/CJGGACCTGCACCTCTATCTTTACCCCTTCCGACACCCAGATGCTGAGATGCC ACACTCTGAGTG







WI-5370	143	T C A T A A A C A A	A A T A A G A T G G T A C C T T A A C T A	C A A A G T T G G T A C A G A G A A T T T C A A A	T G C A T G T T A C T T C T T G A A A T C A T A A A G G G A T C T G A G A G C C T A C A G T A T A T G G C A C A T T A A C C A A T C T T T T G A A A T T A C C T G T A T C C C A T C A T G T T C A T T T G C A A A A A A A A A G A T G G T A C C T T A A C T A A T A A A C A A T C T T G A A A T T C T G T A C C A A C T T T G C T T T T C
WI-9711b	423	T A		---	G A T C T C C T C A T C C C T C T C C A G A G A G A G A G A G A A C A C A A G A A A C G C C T G G T G C A G A G C C C C A A T T C C T A C T T C A T G A T G T A A A T G C C C A G G T G A G A G A C G C C T T G C T G T A G T G G G A A A G C A C T G G A C C T C A A C A G T T G G A A A T G T T G A G T T A G T G T C T G T A T C C T T G A A G C T G T G C A G C A G C T T C A G T T T C T T G C C T G T G G A A A T A T T T C C C T G A T A C T C T T A A A A T T T G A A T G
WI-9711a	390	C A		---	G A T C C C T C A T C C C T C T C C A G A G A G A G A G A G A A C A C A A G A A A C G C C T G G T G C A G A G C C C C A A T T C C T A C T T C A T G A T G T A A A T G C C C A G G T G A G A G A C G C C T T G C T G T A G T G G G A A A G C A C T G G A C C T C A A C A G T T G G A A A T G T T A G T T A G C T G T C T G T A T C C T T G A A G C T G T G C A G C A G C T T C A G T T T C T T G C C T G T G G A A A T A T T T C C C T G A T A C T C T T A A A A T T T G A A T G
WI-9702c	345	G A		---	G G A G A A T T T C A G G G T G A A T G G A C T G C T C C C G C T C C T G A G T T C A C T G C T A C T C A G C C T G A G G T T G C A G A C T G G T C T G A A G G T G A C A G G T G C C C T C T G T G C C T A T T C A G C A A T T C C C T A C T G G T A T G T A T C A G G A T A G A G G T G A A T C A A G C T G A T A T T T G C A A C T T C T C A G T T T A T T C T A A C T T T A A T G A T C T C T G T G A C T T T T A T A C T A G C T T T A A G A G G T T T C A T T C C C A G T G T G C T A C A G C A T C T G A T A G
WI-9702b	344	C T		---	G G A G A A T T T C A G G G T G A A T G G A C T G C T C C C G C T C C T G A G T T C A C T G C T A C T A G C C T G A G G T T G C A G A C T G G T C T G A A G G T G A C A G G T G C C C T C T G T G C C T A T T C A G C A A T T C C C T A C T G G T A T G T A T C A G G A T A G A G G T G A A T C A A G C T G A T A T T T G C A A C T T C T C A G T T T A T T C T A A C T T T A A T G A T C T C T G T G A T T A T A C T A G C T T T A A G A G G T T T C A T T C C A G T G T G C T A C A G C A T C T G A T A G
WI-9702a	179	C T		---	G G A G A A T T T C A G G G T G A A T G G A C T G C T C C C G C T C C T G A G T T C A C T G C T A C T A G C C T G A G G T T G C A G A C T G G T C T G A A G G T G A C A G G T G C C C T C T G T G C C T A T T C A G C A A T T C C C T A C T G G T A T G T A T C A G G A T A G A G G T G A A T C A A G C T G A T A T T T G C A A C T T C T C A G T T T A T T C T A A C T T T A A T G A T C T C T G T G A C T T T A T A C T A G C T T A A G A G G T T T C A T T C C A G T G T G C T A C A G C A T C T G
TIGR- A003N21	49	C A		---	T A T A G T A T T T A A C G A A G C C T A G A A G C A C G G C T G T G G G T G G T G A T T T G G T C A A G C A T A T C T T A G G T A T A T A A T A A C T T T G A A G C C A T A A C T T T A A C T G G A G T G G T T G A T T C T T T T T T A A T T T A T T T G G G A G G G T T G G A T T T A A C T T T T T A A T G T T G T T A A A T A T T A A G T T T T G T A A A A G G A A A A C C A T C T C T G T G A T T A C C T C T C A A T C T A T T T G T
TIGR- A004V30	203	C T		---	A G A A T G G C T A C T T C A T A G G C A G A G C A G C C A C T T T T G G C T A A T T T T A A C A T C C A A A G C T A A T A A T A A T C A A G A A G A A A T A G A G A C A C A T T A C A A A A T A A A T A T G T C T A T T T T G G G A A T A C C T A A T A T C A G A T A C T A A C A A G T A C A G T A T A A G A A T A A A A A G A T A A T A A T C A C A C A T A C C T T C T A G G T A G T A G A A A A G C G T C T T C T T A G G T A G T A G A A A A G T T



TGR- A004W22	232 C A ---				GGATAATCAGTACAATAATGGGACCTTAAACTGCTGTGATGCGAGGTGGGGCTGGGCGAGTG CCCAGGCAGGGAGGAGGAGTGGGACAGGGATGCTCAGTGTGGAGCCACAGCCCTGGGCTCTGGA TGGGCGCATGGGAATGACCAGGTTCCACATCATGACAGAGGGGCTGTAGCTTGAGTCCAGACAG GCCTGCCACATTTGGTGTGCTGCCCGCCCTA[C/A]CTGGAGATGCTCTCTAAAA
TGR- A005D24 b	138 C T ---				CATAGAAAGGAGTCTTTGAGTATTGACAGTTTGAAAATCTCTTTGAGATAATTGATTTCAATTC TGTGGCTTTCAACCTCCATTTACCTCTTGTCATCCAAACATCTTTATAGAGAAATAAACCCAAATTT CTC/TJTTTCAACCATTTAGTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAACTCCTTACCCTTAAATAATTAGGAAACAAT
TGR- A005D24 a	123 A G ---				CATAGAAAGGAGTCTTTGAGTATTGACAGTTTGAAAATCTCTTTGAGATAATTGATTTCAATTC TGTGGCTTTCAACCTCCATTTACCTCTTGTCATCCAAACATCTTTATAGAGAAAT[A/G]AAAAACCCAA TTTCTCTTTCAACCATTTAGTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATTG TTATGTTAAATTCATAAACTCCTTACCCTTAAATAATTAGGAAACAAT
					TGAGTCTGAGCACGAGTTGACGCCAGGGCCAGTGGGAGGGTCTGGGCGAGTGCACCTTCGGGGGCG GCATCC[C/G]TTAGTTTCCACTGCCCTCTGTGACGTGAGGCCCATCTTCACTCTTTGAAGCGAGCAG TCAGCAITTTAGTAGTGGTTCTGTTCTGTGGATGACTTTGAGATTATTTCTTTCTCTCTGTTGGA GTTGTTCAAAATGTTCTCTTTAA
U03735	74 C G ---				GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAGAAAAA[C/C]CAACAGCAAAACAAACCCACA CAACCCAAACCGTCAACAGCATATAAAATCCAAACATATTTTATTTTCACTTTTATGTCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTTATTTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTTCC
U39840b	42 T C ---				GGTTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAGAAAAATCAACAGCAAAACAA[C/C]ACCACA CAACCCAAACCGTCAACAGCATATAAAATCCAAACATATTTTATTTTCACTTTTATGTCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTTATTTGATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTTCC
U39840	56 A C ---				GTGGCCATCGATCTGGACCGTCCCTGCCACCTTGCTCCCG[C/G]ATGAGCACTGCGTACAAACATCCA AAAGTTCAACAACACCAGAACTGTGTCTCATGGT
WI-8997	41 G A OCCC				TATACCACCTCCATTTGATGATGGAATGCTGCTGTTCTATGACCAACTTTATGGCTAGATGGTTCAGAA AGCACCCAGTTTCATGATAGGCAGTTTCAGGTCTATGTTGACTTGATGCCAGAGTCAAAACATTCAG TTTCCACCAAGGCCAGTAACAGGCCAAGAGCTGCTCTCAAAAG[C/G]AGAGTAGTTATCTGCAGA AGATGGCAGGGCCTTGCTCCGAAAGCTAGAGACCGCCACTGTGATTCACCT
WI-7008	180 A G ---				
WI-9005	26 C T TGGGAATCT				GGTCCCACGAATTTGCTGGGGAATCT[C/T]GTTTTCTTCTTAAGACTTTTGGGACATGGTTTGACTCC CGAACATCACCGACGCTCTCTGTTTTCTGGTGG



WI-7593	46 G A ...	...	TTTGTGCTCTGGACACCCACTGCTCCAGGATGAAAGGAGAG/GAATGAGATCAGTTTTGGG CACTTCCTCTTGAATATAAAGAAATCAACAAGTTACAGTCATGTTGGGACTTCTCTCTCCAA
WI-6962	78 A G ...	...	AGTGCATCTTGGGGAAAGGCTCCAGTGTATCTGGACAGTTCCTTCATTTTCAGTGGGACTCTT GATCCAGAGA/GAGACAAAGCTCCTCAGTGAGCTGGTGATATAATCCAAAGACAGAACCCCAAGTCTCC TGACTCCTGGCTTCTATGCCCTCTATCTCTATCATAGATAACATTTCTCCACAGCCTCACTTCATCCAC CTATTCTGAAAATATTCCCTGAGAGAGAACAGAGATTTAGATAAGA
WI-7059	43 C G ...	GCTCTGCTG GGTCA	GCAGAGAAGAGAACCATGCCAGGGGAGAGGCCACCCAGCCATC/GGTGACCCAGCGAGGAGCCAA CTATCCCAAATATACCTGGTGAAATATACCAAATCTGCATCTCCAGAGGAAAAAAGAGAAATAAA GATGAATTGTTGCACTCTTAAAAAA
WI-9063	53 A C TT	TCTACTTTCTG CCCTTGGGT	AGCAGCCATCACATGATCTGTTTTTCACCACTTCACTGAAAGACACCAATTTAT/GTACCCCAAGGG CAGAAAGTAGAACCTTACTATTCAATTAATGTTTGACACAAATTTGGAATTGTC
WI-7079	293 T G ...	...	AAGGGCATTGAGACTATAAGCAGTAGACAATCCACACATACCATCTGTAGAGTTGGAAGTGCATT CTTTAAAGTTTTATATGCATATATTTAGGGCTGCTAGACTTACTTCTCTATTTCTTTCCATTGCT TATCTTGAGCACAAATGATAATCAATTTATACATTTATACATCACCTTTTGTGCTTTTCCAAAGGCC TTTACAGCTCTGGCAATTTCTCGCCTAGGCTGTGAGTAACTGGGAT
WI-9074	38 A G AAAAG	GACAGATTTT GACCTAGTTCC TT	TGGATCCCGAGGTAAAGTCTTTTCTCTAAAGAA/GAAGGAACCTAGGTCAAAAATCTGTCC GTGACCTATCAGTTATTAATTTTAAGGATGTTGCCACTGGCAATGTAACTGT
WI-7104b	249 C T ...	...	GGAGTTGCCCTTCTTAAGGAAGGAGATCTTATCTTCTGTTGGCTTGACCACTACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCTGAGGGCAGCCGGTTCTACTTTGGACTGAGAGAAGGGAGCC CCAGGCTGGAGCAGCATGAGGCCAGCAAGAGGGCTTGGTTCTGAGGAAGCAGATGTTTCATGCT GTGAGGCCCTTGACCCAGGTGGGGCCACAGCACCAAGCATCTTTGCTTT
WI-7104	157 C A ...	...	GGAGTTGCCCTTCTTAAGGAAGGAGATCTTATCTTCTGTTGGCTTGACCACTACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCTGAGGGCAGCCGGTTCTACTTTGGACTGAGAGAAGGGAGCC CCAGGCTGGAGCAGCATGAGGC/CAGCAAGAAAGGGCTTGGTTCTGAGGAAGCAGATGTTTCAT GCTGTAGGCCCTTGACCAAGGTGGGGCCACAGCACCAAGCATCTTTGCT
WI-8974	34 C T AAGAACTCA	TGTAGGGCTGA GCTGGC	CATACAATGAGAGCCCTGAGCCCTCAAGAACTCA/C/TGCCAGCTAGCCCTACACCAGTTTCCACC TGGAGTTTCATGCAAGGGCAAGGAGTGGCATGCAAGCTGTTAA
WI-9161	61 C T OCTGGC	GCTTACAGGAG AGACTAGACA GGAA	CTGTGAGGGTGACGTTAGCATTAACCCCAACCTCATTTTAGTTGCCCTAAGCATTGCTGGC/C/TJTC CTGTCTAGTCTCTCTGTAAAGCCAAAGAAATGAACATTCCA
WI-9014c	93 T C ...	...	CCCTGTTCCCATGCTGACCTGTTTCTCTCCCAAGTCACTTTCTCTGTTCCAGAGAGGTGGGCTGGAT GTCTCCATCTCTGTCTCAACTTTAT/C/GTGACCTGAGCTGCAACTCT



WI-9014b	44 C T ---	---	---	CCCTGTTCCCATGCTGACCTGTGTTTCTCCCTCCAGTCATCTTTC/TTGTTCCAGAGAGGTGGGGCTG GATGCTCCATCTCTGCTCAACTTTATGTGCACTGAGCTGCAACTTCT
WI-7023b	206 C A ---	---	---	TCTGAGAGAAATGACTGTGGGAGACACCCCTGCAGATCCTCATGGGTTTGACAGACCCCTGCGTGCT CAGTGCCCTTTAAGTGATCCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCTACGGGTCCCC TCTTTTGGCCCCAGATTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCACAC A/C/AJACACACATCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C ---	---	---	TCTGAGAGAAATGACTGTGGGAGACACCCCTGCAGATCCTCATGGGTTTGACAG/C/CJCCCTGCGT GCTCAGTGCCCTTTAAGTGATCCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCTACGGGTG CCCTCTTTTGGCCCCAGATTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCAA CACACACACATCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T ---	---	---	CTGAAATCCCTCTCTGCCCTGGCTGGATCCGGGGACCCCTTTGCCCTTCCCT/C/TTGGCTCCAGCC CTACAGACTTGCTGTGACCTCAGGCCAGTGTGCCGACCTCTCTGGGCTCAGTTTCCAGCTATG AAACAGCTATCTCACAAGTTGTGAAGCAGAGAGAGAAAGCTGGAGGAGGCCGTGGGGCCAA GGGAGAGCTCTGTATTATTAATTTGTGCCGCTGTGTGTGTGTTA
WI-9171	62 G A ---	---	---	ACATATCTGAAAAATGTTGAAGCCTAAGCCAGGAATAAAGAAAAAGTAGAGATAATAATCA[G/A] TTCTTTACAACCGATGGTAATTAGCTTGATTCACAAGACTTCATGC
WI-9174	47 T C T	CTAGAGGGTA TATAGGACAGG ACTG	---	GTGTGAGACCATCATGGTCCAGTCTAGGACCCCATTCCTCTATTAT/C/CJGAGTCTGTCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGGTCAAAATGAG
WI-7753	52 A G	CAGAGGCTTG AAATACAGGG A	---	AAGCCAGATGCACATCCCTGGGAAGGACATCCATGTTCCGAGAGAACAGAT/GJATCCCTGTATT TCAAGACCTCTGTGCACCTATTATGAACCTGCCCTGCTCCACAGAACACAGCAATTCCTCAGGCTA AGCTGCCGGTCTTAAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
WI-9186	76 G A	AAAGGGAAG TCTGACCTAGG T	---	AAAGAACTACAGAGGACGATGTCACAAACAAAAATGGCATCACCTGTCAAAAATGGAGTTCCACT TCTCCCGCA[G/A]ACCTAGGTGACACTTTCCCTTTTCATCTT
WI-9193	94 G A CA	AGAAATATTGT CTGCCCTTAAG TAGGGGG	---	TTGGACAAACCTAGAATTTTCTCCCTTATGTATCTATCGATTGTGTAGCAATTTGACAGAGAATAA CTCACAATATTGTCTGCCCTTAAGCA[G/A]TACCCCTTACACACACACCCCTGTGCTC
WI-9015	48 C T ---	---	---	TTTGATTGATATCGTGAATCCTCAGCCGAGAAATTTGGGCTGGATTG/C/TTGCTTTGGTTAATACAT CTTTCCCTAAAGAAGATAAACACAAAATCCATTCCAGGTAGCTCGGCACCACTAAGAA
WI-7254	37 A G	GGTCTGAGAG CATTAGGGA	---	GGAGCCAGGAGACAGGGGTCTGAGAGAGGAGCCAC[G/G]GTCCCTAATGACACCCACTCTAGCC CTGAGGCTGTGCCCTCAGACTGGGGAAGAGTCCAAAGGAGGGGAGCAGGCCACTCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG



WI-9231	32 G	CAGTCCCCA GATTGA	CAGTCCCCA ACTCAGAC	GTGACCCCTGTGAGGTGAGTCCCCCAGATTGACGCTGAGTGGGCAAGTGTGTCAAAGGGGG TGCCCCCAGGAGATGAGGCTGAGAGCAGGAGTTGAGCCGGAAGTCA
WI-7836	120 T C	CAAATAACA ATGCAACGTT C	GCCTCAGAAC CAAGATTAGA AATC	TTGTTGGGAAATAGAGAGTTGAGATAAACACTCTCATTCAGTAGTTACTGAAAGAAAACCTCTGCTA GAATGATAAATGTATGCTGCTATAAAGTCCAAATAAACAATGCAACGTTCCGTCGATTTCTAAT CTGGTCTGAGAGCCATTGGTTTCAAGTTGAGCAATCCCATACCAAGCT
WI-7286	65 T C A	CAGCTTCAGCT TAAGTACAG A	AAACAATCTA ACCAGAAAGCT TTAA	TCCATTCCTTTGGCCCTGCAGCATGTCATGCTCCAGAAATTCAGCTTACGCTTAACTGACAGATT/C GTTAAAGCTTCTGGTTAGATTGTTTACCTTGGTGATCATGCTTTTCCATGTGTACCTGTAAATATT TTCCATCATATCTCAAAGTAAAGTCA
WI-7858	91 T G TAAAT	CTAAGCATGT ACGTGAATTT T	CCCAATTTTA TTAAAAGTTTA CATCTAT	CAAAATCTTGGAATATCTCAAATGTTAATAACAATATGAATTTTCTCATGCATACTATTACTACT AAGCATGTACGTGAATTTTAAAT/GTATAGATGTAAACITTTAATAAAATTTGGGGTGTGG
WI-7860	50 C G	CGTACCTCCAA ACATAAATTGA TTC	---	GAAGATTAGGGAGGGGTGCTCTGTGGTCTCTCCCTGCCCTCTCCCA/C/A.GTGGGGAGAGACC TGATGTTGCCAAGTCCCTGGACCTGGACCCAGCTACTGGGCTTATGGGTTGGGGTGTAGGCAGG TGAGCGTAAGTGGGAGGGAATGGTAAGTCTACTCCAAACCTAGGTCTCTATGTGACAGCCAG ACCTAGGTGCTCTCTAGGAGGGAACAGGGAGACCTGGGGTCTGTGGAT
WI-9064	29 A G TTC	CGTACCTCCAA ACATAAATTGA TTC	GCCTGAGTGA AGTCTCGCAGA	CAAGGCGTACCTCCAAACATAATTGATTG/A/GTATCTCGAGACTTACACTCAAGCAATCCTGAGG AATAGTGGGAGGGCTGGCTACTGCTCTCTGCACTCTGCTGCTTG
WI-7307	128 G T	---	---	CACACTTGCTGTTCTCAGTGTGGAGGCTCTGGCAGGTGAGGCTGGGTAGCCGGGGTTCACACA GGGCCAGCCCTGGCAGGGGTCTGGCCCCCAGGTAGGGGAGAGCAGTCCCTCCCTCAG/GTAACT GGAGGAGGGGACTCCAGGAATGGGAAATGTGACACCAACATCCTGAAGCCAGCTTGACCCCTCCAGT TTGCACAGGGAATTTGTCTGGGGCTGAGGGCCCTGTCCCCACCCCGCCC
WI-9274	25 C T G	GAAATGTGAC TTCACTTTGGT G	CAGGTAGAATT TTCTGTCCATT G	GAGGAAATGTGACTTCACTTTGGTG/C/TJCAATGGACAGAAAATCTACCTGTGCTACATAGGAGAA GTTTGGAAATGCACITTAATAGCTGGTTTACACCTTGATTCGAGGTGGAA
WI-7313e	266 T C	---	---	AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTGATTAGTAGGCTGTGATTAAAGTCTTAAAT TGTTTGCAGCTTTTATGTTTATATCATAGGTATAGGTGGACCTAAATTCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACGATTTTGTATGTTTTAAGTAACCTATTATCTCTGGAATTCATG AAGGTGAATACTGTTTTGTAACTGAATAGAAATGTATAGCGATGA
WI-7313c	256 C T	---	---	AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTGATTAGTAGGCTGTGATTAAAGTCTTAAAT TGTTTGCAGCTTTTATGTTTATATCATAGGTATAGGTGGACCTAAATTCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACGATTTTGTATGTTTTAAGTAACCTATTATCTCTGGAATTCATG AAGGTGAATACTGTTTTGTAACTGAATAGAAATGTATAGCGATGA



WI-9281	68	G A	---	---	ACTGTGGGAGACTGTGAGGATCCAGGATTCAGTATTCCTGGCCAGAGGGCCCTTGCTGGCTACTGG [G/A]TGTTAGTTGCAGTCCTGTGTGCTTCCCTCCTTAAGACTGTGTC
WI-7848	142	A G CTC	GTATATTACA ATGATCACC G	CATTATTG AAAGCTATTCA GACA	TTCTGAAAATATAACAGCCATTGAGCTATTAAACCTTGTAATTTTAAATTTACAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTGCGTGACAAATAAACATTAATGCTAACACTTTTAAAA ACCGTCTC[A/G]TGCTGAATAGCTTCAAAATAAATGTGAAATGGT
WI-9304	70	G A ACTGA	GTATATTACA ATGATCACC G	CCCCACAGAAC TATTGTAAAC AA	TCACGTTTGGTGCTTCTCAGATTCTGAGGAAATGCTTTGATTGTATATTACAATGATCACCAGCT GA[G/A]AATATTGTTTACAATAGTTCTGTGGGGCTGTTTTTGT
WI-7933b	314	C A	---	---	TTACAGAACTTGCCCTGTGCCTGTGTGCCCCATGCTAGGGGGGAGGGGCTTTTCCTTCTTCTTCC TACCTACCCCTTTTCTTGGCCAGGGCTCGTATCTACCTTCCCTTGTCCCTGGGCTGGCTGCAC AGAGGATTGCCCTTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTGCACAA AGTCTAAGGGACCATGGCTGCCTGGCTGGGGAGGAACCATAGCTCCCT
WI-7933	96	G C	---	---	TTACAGAACTTGCCCTGTGCCTGTGTGCCCCATGCTAGGGGGGAGGGGCTTTTCCTTCTTCTTCC TACCTACCCCTTTTCTTGGCCAGGG[G/C]CTCGTATCTACCTTCCCTTGTCCCTGGGCTGGCTG CACAGAGGATTGCCCTTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTGCA CAAAGTCTAAGGGACCATGGCTGCCTGGCTGGGGAGGAACCATAGCT
WI-7374	182	T A	---	---	CCAGATGTGCCCATCAGTTTTTCTGAGGCTTTGTACTTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTGACTTTGTTAAATATTTGAAATGTAATGAAAGAAAGTACTGTATATTA AAAGTTGGTTGAACCAACTTCTAGCTGCTGTGAAGAATATTTGTTA[A/G]GTGTTAGAAATCAGAAATTTGATTTTGA GAT
WI-9343	78	C T CCTCTGCCA	CCAACAACAT CCTCTGCCA	AAATGAAACTT ACGTTTGTG TG	GGTCTGCTCCTGCTACCTGACCCCTTCCCTTCTCTCTGCTTCTCTCTCATCATCATCCCAACACAT CCTCTGCCA[C/T]ACACAACAACAAACGTAAAGTTTCATTTGGGCAAA
WI-7386b	104	T A	---	---	CTATATGTGAGAGGCGTGATATCTGGATGGAAGTTGGGCTGGATGATCTCCAAAGTCGTTTCAACTCT TAAAGACATCTTAATCCTGAATGTAACAATTTGTTA[A/G]GTGTTAGAAATCAGAAATTTGATTTTGA ACTTGAGTAATTCATCCTT
WI-9357	75	A G	---	---	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTTCATGAAAACCTGAAGAGTTTCACTTTGTATTAT GCTCTT[A/G]TGATTACAGACTGATCCAGACAAACCTTTGGGAAGA
WI-9360	79	T C TTGG	CTTTAGAAA TCTGCTTTAAC A	CCTAGGGAACA CAATTAGAGGA A	TGAAGGGGTGGCATCTGTGTTTCTGATGCTTACTACAATATGAACCACTACTTTAGAAAATCTG CTTTAACTTGGT[C/A]TCTCTCTAATTTGTTCCCTAGGAAATGACTGTCCCAAG
WI-7423	107	T C GTTC	TTGCTGGGCTGT G	GGTCCAGAAAGA G	TGCTCCCTGTCCCATCTGCAGTGGACCCCGAGCCACCCCTTTGAGGAGGTGGGTGAACCTGCTCCTT GGCAGGGATTGTGACACTGCAATGCTGGGCTGTGTTCC[C/G]GGGCTTCTCTGGACCTTGCACCGTG GATACAGGGCCATGTGCCATGGTATTGGGCTCTGGGAGGTGGGTGAAATAAAGGCATACTGTCT



WI-7424	131 T A	CAAGAGAGAG AGAGGAAAGA AAAA	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGAGGGAAGAGCAGAAAGTTAGAGAAAAAGCCACCGGAGGAAAGG AAAAACATCGCCAAACCTAGAAACGTTTTCATTCGTCAATCCCAAGAGAGAGAGGAAAGAAAAA T/AJACAACCTTCATCTCTTTGCACGTTTCATAAACATCTACATA
X86400	118 A C	---	---	TCCTGCAAGAAGTTCTCAAGCCTTTTGGATTTTGTGCAATAAAGTACAGCTTTGCATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACCTTCTCTTAATTTAAGTGAGA/A/CJTCTTTTAAACACCT GTTAAATTTAATGTAGCAGCTGAGAATCTAAATAATATGTACCACCTCGTTTATTTGTTTCATTCATCCA TCCCTTTTCCCATGAATTTCA
WI-8053	242 T A	---	---	GTGGCCACTACATGTTATAGAAACCATCATCTTGTACACAGCAGCAGCTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGAAAGCATTAAGAGTGTCCTTAAAGGGACTTTTAAATCAACCTAA TAACTCTAATCTGCTGACTTTTAAAGATCTAAGGTCATTTAATACATGCTGAAAGGGTCACA ATTAACTCTTTGATCTTTTACTCACTGTTAACTTATATAAT/AJTTCAGAAC
WI-6190	165 G A	---	---	TACACAATGAATTCCTTTTATTTCGGTATGCATCCACATTTCAAGCATTTAGTGTCTGTAACAGCAAG TGGAAAGAGCGCAGCAATTTGCCAGGAGGTCAAGCCCAATTTCCGGGATCTGCTGTGCACACCCGG GTTCCCTTCTTAATCCCTGCTGAGGATCTTG/GA/GAAGCAGCAGCAGCACCACCAAAACCAAGGCATGCA COGGATTCAAGGTTCTTTTGTCCAGTTGTCAGATTCCAAACTAGACCCCA
WI-6275	148 G C	---	---	AACAGTCACCACCAACCATGACAACTGCCAGGCAAGGCTTCTCCCTCCCTCTTTCGCTGCTCCG ATGTGCTAGTCAGCAAGTCCGGGAGGCACCGATGTTAGCTTCGCCCAAGGGAGTATTACAGAGA GAGGCTTGGGAAAG/GC/GGAAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAAACTG ATTTGCTTTTCAGTAACGGTATGTCTGAA
WI-6421	41 G T	---	---	ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTGTGATTGT/GTGGGCTTCTGTAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGACGGAACCGTACCTGAGAGGGGATGGGGGCTCTCTCACAAAA GAATATTTGGGGCAGAAACCTGGAACCTGGCCACAGGGACATCCCAATATCCCTCCTCCTCAGGG CTCACCCCGACATCCTCAGCCAAATGAAGGCTCTGAA
WI-6905	215 T A	---	---	GGGTGAGACGGGTTTATTGTGCACATTTACACAGCTCAGCGCTGCGGCTGGCAGCGGCCATGCTC CTGTGGTGGGCTGCTCTACAAGGGGCTTCACTTTTCTCCACACATGTACAGTCAGTGCTCCAA GGTGATGGGCTACAGTGTGCTCAGTGAGTCTGTACACACATTTTACATAAATACACACGACTC ATACATGAAAAAT/AJAGAGCCTAAGGGCCTGTATTTTAAATGAGAAAAAA
WI-9420	202 G A	---	---	AACTTGTTTACAAAATAGGCTTTGCAAACTTCAATTACTGAATGTAAAGTCAATGACTGTGTTTT TAAAAATATGTACCAAGGAAATACAAAATGGATAATGATCATTTTTCATGCTCAGGAGAACAGCAC AGAAATAAGGATACTGCACAAGGTGCAAGGAAACCGGAACCCATTGTGTACACTGTCTTCACACAG G/A/GCATCTTCTCACCTTAACCTGACGCTGTGCAAGATGCCTCAGTG



WI-9448	184	G A	---			TGGGGCTGCTTTAGACTTCATTTCTAGAGCAGACACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCTTGCCCATGGTGGTTAAACCTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAAAATGGGCTTGTTCCAAAGGCTGAGAGCTGGCACCAC[G/A]CACTGGTTCTTAA TCTCTGGCTTGGATTTATCCAAAGCGCATGTTCCTAACGTGCCCGTGAGCAG
WI-9470	204	G A	---			ATGTCAGAAGAGACACAGACAAGGAGTTTTTCCCTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGGTTGATAAATCAGATCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCACGAATATGATCTCCCTAAAGCCACAGATCTCTACTAGAGCCGCTGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCCTCAAGCTCACAGGGCTCACCTTCCCAAG
WI-1245b	201	G T	---			GATGATTTCTGAAGTCTCAGCAGCCCTGATTTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCTGATGCAGATCTGCTGAGCCATGTGCTGGCATCACAGGGGTGGT TTATTAAATTCATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGC[G/ T]CTAAGATCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T C	---			GATGATTTCTGAAGTCTCAGCAGCCCTGATTTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGT[G/C]GCTGATGCAGATCTGCTGAGCCATGTGCTGGCATCACAGGGGT GGTTATTAAATTCATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGC GCTAAGATCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G A	---			TTCAAGTATAAGGACAGGCTAGAAACAAGCGTTCCCAACCTGGCAACCAATGACAGTTTGGACCAAA TAACCTCTTTGTTTCAGGGGACTGCTACACATTTGGGATTTAGAGCCCTCGTGGCTTCTACCCA CTAGATGCCAGCA[G/A]CACAAACACCCCTCCCAACAATCATGACAATGAAAATGTCTTTAGACATT GCCAAATATACCTTGTGGGACAAAATGGCCCTGATTGAGAACCCTGGTT
WI-5385	110	G A	---			AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCCAATGGTGGGATTTGAAGAGG GAAGTCTCGATAATTTTAAACATATGTTTCTTCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TCTTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCCCTGAC CCCTGCTACGGGAAACATTGAATGCA
WI-5403	199	T G	---			ACCAACCGTTGGCAAGGCTCCCAAGACTCACACCCCACTTTGGTGCTTACCCTATGCCGGGTG GGATTGAAGAAATAACCAATAAATTGCTACAAATTTTCCAGTAGTTACCAGGCACCGCCTAT TGGAAGAAATCATAAATGTAACCCCTACAATGTATTGCTCTGTGGCTTGGTCCAGGCATAGAGTT/G JGGCTACAACCCCATTTTATCATTTGAACCTCAGAAGCATCCAGTTGGGGCT
WI-5801b	157	G A	---			TGGTATTTTCTTTCTTAAATGTTATGATTAATTAGTGCTTTGTAGAAATTTGAAAAAATGTAAA TCAGAGAACAGAGAAAGAAATAAGTATAGTTGAAACCTCTAACAAATTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCTGGGA[G/A]AGGGGAATGAGAAAAGCACACCAAGAAAAAAGTGTGT GGCTTAAGGGAGGCCAAGGAAAGTTAAGT



WI-5801a	48 A G ---	---	TGGTATTTTCCTTTCTAAATGTTATGATTAAATAGTGTCTTTGTJAGJGAATTTGAAAAAATGT AAATCAGAGAACAGAAAAAATAAGTATAGTTGAAACCTCTAACAAATTTTAGATTTTAAAGGCC TAGGGAAAGAAAGAGCCTGGGAAGAGGGAATGAGAAAAGCACAAACCAGAAAAAAAGTGTGT GGCTTAAGGGAAGCCAAAGGAAAGTTAAGT
WI-5696	61 C A ---	---	TTCTATTTAAATCCTGTGCCCATTCGAAGACTGCATTAGTCTGCATGAGCCTTAGTTTCJAJTAA AAGCCCCCTCACCCGAGGACAATGTTCAGAACTAAATGACTGCAGGTGAGCAATTCCTGTATTA TACAACTGGGACCAAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGTGGTGAGTTTATTTAACTT
WI-7461	153 C T ---	---	TATTACTAGGTTTCATAGAGCCCCGTTGTAATGATAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTCCTAAGCTCCTCACTTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCTG TGGCAGGGACTGTCTCTCTGTTCCCTGTTGGGTCCCGGAACCCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTAGCATGTGTGCA
WI-9716	221 G A ---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAATCTGAGGCTTTAATGGTCCCTTGCTCTAAC GCTTTTGGTATCTTCTCTCTGAAGACCAACCCCTTCAAACCTCTCAGAACACAGGCAAGATGCAT ATTCGTAGTTTTCAGATGTGACTTCTACATCTCGAAACCTAGATGAGTAGGCTCTCTTCACTCT CAATTGAAAATTTAGAAJGJAAAAACACCTAATTGGCTCATCTTGGATCA
WI-9760	49 C T ---	---	TTTTCGTTAAGTCTGTGAAGCCACACAGAGTGATCTACTCTCTTACJCTJAAAGTGTACTTTGCA TATATTTATGGGATGATTCATCCCTACTTAAGATTTCTCTCTCAGGTAAATATCCATTTCTCT TTGTTCAAGGATTTCTTATTTGGCCTCTTTCTAAACCCCTAACCATCTGCTTATCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31 A C ---	---	GAAAAACCTCGTTGGCTCAAAGGAAACTGTAGJAJCAAATCTTTTATTTTATTTTGTATTTTAACTC AAAGAGTGGAGTTTGCAATTGACCTTGATGGCACGCTGCTCTTTGTTTGGTGAAATCCTCTAGT GGGCACTTTGCAAAAGCAATTTTAGAGCAAAAGGTGGTGGCATGGAGTTGTGTGAGGTTGCTGAAAAG TAGCAAAATGGAAGAAAGGTTAATGGA
WI-10312	41 A G ---	---	AAGGCCAGTGGGAAAAGCAGACAAAACACTCCAAGAATACJAJGAGATATAAAACATCATCATCA GTAGAGATGGGATGACCTAGGAGGTGATGCTGATGAGGGCATGTGAGCCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTGTCTGGTGAGTCTTGCCAGTCCCATAGTAGGTGTTCCATAAAATAAG AGTGACTAACTGAGGTAGAGTCACAGAAAGAAATTTCA
WI-11152	179 C T ---	---	GATTCCTTTCGACATGCAGAGCAGATACGGCAAGGCATCTTGGGCATTTGGAAGGAAACAGGCCCTA ATTTCATAGAAACAGACTCTACAAAGGACCAAGTTAAAGGTCTCGACCCAGGGACTGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGGACAAGTGGGACAAAAGGCTTGTCAJCTJCTGTCAAGAAACATTGAA AACAGCCAGTACATGCCACTGATAGA



WI-1968	167	A G ---	---	TGGTGAGGAGCTGAAGGCTGAAAGAATAGTCTCTGCTCTGGTCTTCGTTGGAAATGGATGAGTCCTTTACAAAAATTTTCCCTTGCCATGGGTGTTATGTTTAGAATCATGGAGTTGGAAGACTTAGATTCAATTTGGGGCTGTACAGTTTACTGGAAGTTGTA/GJTGAACCTTGAGCAAGTGCTCTTAATGTCTCTCA
WI-4701	198	G A ---	---	GCCTCAATGCCCTTCCCTGTAA GGGTTCATTTAACAGCCTCCACTGGTCTCAGATTGCACGGAGATGTAAAAATAGGAAGAGATAGAAAAATGGTGCCCACTATTGACTTGATAACACCTACAAAACAACACATTAAACTCCTCCCCACTCTACCGCCAAAGTCTACCTTTTGGTTCTTTTATTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A]CCATGTCATTTTTCAGAAAAGCAGTATA
WI-4823	164	C A ---	---	TTTATCTTTCCAAACCATGTGTGTTTTCTTCACATACTTTACGTAATTTTAAATCATGTCAATTAATTGCACTTACTTGTGGCTACCAGACATTGCTTCCAAATTGTAATTCCTTAACAACAGCAAGCATAACTGATGTCCATCTTTGTATTCTTAAAC[C/A]AAAGAAAGTGCTTTTGTGCATCTGCCCTCTCTGTCTTCTCTGTTTCACCTCCTGTATTTCCTATTCCAGCATTCATGATTA
WI-4860	72	A G ---	---	AAAAACAACCTTCATTTGACATCTAAGAAGATAAAGAAAAACAACGATCCACTGTGTGTTTGCCTTGATTT[A/G]GGAGATAAACCTGATCTCTAAGAAAAATTAAACCAAGCAGTACACTAAAATAGCCTTTGTGTGTGTTTTCAGGAAAGAAAGCCAAATCCAACCTAAGTTGCTAAGAAAAATAATGTTTCATATCACTCTAACTCCACATAGAGCATTAAATAGCA
WI-9705	111	C A ---	---	TGAAAGGACCAGTTGCAATGCTACCAAGGTAAAGTAAATCGAGGGGCGAGGAAGTAGGAGTTGCTTCCGGATGTTGCATAAAATTCAGGTTCTTTAAGGAGTTGCGTGCC[C/A]AAAATTGTTAACACTGATGCCGTCTACAAACGCACATAGAAATCGGTGGTAGATTGCGGTTCTCTAGTAGTAACTAATGTTTAGATA
TIGR-A004Z48	177	A G ---	---	TGATTGTTGAATTTATTGTTGCTGTGTTCTTGGTG CAAATACTCTCTGCTTAGAAGTTGCTCTAGGGCCATGGATTTCATGTAAGGGTGGGCGAGGTGGACTGAAGATCTGTGGCAGGCTCACAGAGACGGGGTGAGGGGAGAGATCGTGGGTTTCATGAGATCCCATCTTGGGCAATACGGTTATCCCGTGGTCTCATACGCCACAGA[A/G]TCTCCAATTTTCAGGGGCTCCC
U17579	34	T G ---	---	GTGGGATGGTGGAGCCAAATGAAGACCAGGTAGATGATGCCACCTAGAGATG GGGATTCATGTGTCTCTCATCCAATAAGCAC[T/G]CATGACCTCAGCCCCATACTCTTTCTTCCC TATGTTCCCAGAGACAGAATAGACCTGGCCCCCTTCTCTAGGGGATCACAATATTGGAAGGATGAGGACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTGGGATCAATTTCTATGGGAGCC
WI-7747b	88	T G ---	---	TGGGAGAGGGATCCTTCTAGTTGA GTGAGAGCGAGGCTGAGCCTACAGATGAACCTTTCTGGCCTGCTTTCGTTAACTGTGTATGTACATA TATATATTTTAAATTTGAT[T/G]AAAGCTGATTACTGTCAATAAACAGCTTCATGCCTTTGTAAAGTT ATTTCTGTTGTTGTTGGGTATCCTGCCAGTGTTGTTGTTAAAGAGATTGGAGCACTCTGA GTTTACCATTGTAATAAGTATATAATTTTAAAGTTTGTCTCTGA



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WI-7805	101 A G ---	---	TTTCTAGGCTGTACAGTCTGATGATGATTTTATAAATATTTCATACTCTTGTGAATTTGGATCTT TTTACTTTGAGCATATATTTAGAAATATGTGTA/GJTGTTAAAGGATCTCCACAATGTCTGCAGTGTG AAGCGAGTTTCATTGTGGAATAGTTTAAACAGTCAGGAAGGCTAACTGGTCAGTATTAATGTGTAGC CCTACCAAAATAGCCAGTAGTATCTGAAAATGAAAAATAAATGAAGTAT
WI-7416	137 G T ---	---	GGCAGGAGATTAGCAACAAGGATTCATTCTGTTACTTACTTGCCCTTTTATCTTCCCTCTTGCC CAGTCCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAAGACACTCAGTGTCTTGCGAGTGT [G/J]CTACTCCTCAGGTGCAGCATACATAACCAAGTAAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACAACACTCAAAAATGGCAATGTCATCAG
WI-140	252 C T ---	---	ATTTGAAGATTGGAGGGCTTTCAGAGGAAATAGATTCAATTTGATCCCCAACTATAATGACA AGTTTTTAATTAGGTGTGATCAAGGCTTCTAAAGTGAAATGCAAGTTGTTACCAGTAAAGTTTATA TCTTCCATTGAGCCAGCTCATTGGCCAGAAAATTCAGGTGAGTGGATGGCCAGACTATCTGGCAAG GATGAAAATTTTAGTTTAAAAATGTGTCATTGTCTGTATTGGCATTCCT[C/
WI-198	218 C T ---	---	GAGGCTTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCCGAGTCCCGGATCAAGTGTGGCAAC CATGATGGAAACTCTTGCCATGGTTTAGTACCCCTGGACCAAGTAGTCAATCCATCCTGACTTTAAAA TTCTAAACAGCCTTTGATGGGACAATCTCTGCTAAAGACTAACCACTTCTTATCTTATCTTCAGCTA CCTGCTCCCTTTCT[C/J]TTTAAACAAGCATAGAAATATCTGAACAAC
WI-205c	146 T C ---	---	TTCTGTCCTCCAAAGACAGATTTTAAAGAAAGAAAATAGCCCTCATCTCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTCAAT GCATGAGTTTG[C/J]CCAAAGGCTTGATGGGAAAATCTCAACATTTGTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATATGCCCTTTATTTTGTAGTTCCC
WI-205b	146 T C ---	---	TTCTGTCCTCCAAAGACAGATTTTAAAGAAAGAAAATAGCCCTCATCTCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTCAAT GCATGAGTTTG[C/J]CCAAAGGCTTGATGGGAAAATCTCAACATTTGTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATATGCCCTTTATTTTGTAGTTCCC
WI-234	165 G C ---	---	GAAAGACTGAGTTTCCAGGAGGTTCAGCCGTTTCTCTCGGGCCATATGGCTAATAGAGAGCTTGAGCA GGGATTCAACCTGTTTGCAACCCCAAGTNCCTTCCAAGAGGTCTCAGACTACCTCCTCCATCTCCCT CTCCCCACACACACAAATACAGAGATT[G/C]AATTCAGAGGCCAGTTCTAGGTGGGCTTTGAGC AATCATACACAGTAATCTCTGGGCTTTAGTTTCTCAAAATGGAAATGG
WI-276b	25 A G ---	---	AGCTTTTGAAATCCAAAAACACAT[AG/C]TTGACTCTCTTATCCTCTCTTGTGTAACTATCTCC CTGAGGCAGAAAATACAGAACACCCCTGTGGCTGCTTGAACGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAAAGCATCTCTGCTGCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGCTTATCCTCTCTGCTATCCTGATGACTGGGCAAA



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WI-276	25 A G ---	---	AGCTTTGAAATCCAAAAACCACATAGCTTGACTCTCTTATCTCTCTCTTGTGTAACATCTATCC CTGAGGCAGAAAAATACAGAACACCCCTGTGGCTGCCTGAACGGAGGAAAGATGGGGCGGGGAGACAT CGGTCAATGTATCAAAAGCATCTCTCGCTGAAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTGCTTATCTCTCTCTGCTATCCCTGATGACTGGGCAA
WI-427	59 G A ---	---	TTTCCCAATCCACAGGTAAACTAATAATGGATGATAGAAATTTAGAACTACTTC[G/A]GTTT TTCCCTGGGAAATATTCACAAACATTTGTGGTCTGCAATCAGGTTAAAGACATAGTGTGCCA TTTGTCTATCAGACAGGTAGAGGCTGACTCTGGCAGGATTAGTACCCTAGCTGTGAGACTTTATGT ATTCAATTTATAGAGCCAGGGTCTTGCTCTGTCAACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---	---	CTCTTCACTCCAAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCGAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAITCJAATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAACCATAATAATCTCAGGTAATTATGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106 T C ---	---	CTCTTCACTCCAAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCGAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAITCJAATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAACCATAATAATCTCAGGTAATTATGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103 T C ---	---	CTCTTCACTCCAAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCGAGAAAGGAGCCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAITCJAATGGTCTTTTATTAAAAAAA AAAGNTATCTAAAGAGAAACCATAATAATCTCAGGTAATTATGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141 A G ---	---	GTGTAATTTGGTGGCTTGGCACTTTCCACAGTAACTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAAGATGCTATGTTGAAGAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAATTATTAAAC TTGATCTAATATTCTCACAACATAATACCTGAGAGAAATAAGTCTATTAAAT
WI-597b	141 A G ---	---	GTGTAATTTGGTGGCTTGGCACTTTCCACAGTAACTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAAGATGCTATGTTGAAGAGTATCCTTAGGATATTCT GATACATG[A/G]TAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAATTATTAAAC TTGATCTAATATTCTCACAACATAATACCTGAGAGAAATAAGTCTATTAAAT
WI-597	136 A G ---	---	GTGTAATTTGGTGGCTTGGCACTTTCCACAGTAACTTTAGAAATNAAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAAGATGCTATGTTGAAGAGTATCCTTAGGATATTCT GAT[A/G]CATGATAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAATTATTAAAC TTGATCTAATATTCTCACAACATAATACCTGAGAGAAATAAGTCTATTAAAT



WI-811	66 G C ---			TTCAAAATTAACACCATTGGGTATATTATAATTINGCTCTATCATAGTTCTAACCCCTCTCTCTG/ CJACAGTGAGACACCTGCTTCTATTGTCTTGACGTATTACGTATTCGATCAGTCACCCATCTGGA ACCAAGTTTCATTTCTGCTGACCCCTCCCTCTCACCTACTTGGGCTGACTTCCTTCTCTGGGCT GAACCTTCTCTGTGGCTGCCGCTTCTCTGCTTGGGCTCCAATAC
WI-811b	156 A G ---			TGAAGCCCTCTCTATACCCAAGTGCTTTATCTTAAATGCTGTGGTGAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTCATACAGGGGAAGCACCTTGTNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTG/JTTATACATATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCTATGGTTT
WI-881	156 A G ---			TGAAGCCCTCTCTATACCCAAGTGCTTTATCTTAAATGCTGTGGTGAAGTATCTACCCCTTA GGGATATTGTGAGAAATCAATAAGTTCATACAGGGGAAGCACCTTGTNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTG/JTTATACATATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCTATGGTTT
WI-857b	119 G A ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTTCAGTCTTAATTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCGAGTATCTGGCACATCTTTCCCTTTTCATCTCC[G/A]TTGTGTTTGGC CAATAATATCTCCCGAGGACGTCCTCTTCTAATCCCTGAACCTGAGAAATGTTATCTTATGC AGTGCTATGGTTTGAATGTGTCCTCCACAAAGCACACATTAGAACTTA
WI-867	113 A G ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTTCAGTCTTAATTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCGAGTATCTGGCACATCTTTCCCTTTTCATCTCC[G/A]TTGTGTTTGGC CAATAATATCTCCCGAGGACGTCCTCTTCTAATCCCTGAACCTGAGAAATGTTATCTTATGC AGTGCTATGGTTTGAATGTGTCCTCCACAAAGCACACATTAGAACTTA
WI-867	119 G A ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTTCAGTCTTAATTTTGGAGCCTAAGATCAGTG CAACCTCCAAAGGCTCCCGAGTATCTGGCACATCTTTCCCTTTTCATCTCC[G/A]TTGTGTTTGGC CAATAATATCTCCCGAGGACGTCCTCTTCTAATCCCTGAACCTGAGAAATGTTATCTTATGC AGTGCTATGGTTTGAATGTGTCCTCCACAAAGCACACATTAGAACTTA
WI-871b	123 C G ---			TCATCAGACCTGAGATTGAGCATGAAATCTACCAAGGTACCAAAATGTAACCTTGTCACAAACGA ATCTCAGTTTCTGCATATGTAATAATGGGAATGATAAGAGCACCCACCTACCTCATG[G/A]ACTGTT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTATGCACTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCAATATGCTGTTTGTACATAA
WI-871	123 C G ---			TCATCAGACCTGAGATTGAGCATGAAATCTACCAAGGTACCAAAATGTAACCTTGTCACAAACGA ATCTCAGTTTCTGCATATGTAATAATGGGAATGATAAGAGCACCCACCTACCTCATG[G/A]ACTGTT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTATGCACTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCAATATGCTGTTTGTACATAA



WI-884	198	T C ---	---	AGGTTCTGGACTTGATGCTGGGAAACAATTGGTNGTGGAGAAATTCCTATTTTGAGTNTTTACAGAT CAGTAGGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACCTTCCTGATCTATTGGGA ACTTCCTCCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATAIT/C]G ATCCGCGATGCAACATTTATTAGTGAAACATGATGAAAATGAACATAAT
WI-921b	205	G A ---	---	CACITCCCAAGGGCTCTGGGGANGAGCGGTGGGGACGCTCCCGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATACTGG CAGTGATGCCCTCTCAGCCCTGCCCGCCCAAGAAAGTCTTNGCAGGAAAAAGCACGATCCATCTAC TCT/GA]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTTCTCCGAG
WI-921	205	G A ---	---	CACITCCCAAGGGCTCTGGGGANGAGCGGTGGGGACGCTCCCGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATACTGG CAGTGATGCCCTCTCAGCCCTGCCCGCCCAAGAAAGTCTTNGCAGGAAAAAGCACGATCCATCTAC TCT/GA]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTTCTCCGAG
WI-945c	90	G C ---	---	GGTGGGATGAGAGGTCTACTTGTTGCTGAGGTTTCACTGGCTTGCTAGAACTAGNAAAGNA GAAAGACACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAAAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAACTCTTTAAAGGGAAATCATGACAGATTTCTTGGCTTTA
WI-945b	90	G C ---	---	GGCTGGGATGAGAGGTCTACTTGTTGCTGAGGTTTCACTGGCTTGCTAGAACTAGNAAAGNA GAAAGACACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCCAAGGCCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAAAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAACTCTTTAAAGGGAAATCATGACAGATTTCTTGGCTTTA
WI-960b	167	C T ---	---	TTGCTTCAAAGAAAGTTCTTGCTCAGGAAGTTATTATTTCAGCAACCTAAAAATGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAATGAGTGTTCCTACC CTGAGGAATTTATCAAAAGATGTTAAGTTATCTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155	G A ---	---	TTGCTTCAAAGAAAGTTCTTGCTCAGGAAGTTATTATTTCAGCAACCTAAAAATGTTTTTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAATGAGTGTTCCTACC CTGAGGAATTTATCAAAAGAT[G/A]TTAAGTTATCTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181	T C ---	---	TCCCACTGAGTATGGCTTTCAGTAGTTTTATTATGATGTGCCTAGGTACATTTGTTTTATTGTTCTG CGAATTGTTGTTTACTTGGGAGAAATGCTCAACTATAAATATTGCTCTGACCCCTTTCTGTGTTTC CTTCTTAAAGATACAAAAATAAATGTAACATTAGACCTCTCACTA[T/C]GCTGTTTTTACTCTCCTCTG ATTTTTTTTCCATTATTTTATTGCTCTGGCTTCATTTTGTAATNTG



WI-1147b	204	G A ---	---	---	TTGCCATTATTGAAGATAACCCACACACCTTGGTGTCCAGGGTTTTCACAGGTATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCAGGCCACCGCAAACCTCTCCTCTGCTGGCTC CTGAGCCAAAACAGGCATTTACCATAAATCACCTTTGTTAGGATGAACCTATCTGGCCAAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAAACACTCTCATCAGGCAGA
WI-1158b	147	C T ---	---	---	GCATTGAGAGGGTTCGTTTAATGACATTCACTGAGGCCCTGTCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGT TAAGTGTCTGGGG/C/TCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124	C G ---	---	---	GCATTGAGAGGGTTCGTTTAATGACATTCACTGAGGCCCTGTCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAAATGAAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGT GGCTAAGTGTCTGGGGCTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124	T C ---	---	---	AAGTTTACAGAAAAAATACAGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTNCACAGACACTTATCCCTAGACAGGCATTTCTTTGAATGNT/C/GINCANT AAAAATGATTTGAAATTGGGAATAAAGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTGCCTAG GGC
WI-1305d	202	C T ---	---	---	TTCTCAATCCAACTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNINATATG/C /TAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305c	46	C T ---	---	---	TTCTCAATCCAACTGTGTGTTACTTTTATTTCTTTCTTCCATT/C/TATGTTGGTAAATATAAAGATG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTNCAGAAAGATAAGGTTTTCCTC ACATCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNINATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305b	153	T C ---	---	---	TTCTCAATCCAACTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAA/T/C/TNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNINATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305	202	C T ---	---	---	TTCTCAATCCAACTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAAATNACACTGTTTAAANTGNINATATG/C /TAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA



WI-1306b	248 A G ---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNGCAATAATAATGGACAATCTTGTNGNNNTNG GGCTGGGTGACTGTGCCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGAACCTAAGGNGAGAAAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTTIGGAAGGCCAGTTGAAATTTATCTCTT[A/G]GC
WI-1306	240 A G ---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNGCAATAATAATGGACAATCTTGTNGNNNTNG GGCTGGGTGACTGTGCCTGGGTCAATTTAGAAGCCATAGAGATGAAGTAGCCTGCAATAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGAACCTAAGGNGAGAAAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTTGTGAAGGCCAGTTGAAATTT[A/G]TCTCTAGC
WI-1307b	118 T C ---	---	GACAAGGCTGGTACTAGTTCCAATTCCAAATCTATGTACACTTTCCTCTCACTTTCTCAAGTGGACA GATTTCTGCATTACTGCTGGGGTGGGGGAGCAGTGGTGTAGGCAAT[C]GTGAGATTGTCTTT CCTACCCCTTAAATGTATCTTNTCTAATTATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTTGTTGCTGTGTTTCTCCTGTAAAGNTGTT
WI-1307	118 T C ---	---	GACAAGGCTGGTACTAGTTCCAATTCCAAATCTATGTACACTTTCCTCTCACTTTCTCAAGTGGACA GATTTCTGCATTACTGCTGGGGTGGGGGAGCAGTGGTGTAGGCAAT[C]GTGAGATTGTCTTT CCTACCCCTTAAATGTATCTTNTCTAATTATNATGCTAAACCCGGTACTGTGATCTATCACTGGTT TCTTTTGGTGTGTTGTTGCTGTGTTTCTCCTGTAAAGNTGTT
WI-1325b	169 T C ---	---	GAGAGATGGCCAAAGACAAGCAGAGGGGAGAGAGAGCAACCNCTGTGGTTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATTAGGCAACTACAATGTGCCCTTGGCTCTT[C]ACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165 C T ---	---	GAGAGATGGCCAAAGACAAGCAGAGGGGAGAGAGAGCAACCNCTGTGGTTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATTAGGCAACTACAATGTGCCCTTGGCTCTT[C]TCTACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162 T C ---	---	CTACGATAATTAGGTTTGGCAGTGAAGGTATTAAAGCTGTGTAGTGAAGAAGTCTGTTATTTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTAGTNCATATTACAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTG[C]GAAGTTGGTGTAGTACCAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCCTTACTGAAGAGGCAATGGTTCATCTCTAAG
WI-1327	175 C G ---	---	CTACGATAATTAGGTTTGGCAGTGAAGGTATTAAAGCTGTGTAGTGAAGAAGTCTGTTATTTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTAGTNCATATTACAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGTGTAGTACCAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCCTTACTGAAGAGGCAATGGTTCATCTCTAAG



WI-1341b	136 G A ---			TATCAGCATGATTGGCTGTTGGACACAAAGTCAATTTGTACTTTTGNNGNNTCCCTTTCTNTTT ACCTGATCCACTATCTTCTCAAGATCANGTTCAAAATTTGGCTTNCCTTTGTTNAATATACCCAAAGC [G/A]GGATTGTGATGGATCTGTTATTTTCTGTCTTGGAAACAGCAGAGTCTCTGNGAGTNTG GTTTCAGGATTGTCTCTGTTTCCCGAGCCACCTTGCACCTAGCAAGTGT
WI-1349e	192 G C ---			CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTCTGGCCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGTAGTGTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATA
WI-1349d	264 C A ---			CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTCTGGCCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGTAGTGTGAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1349c	192 G C ---			CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTCTGGCCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGTAGTGTGAATTTCCATCTCTGA[G/C]TTCAAA ATAATTTGAGAAAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATA
WI-1349b	264 C A ---			CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTCTGGCCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGTAGTGTGAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1349	264 C A ---			CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGCGAGGTGGTAGGTCTGGCCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGTAGTGTGAATTTCCATCTCTGAGTTCAAAATA ATTTGAGAAAAATATGATAGAAATTTGTGAAGTACTAGATTTTCAGAAAAATATGAT
WI-1403b	57 C T ---			TGGTATTTGGAATGGGTTCAAGTCCGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/T]TCCGAAT GCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATACGT AAAGTTTACATCAACATAAATCTTGGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCCTCA TAATCCCAAGTGCCAAAAAGGGTTGTATCTGATTGT
WI-1403	58 T C ---			TGGTATTTGGAATGGGTTCAAGTCCGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/T]TCCGA TGCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATACG TAAAGTTTACATCAACATAAATCTTGGCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCCCTC ATAATCCCAAGTGCCAAAAAGGGTTGTATCTGATTGT



WI-1417c	31 C T ---	---	CAGGCCGGAAGAGATTACGTGGAGAGATGTC/TTGGCCAGGGGGGCGAGATGTGAGCCACGGG GGTGACAGCATGCCCTGGCATTGGAGGGCCCCAGAGGAATCCAGTGGCCCTCTCAATGACTTG GGTCTCGACTTCGGAAGTTTAAAGGGCTCGCTTCAAAAAGCTGGTCCGGTTTGAGGCGGTTGC AGCGAGGCCCTTAGGTCGGTATTAAATGTTGCTTTGTAGAAAAAGTCGC
WI-1417b	31 C T ---	---	CAGGCCGGAAGAGATTACGTGGAGAGATGTC/TTGGCCAGGGGGGCGAGATGTGAGCCACGGG GGTGACAGCATGCCCTGGCATTGGAGGGCCCCAGAGGAATCCAGTGGCCCTCTCAATGACTTG GGTCTCGACTTCGGAAGTTTAAAGGGCTCGCTTCAAAAAGCTGGTCCGGTTTGAGGCGGTTGC AGCGAGGCCCTTAGGTCGGTATTAAATGTTGCTTTGTAGAAAAAGTCGC
WI-1729	172 A ---	---	CCATGAGCAACAGCATGTTCTACTCTGTGATGTGATGTAGGGGGCATGTATCTGTATTTCTT TTTTATTCTCTCCAAAAGAAATTTCAATTATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAGA TGTTGGAGAACTGAAAAGAGAGCTTACATGCACCCCAATAGCAAACTCTCCACACATTTCCAGCA GATGATGTGCTCCGTGGTNACTTCTCTCCACCATCACCTGTTTTT
WI-1732b	122 T C ---	---	TGCCTTACTTCTTTGTTTCATTCACCACATTACATTTTGTAATTTGGAACCTCTAGGAGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGGTCAACCTTTT/C/ATTCAGTCT CTGCCACATGTCTAGTAACGTGAGTGATGGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACACTATTTCATCATATTGGCTAAGGTATTTCATCATATTGGCTAAG
WI-1732	114 C T ---	---	TGCCTTACTTCTTTGTTTCATTCACCACATTACATTTTGTAATTTGGAACCTCTAGGAGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAAGGAGTNTCCCTGGGTCAACCTTTT/C/ATTCAGTCT CTGCCACATGTCTAGTAACGTGAGTGATGGGTGCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACACTATTTCATCATATTGGCTAAGGTATTTCATCATATTGGCTAAG
WI-1750	97 A G ---	---	GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTCCCCAAAAAGGTTTTAAATCTGTGTTGGA CATAATGTTTGAATTTGCAGTTACCTTGGI/G/TTTAAAGGTGCTGTTTTCTGGCAAAGAGTCAG TGGGAGTGTCCGGGAAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGACGTCCTGACTGAG CTACATTCACTTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31 A G ---	---	GGTACACAAAGAAATGCTTCTGGAAATCTACI/G/TTAGCGCCTTAACATTTGGCTGAGTATTAATC TGTACATGTGTAATGTGAACCCCATGAAGCTGGGCAAGAACAAATTCCTAGGAAAAGTACAAATTAC TGGGAAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGAATCACTCATGTTCCCATCA ACTGGAGAGACCTTGTGAGTACAGAGGACATTCAGAATAATCATAAAAAT
WI-1803c	77 A G ---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGAT/G/AGTAGGTTAGAGCATCACACTTGGGAGGACATATTCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATTACTCTTGTCTCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAATAACTGGAATCA



WI-1803b	77 A G ---	---	CCACTCAGTAATAAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGATAGTAGAGGTAGGATAGCATCACACTTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAATTTCAATATATCTACTAAGCATGACTTCTAGAAAATTACTTATTACTCTTGTCTCAA GGAATGGGAATACCTATAACAGCTTATTGAGGAAAATAACIGGAATCA
WI-1837b	112 C T ---	---	TTTACTTGGGATTTTTCATAGCTGATCATAATTTACCATTTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATAC/TTCTGTGCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGTAAACACTGGGAAGTCTGGGGAACGTTTGTCTGTGGCT
WI-1837	112 C T ---	---	TTTACTTGGGATTTTTCATAGCTGATCATAATTTACCATTTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGACCCGTTTATAC/TTCTGTGCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAAACAAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGTAAACACTGGGAAGTCTGGGGAACGTTTGTCTGTGGCT
WI-1840b	79 G T ---	---	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACT[G/TTGAGAACTCTGAATATTCAGCACATACAAAGTGTGACAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTGTGAATTTACTAAAAAGTTCTTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1840	79 G T ---	---	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACT[G/TTGAGAACTCTGAATATTCAGCACATACAAAGTGTGACAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTGTGAATTTACTAAAAAGTTCTTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1879b	110 C T ---	---	GGGCTCACTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCCCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTCTTTGAGGTNAAGGACCTGCCNTTTTAC/TTGTCTGCNAAATAAACTCCCAAAA AAGTGGTAGTCCACAGGGTTTAAATAGTCTTGTGAATGAATTTCTGTGCGCACCCCTGTGCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1879	110 C T ---	---	GGGCTCACTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCCCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTCTTTGAGGTNAAGGACCTGCCNTTTTAC/TTGTCTGCNAAATAAACTCCCAAAA AAGTGGTAGTCCACAGGGTTTAAATAGTCTTGTGAATGAATTTCTGTGCGCACCCCTGTGCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1900b	119 C T ---	---	TGTTCTCTGGTCCAGGACCGGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[C/TTGCTCTGAGAGGT AAAGTGCCCTGCCCAACGCGCACAACTAGAGAGCAGCAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTGCTTAACTGCCATGAGAAACCACTTTTCTTTGTCTCC



WI-1900	119 C T ---	---	TGTTCTCTGGTCCAGGCACCGGGCTAAGTCTTGCTGCATAATGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTCCCTGCCCAACGGGCACAACTAGAGAGCAGCAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTCTTAAGTCCCATGAGAAACCATTTCTTTGCTCC
WI-1943c	165 C T ---	---	ATTCCAGTTTACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGTAGGGAAAGACCAGC[C/T]CTCTGAANCTGGTCCACGTGGAGATAGTGAA TACAGGGCACCGNTAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943b	165 C T ---	---	ATTCCAGTTTACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGTAGGGAAAGACCAGC[C/T]CTCTGAANCTGGTCCACGTGGAGATAGTGAA TACAGGGCACCGNTAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943	164 C T ---	---	ATTCCAGTTTACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAATGGTAGGGAAAGACCAGC[C/T]CTCTGAANCTGGTCCACGTGGAGATAGTGAA TACAGGGCACCGNTAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1960c	270 A T ---	---	CCAGGTGAGGCTGAAAGAAAGGAGGGCAATTGCTGTTGGAGTGAGGGATTCTGGAAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGTCTGTTGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAATGCACCTCCCAACTTT
WI-1960b	270 A T ---	---	CCAGGTGAGGCTGAAAGAAAGGAGGGCAATTGCTGTTGGAGTGAGGGATTCTGGAAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGTCTGTTGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAATGCACCTCCCAACTTT
WI-1977	203 T C ---	---	CTGATGGCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGGTAAGTAGGTCA TTCTGGGCAATTTCTCATAGAGNTTGTGTTTGTAGTCTGTAATAATACTGTTGCCCTAGGAAGGTTGTT TTTCTACTGCTGTGAAAGCCCTTCCCATCGAGTGATACAGTACTTCCAGTTATGGAGATTIT /C/TAAACAATCAAACTGGCTGAGGCTGTTGG
WI-2012	102 T C ---	---	AAATTTAGAAGCCAGAAGTCAGCTCAGGATTATAAAGTTGAAGTAAATGCAATTGTAGTTTCATGT TTTCTCTTAATCTGCACAAAAGTAAATC/TGTTTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAAGCACTCAAAAGTTATGTAGAGTAGCTGTCTCTGAGTCACITTTTTTCTACTCTCAT GGCTTACCAATGCTCCACTGGATC



WI-2013	127 C T ---	---	---	CTTTAGAGTGGTCAATTCGGTTCCTCTCGAAAGTATCGTGTAAAGAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATACACTC/TCTCA CCAGAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTCACTGGAGGGATATCTAGCTTCTGAGCCCTGGTTACTGCAATCC
WI-2032c	166 G A ---	---	---	ACCAGACATCCCATCAGGAGTAGTCTTCTGGCAAGCCAGCCCTCTGATTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACACG/ATGTGGGACCTCTGTCTCAACCTCCGACTTTTCAG AGATCATTTGGTTAGGCTCACCTTCCTGTAATGCTTCTGTTTTCAAAGGG
WI-2032b	219 C G ---	---	---	ACCAGACATCCCATCAGGAGTAGTCTTCTGGCAAGCCAGCCCTCTGATTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACACGTTGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTGGTTAGGCTCA/C/GCTTCTCTGTAATGCTTCTGTTTTCAAAGGG
WI-2032	219 C G ---	---	---	ACCAGACATCCCATCAGGAGTAGTCTTCTGGCAAGCCAGCCCTCTGATTCCCAAAAACC TCAATTTTCTTNACTTACTCATAATATTTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACACGTTGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTGGTTAGGCTCA/C/GCTTCTCTGTAATGCTTCTGTTTTCAAAGGG
WI-2054b	188 C T ---	---	---	CGTTTCTTCTACATCTTGGGNACATAAAGANGAAAGAGNAGCTGCTTTTGTGGTAGTTTGGCT CAGAGCTGCCTAGAGCNAGGACAAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTGGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGTC/C/TCTGCTCCAC CAGCCCTATCTCTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
WI-2054	183 T C ---	---	---	CGTTTCTTCTACATCTTGGGNACATAAAGANGAAAGAGNAGCTGCTTTTGTGGTAGTTTGGCT CAGAGCTGCCTAGAGCNAGGACAAAGACAGGTGACCTTTCAAATACCTTACAGACTTAGGATTGGGA TTTTCATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGTC/C/TCTGCTCCAC CAGCCCTATCTCTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
WI-2573d	129 T C ---	---	---	TGGGATTAAACCCCTGTTTCTTCTCTCCAGTTCAGTGTGCCTTAATGTTGTGTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTCAAGGTTTCCGTGCTT/C/JGA TATCATCTGATCTCCCAACAGGGCTTATTTATGCCTAGGTAGGGGTAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGTCAATGCGTGGGCTTGGACGAG
WI-2573c	165 A C ---	---	---	TGGGATTAAACCCCTGTTTCTTCTCTCCAGTTCAGTGTGCCTTAATGTTGTGTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTCAAGGTTTCCGTGCTTTCGTGATAT CATCTGATCTCCCAACAGGGCTTATTTA/C/JGCTAGGTAGGGGTAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAAGTCAATGCGTGGGCTTGGACGAG



WI-2573d	129 T C ---	---	TGGGATTAAACCCCTGTTTCTTCCCTCCAGTTCAGTGTGCCTTAATGTTTGTGTAGAAATTAAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTTGCGTTTCAAGAGTGTTCCTGCTTT[C]JGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTCAATATGGCTGGCTTGGACGAG
WI-2573c	165 A C ---	---	TGGGATTAAACCCCTGTTTCTTCCCTCCAGTTCAGTGTGCCTTAATGTTTGTGTAGAAATTAAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTTGCGTTTCAAGAGTGTTCCTGCTTTTATGATAT CATCTGATCTTCCCAACAGGGCTTATTT[C]JGCTAGGTAAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAAGGTCAATATGGCTGGCTTGGACGAG
WI-2573b	165 A C ---	---	TGGGATTAAACCCCTGTTTCTTCCCTCCAGTTCAGTGTGCCTTAATGTTTGTGTAGAAATTAAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTTGCGTTTCAAGAGTGTTCCTGCTTTTATGATAT CATCTGATCTTCCCAACAGGGCTTATTT[C]JGCTAGGTAAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAAGGTCAATATGGCTGGCTTGGACGAG
WI-2573a	129 T C ---	---	TGGGATTAAACCCCTGTTTCTTCCCTCCAGTTCAGTGTGCCTTAATGTTTGTGTAGAAATTAAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTTGCGTTTCAAGAGTGTTCCTGCTTT[C]JGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTCAATATGGCTGGCTTGGACGAG
WI-2868b	60 A G ---	---	GACTTCATGCTCATGAACAAGCATTTGTCTTAATTTACAGACATTAAAGCAAGCTTTCC[C]A/GJCTC CCACTTCCCTCCCACTATCACTCAACCTCTTCCATCCACTTTAAAGAGGTTTCTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTACGCTTTCCCAATGATGCAGCCCACTTCTGCATACAGTTTGT CAGAAATGCTATATTATGGAACACAGCTGAAAAATGAATAICGATATAC
WI-2868	60 A G ---	---	GACTTCATGCTCATGAACAAGCATTTGTCTTAATTTACAGACATTAAAGCAAGCTTTCC[C]A/GJCTC CCACTTCCCTCCCACTATCACTCAACCTCTTCCATCCACTTTAAAGAGGTTTCTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTACGCTTTCCCAATGATGCAGCCCACTTCTGCATACAGTTTGT CAGAAATGCTATATTATGGAACACAGCTGAAAAATGAATAICGATATAC
WI-2870b	131 T C ---	---	CATGCTGTGAACCTCTGTGCTGCTTGTCTGCTGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCCATTTTAAATTATATCAGAGCTTTATGTCCACTTCTGTTCCCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT
WI-2870	131 T C ---	---	CATGCTGTGAACCTCTGTGCTGCTTGTCTGCTGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCCATTTTAAATTATATCAGAGCTTTATGTCCACTTCTGTTCCCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT



WI-2954c	49 T A ---	---	TTAGCACACATATCTGTGTGGGACTTAACCTGAGACAAGGCATAAAAA[T/A]CAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954b	41 A G ---	---	TTAGCACACATATCTGTGTGGGACTTAACCTGAGACAAGGC[T/A]GATAAAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954a	38 G T ---	---	TTAGCACACATATCTGTGTGGGACTTAACCTGAGACA[A/G]GCATAAAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2971b	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACITCCCAGTTAGACTCACCAGCATTTCTAAGA[T/C]G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTAACTCCTCCTCTCCTTAATAAACCTAAC ATTCCCTTTGTTCCCTGACATTTCTGAAGGCCACGCTGGTCTAGATGATGTCCCAGATTGCAATCCT AGTTCTTTAATGTTATCTGAAAGAAAACCTTTTACTTAGGGATTGCT
WI-2971	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACITCCCAGTTAGACTCACCAGCATTTCTAAGA[T/C]G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTAACTCCTCCTCTCCTTAATAAACCTAAC ATTCCCTTTGTTCCCTGACATTTCTGAAGGCCACGCTGGTCTAGATGATGTCCCAGATTGCAATCCT AGTTCTTTAATGTTATCTGAAAGAAAACCTTTTACTTAGGGATTGCT
WI-2995d	133 A T ---	---	TTCCCTGGGAAAGAAAAGATGGGGGTTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTT[A /T]AAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151 G C ---	---	TTCCCTGGGAAAGAAAAGATGGGGGTTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTT[A AATCTTTCTTTCTGGT[G/C]JTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133 A T ---	---	TTCCCTGGGAAAGAAAAGATGGGGGTTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAAGGAGCTGGANTTTTTT[A /T]AAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT



WI-2995c	151	G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTT NATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGAGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133	A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTT NATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGAGAGCTGGANTTTTTTNA /TAAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151	G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTT NATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGAGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995b	151	G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTT NATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGAGAGCTGGANTTTTTTNA /TAAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995a	133	A T ---	---	GTGGTGCAGTTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACAC ATCTCACTTAGCTCCTT[C/T]CCTGCCATATCCTGTTTCTTACTCCTATCTCCTGAGACTTCTTCT GAATGAATTACATGCACCTCAATCCCTGCCTCAGTCTCTGCTTINAGGGAACCTTGACCTAAGACAGAA ATCTTAGTACCAATACITTTGCAAGG
WI-3147	85	C T ---	---	ATTCTGTAATGTTTTCAGTCTCCAGTAAATTTCTTTATTGAGGTCCATGTCCATTACCTTACTTA[ T/C]GACAAGCAAGAACACACAGAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACITTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATCATCCTTAAATAGCATATCAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAATGGAATGTACTTATTTTINATATCTTAT
WI-3234b	68	T C ---	---	ATTCGTATGTTTTCAGTCTCCAGTAAATTTCTTTATTGAGGTCCATGTCCATTACCTTACTTA[ T/C]GACAAGCAAGAACACACAGAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACITTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATCATCCTTAAATAGCATATCAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAATGGAATGTACTTATTTTINATATCTTAT
WI-3234	68	T C ---	---	ATTCGTATGTTTTCAGTCTCCAGTAAATTTCTTTATTGAGGTCCATGTCCATTACCTTACTTA[ T/C]GACAAGCAAGAACACACAGAAAGCCTCTGTTTGCAATCTGGCCTCTTATAAATACITTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATCATCCTTAAATAGCATATCAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAATGGAATGTACTTATTTTINATATCTTAT



WI-3292b	106	GA ---	---		GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCT[G/A]TGGTATTGGATGGGATGGAATTACTT GCCATGAATATTTCCATTGTTCTCATTAAATGTTAAATTAATTAAGTAAATATTATTNNCCATGA GACAAATGGAAAATGGAAAACATTTCATGGAAAAAACCCATTTCATC
WI-3292	106	GA ---	---		GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCT[G/A]TGGTATTGGATGGGATGGAATTACTT GCCATGAATATTTCCATTGTTCTCATTAAATGTTAAATTAATTAAGTAAATATTATTNNCCATGA GACAAATGGAAAATGGAAAACATTTCATGGAAAAAACCCATTTCATC
WI-3355	19	GC ---	---		CCATGAACCATGGGCTACA[G/C]ATATTCCTAAACTTCAGAGTCCCTCCTTACTGGAGGGGATCCA CTTTTAAATATGATTTCTTGAAGTGGCTGCATACCTATTCCTTCCAAGCACCTTAAAACTCATCAGAA AAAAAATCATCAAAAAGTCGAAGTTAGTTTNNATTACCTTCACCTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGATGACTTTNAGTTG
WI-3408	194	GA ---	---		CCATGAAGAATGAGTTCCCTCCCTCCCGTGGTCAAGTCTAAGAATAGCACACCCCTTGAGAAATTTNACT TAGCACGTGGCATTGTAATGGCTGGATTTCCCTCCGCTCTAAGACACACCTTTATGCTTTCNAAGCTTT CTGGAAATGGGATGAATCTNACATTCATGTCACCCCTCGTGTGGGATCAGTCTCC[G/A]TGCCTCC ATCTCTGNAGAAGCCACTGGGAAGTCGAAGGAGTGACTTCAAAATCAGG
WI-3505b	131	GA ---	---		TAACCTATGCTCATCTGGCTTACTGCTTAGTCCCATTTGTCATCAGTGCACCTTAAAAAATTTATTT GAAAAATTGCCATTTTAAATATCTTTGGAACTTCCTAACACATTACCTATTTTNAACCAAAC[G/A] AGGTGATTCCTTATGGGAAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAITGGGAAATATGTTGCATAT
WI-3505	131	GA ---	---		TAACCTATGCTCATCTGGCTTACTGCTTAGTCCCATTTGTCATCAGTGCACCTTAAAAAATTTATTT GAAAAATTGCCATTTTAAATATCTTTGGAACTTCCTAACACATTACCTATTTTNAACCAAAC[G/A] AGGTGATTCCTTATGGGAAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAITGGGAAATATGTTGCATAT
WI-3564b	177	CT ---	---		GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGTCACTAAATGTTTGAGAAATAAAAGT GAAATCAATGTGCTTCCAGTGATTCACATGGCAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTTC[CTT]AACAAAGTGTGTTGTTGTCATC AGTGTACACATGCTACCTTCCCTCACAAAACAAA
WI-3564	177	CT ---	---		GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGTCACTAAATGTTTGAGAAATAAAAGT GAAATCAATGTGCTTCCAGTGATTCACATGGCAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTTC[CTT]AACAAAGTGTGTTGTTGTCATC AGTGTACACATGCTACCTTCCCTCACAAAACAAA







WI-4110	130 T C ---	---	GAAAAATGATGTTTTGATTCCCTCCTATCTTCAGATTATTGGAGTGTGCATTAGAAAACTGATAGT AACCTTTTATTTGATGAAACTCTGTCTATAATTAAACCTTCCTCTCCCTGCTTATTTTGCCTTC/JACA GTTTAGGTAATAAAGATGCCCAAGATTTCAGTATTCAGTACAGTAAAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAAGGGAGGAGGTTCTCTGGGAAGA
WI-4119b	168 G A ---	---	ACCTCTATGCCTGAAAGCCCTCATGAGTGCAGCAAGGGCTTGGTGGGAAAAAGTAATAATAG AATGGAAGGATAAATAAGGTAACACTACGGGGAAGAACAGAGAACAGACAGAGAAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA/GA/CAAGGTACCAAAATTTGTTTTCTTTCA TGAGACCGTCTGCATTCTTTTGTTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4119	168 G A ---	---	ACCTCTATGCCTGAAAGCCCTCATGAGTGCAGCAAGGGCTTGGTGGGAAAAAGTAATAATAG AATGGAAGGATAAATAAGGTAACACTACGGGGAAGAACAGAGAACAGACAGAGAAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA/GA/CAAGGTACCAAAATTTGTTTTCTTTCA TGAGACCGTCTGCATTCTTTTGTTTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4123b	51 T G ---	---	CAAAGTCAGATTTTGTATTTCAGGATAACAAATTTGAAATAGAAAAAGTG/T/GJTTAAACTATTT CAAATAACAATAAAGAAAAACATGATGAAATCTTCGTTACATAATTGATAGAAATTTAGTGGG TTCTCCATGACATTGGCTTGTCTCTCAACAGTGGGTGTTGGATGTTTCTATGCTTTCTC AGGCACAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4123	51 T G ---	---	CAAAGTCAGATTTTGTATTTCAGGATAACAAATTTGAAATAGAAAAAGTG/T/GJTTAAACTATTT CAAATAACAATAAAGAAAAACATGATGAAATCTTCGTTACATAATTGATAGAAATTTAGTGGG TTCTCCATGACATTGGCTTGTCTCTCAACAGTGGGTGTTGGATGTTTCTATGCTTTCTC AGGCACAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4149b	145 G C ---	---	TTGTACATGTTTCATTTCATCCCTCCCTCCTTTCTGCTTATAAAGAACCTCGCTTCCTCCAAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTTCCATCAAAGCTTTCTCAGCATCTCTATATACT GTGCTGT/GC/JCCTTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGAACTGTAGT AGGAGAGACAAGACAGATGTGCGGGTCCCTCATGATATAAGGTAATTG
WI-4149a	137 T C ---	---	TTGTACATGTTTCATTTCATCCCTCCCTCCTTTCTGCTTATAAAGAACCTCGCTTCCTCCAAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTTCCATCAAAGCTTTCTCAGCATCTCTATATACT T/C/JGTGCTGTCCTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGAACTGTAG TAGGAGAGACAAGACAGATGTGCGGGTCCCTCATGATATAAGGTAATTG
WI-4182	188 G A ---	---	TAAACACATTTTCATTTTGGTTTCTTACTGAGTTAAAGGACCATCCATTATATTAACAATTCCTC AGTTCTATGCTTTAGAGTNCATTTATAGGACTACTGTAAAAATTCAGAGGGAATTAACCTCTGGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAATTCAGGGGACTGTGGTTAA/GA/JATGTCCTCTCT TGCCCCCTTCCCAAGTCTTAAATTCCTAG



WI-4230	93 T	---	---	AGAGACGTTGAATGGGGACATCTTTCTATTTTCGATTTTGTGATTTTAAACATTTGATAAGAATTGATGAAA GTTTGACATTCAGATTATCTTTATAGCAGCAGAGTCTGGCAATTAATAACAGCACACTGACT TTTCCATGGTAAAGAGTTAGAGAAAAACAGCCTATTTCTTAATGTTAAATGTAATTTCTGAAT ACATTTTAAATGGAGGAGATGAATAGTGACCTTTGAAATTTTGAAATTTATGG
WI-4241	118 C T	---	---	GAAAAATCCATTGAAGTTTGACCTTGAACCTGATCTCAATTAATACCTTTTNCCTGAGTGGTTGTAATTT CATTTTGGACAAACAGACAGCAAAATTTCCACTTAAATTAATCTC[CT/TAAGTATCTATGAT TTAGCACTGTTAGCACCAGAAACTGTGAAATTAATCTCTAGATATCTTCAGAAATCTAGGATGGAAG AA
WI-4271b	151 A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTNTCTACAGGGAGCCCCAACCCCTTTTGTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
WI-4271	151 A	---	---	CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTNTCTACAGGGAGCCCCAACCCCTTTTGTCTCAGG CTCTTAGAAGGTCCAGTCAGGGGC
WI-4389b	156 G A	---	---	AATCGAAACATTGATTTTTTTGTAAGGAACCACTATTATGATATTTGTGCCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATGTCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/ATNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4389	156 G A	---	---	AATCGAAACATTGATTTTTTTGTAAGGAACCACTATTATGATATTTGTGCCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATGTCATAACCTTTGGA AGGTAAGATGTGAACCTATACA[G/ATNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACCTGGAAGCGGTAA
WI-4488	31 A G	---	---	GATGACAAATTATTGTGATTTGGCATTTTAA[A/G]GTACCATTCATTTCTTCTGGCTTTCGIGTGT TGTTGTTGAGAAAGTCAGGGGTAGTCGTATTGCTCTCTTTCTAGTTCTCTCAGTAGGAAGACTGATC CTAAACAACCTTAATACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAATCAAATTTG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145 G C	---	---	ACCATCAATGTATCACCCTCTAAAAATTTATAGATGATTAACTGGCTCTGTAAAAAATAAAAAACCT GTCTGGACATTGAAAAATAAACATTACTATTGGTCATTTCTGCTACTTACAAAGGTACTGCACATA AACAAAGTTAAG[G/C]GTTTTTTGGAGGGGAAAAATCATAAAAATGCATAAAAAATTTCTACCACCTGTCA TTTCTGTCCCAATAAATAAATTTTACATGCCT



WI-4584	144 A G ---	---	TTGGTTGGCAATTTAGCCTCATAACAACATATTTACAATCATAAATGTTACTCTTATTTACAAACAAG AAAATGAGGCTTAACATCACACTCTGCTTAGTCGAGAGCAAGATTTGAACCCAGGAATCCATT CACCGGTACAGTGCTACCTGGGTAAAAATGTTTAAATCTATGGCATTAGATTTCAAAGA GTCCTAATGTGGTTTTGAAATAGGTGTGCTTTAATTTGTTTATCAGTATGC
WI-4639	185 C T ---	---	TTTCTGCATTTGAATGTGATGGTCAGACTTCAGAGGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTAACTTTCAATTCACCAATTTAC TGACCATATGACTTGGGAACATTATCTCACCTATCTGAGTCTGTATCC[C/TT]CATCTTTAAATTTGTA AATTTAAGGACACCTATCATAGTAATATTGTGAGGATAAAAATGAAATAA
WI-5327	63 A -- ---	---	AAATGAATCCGCTTTAGAGCAATACCAGTAAGGGCTGGTGCAGGATGGTGGCTGAGAGA/- JGATTACTCATAAAAGCATATTAAATTTATAATATGGAATAATTAAGTATAATTAATGTAAT TGAGTTGAAGGTTGCATGAGAGTAGGAGGAGGTAGTTCTACTTATAGGGTTTATAAAGTNGCT TCAATAGAAATGGCTCTTTCCGATGACAATGATGAAGTGTCTAAGCAGACAG
WI-5390	87 C T ---	---	GCTTTGAGAAATGAAAAGGGAGCCTGGACCATTGCAGGGCTTCTCATCTCTGATTTTGTGTAT TTATTGTTCACTTATTAT[C/TT]GCTGCTCCCCCTCTGGTATGCTTGTGTCATGAAACAATGAATTC CCCAGTGCCTGGCCCGATTCTGGCTCCTAGAGGTGTCAGAAAAAAGTTTGGTGAATAGAAATTG ACGAATGGGTTTCAGAAATGAAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87 G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAGAAATCAATTTAAGCAGT GCAACATTTATTTAATTT[G/A]AAAGAAACTTTGTTCTGAAACTTTGTACTCTTGTAGTNAATTTG AATCTTCCCTCTCAGCAGTTCCCATGGTCGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTTAGAGTTTCATAACA
WI-5404	87 G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAAATAGAGTTGACTCTCCTGTCAGAAATCAATTTAAGCAGT GCAACATTTATTTAATTT[G/A]AAAGAAACTTTGTTCTGAAACTTTGTACTCTTGTAGTNAATTTG AATCTTCCCTCTCAGCAGTTCCCATGGTCGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTTAGAGTTTCATAACA
WI-5545b	77 A C ---	---	TAGGAAAGGGGATGGTATGGCCTCTGAGACATTTAAATCTATCTTTACCACCTCACACTGCCGCCA TATCTCTC[C/A/C]CCACACCTCTGTTTCTGACAGCCCAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTCA
WI-5545	77 A C ---	---	TAGGAAAGGGGATGGTATGGCCTCTGAGACATTTAAATCTATCTTTACCACCTCACACTGCCGCCA TATCTCTC[C/A/C]CCACACCTCTGTTTCTGACAGCCCAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCATTCA



WI-5860b	134 A G ---	---	ACTCAAGTTGGGGATAAAATCAGAAGTTCTATGTACAACCTAAATTTGCTAAGATTTTATTGT TTCCTTTTATATAAAATATGGATTGTTTCTTCTCCCTAACCAACCTTCTAACTGAGGAACCTAC[A/ G]TTACTGGAATCATGTGAAGACATCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
WI-5860	134 A G ---	---	ACTCAAGTTGGGGATAAAATCAGAAGTTCTATGTACAACCTAAATTTGCTAAGATTTTATTGT TTCCTTTTATATAAAATATGGATTGTTTCTTCTCCCTAACCAACCTTCTAACTGAGGAACCTAC[A/ G]TTACTGGAATCATGTGAAGACATCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTCCAAATCATCAACTTCTGTAT
WI-6106	208 C G ---	---	GCAACAACCTATTATACCTGATTCCAAACCCAGGTCTACTAACATTAAATCAACCTAACCAACAATAC TATATATTGTCCTGTTCTGAATTATTTTCAATTAGAATCTGATGAGATTAGCATGGGATAAGTGCAG TGCAGAGATAGTAAACACTGCTCTTTTGGTCCAGGAGTCTCAATGTGAAGTATAATTCTTACAGAG TAATT[C/G]ATAGTAGGTCAACCAAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129 T C ---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAAAAAACCT[C/ A]AACCTATATTNCTGCTTGTGCATACCTTAAATGTATAATGTGGGAGAGAAGGAATTTTGATGT GNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109c	147 T C ---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAAAAAACCTAA ACCCTATATTNCTG[C/T]CTTGTGCATACCTTAAATGTATAATGTGGGAGAGAAGGAATTTTGATG TGNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109b	147 T C ---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAAAAAACCTAA ACCCTATATTNCTG[C/T]CTTGTGCATACCTTAAATGTATAATGTGGGAGAGAAGGAATTTTGATG TGNAAAATTATCCCCTGAAAATTTTATACCA
WI-6109a	129 T C ---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTCTGAGAGAAATGTAC ATTGAGTCTTCCTTCTCTGGACTATAAGGAGATCAGGTGGAATAAAACGAAGGAAAAAACCT[C/ A]AACCTATATTNCTGCTTGTGCATACCTTAAATGTATAATGTGGGAGAGAAGGAATTTTGATGT GNAAAATTATCCCCTGAAAATTTTATACCA
WI-6112	96 T C ---	---	AATGCCTATCACCTTCCATCATGCTGCATAACTGATTGATTCAATAATGCTTATTGTTAGCACCTGTC TTCCAAACACATGCTGTTTGTTCATGAT[C/G]GCATATCCCAAGTGCCTTAGACAATGCCCTCCCATAC AGTGAACAGTATTGACTAAACACATACCTGTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC



WI-6244	103	T C ---	---	TAATTGCACAACCTACATATCAGGGTTCTGATTGAAAGGAGAGAATATCCTTTCTTTAGTGATT GCTTAATATTAATTCATAATAAGTGCACCATCTCTTC/GCTCCTTAATAATGTGTTTAGAAGAAGG AAATTGAGTGTGGGAATTAGCAACCCAGGAGACATTTTATATATACTCCTACAGTGGGGAAGACTT CCTATTTCTTCCCAAGGATGGATACATTTCTAC
WI-6268	124	C T ---	---	CTGGCCTTATAATCCAAAGTTTAGGATTAACTTACCCCAACTTAATAGACTCCAGACAGTTGCAGTT GTCTACAAGATTTCCTCCTAGTAGGGCTTTGGGTGTTGGCACCGTTTGGCTCATTTC/TTACTCTCCCT GGGTCTTATTGACTTTCAGGGAGCCTAGAAGAGCTGGACAAAACCTGCTTCTTTGCAGAAAGAGTCG GGGTTCCAAAGATTTCGTACGATTTTATA
WI-6336b	234	C T ---	---	AGGTGCCATTTAATCCATTCAAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTTACATGTTTTCTTATAAGACATACAGTTTAACTTAACAACCTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCCGAGTGCAATTATGCTCTGGTAGAGCC/C/TTGAGGACACTGACAGT
WI-6336	234	C T ---	---	AGGTGCCATTTAATCCATTCAAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTTACATGTTTTCTTATAAGACATACAGTTTAACTTAACAACCTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCCGAGTGCAATTATGCTCTGGTAGAGCC/C/TTGAGGACACTGACAGT
WI-6381	92	C A ---	---	TTGGATACAAAATTCAGTTACACAATCAGTAGCATTCAAAATTAGTTATGAGTATTTATACAATT CAAAAATGGNTTCATGTTTTAACAA/C/AJGTATTTTAAAGCTCAACATTTTAAACAGGCACAAT ATTCTAANGGCATATGCATTCACCATGGGCTTTTGAATGTCCTCACTCCCAACTTCACAATCAAAATC TACAGANGCGGCAAAAGATCAGAGTTTCAG
WI-6436	198	C G ---	---	GGTTGAGGCATTGGGAAAGGCAGAAAATTGAGGCAGTAGAAAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAAAGTCATGACAGACAGGAAATACAAAGGCTTAGGAAGACAGTAGTCTGTGGTTGAA ATTTTGGTGTCATAATAAGAAAGTTAGACTTTGGTGGTTGTAGTAGTTGTAGTAGGTTAGCGTT/C/ G/ATTGGGTGATTCCACAGACAAGGTGATGTTCTAAGATTGTATTTATTGT
WI-6449	186	C T ---	---	GAGGCTCTTTGCTTTCCCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTTTGTCTGATTGGTTGGTCTCACACTGCCAGATTGTTAAATATTTTGAAAATC GTAICTGGTTCTATTCACTGCACTCTGATCTATGTCGGCTCTATT/C/TTATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCTCTAATTTTCTGTGGGTATTATA
WI-6449	186	C T ---	---	GAGGCTCTTTGCTTTCCCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTTTGTCTGATTGGTTGGTCTCACACTGCCAGATTGTTAAATATTTTGAAAATC GTATCTGGTTCTATTCACTGCACTCTGATCTATGTCGGCTCTATT/C/TTATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCTCTAATTTTCTGTGGGTATTATA



WI-6463	72	T C	---			GCTGGAGAGAAAAGACCTCCAAAAGAAAGAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAA AGAACAT/CJTGAAGAAAATTTAAAGTAGAACTCAAAGAGCCAAAAGTCCCCAATTGTGTCCATT TAAGAAATATTTGAATGGAAATCTTAAGAATGATTTTATTGATCAGTTAAATGTTCTTCTCCTCCTC CAGTCCCATTTATATGACATCCGCATGCTG
WI-6474b	76	C T	---			AAGCAGTAAATCTTCCATCGCATGCCATGGATGCCAGTGGGTAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA/CJTGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACITGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76	C T	---			AAGCAGTAAATCTTCCATCGCATGCCATGGATGCCAGTGGGTAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA/CJTGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACITGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAAGGGGTGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175	T A	---			GAACCTAAATTAACCTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCACGCTCGAGGCTGTCTATATGCTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGGAGAAATCAGAGT/AJGCTCCTTGTGAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175	T A	---			GAACCTAAATTAACCTTGCAACACTGAGAAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCACGCTCGAGGCTGTCTATATGCTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGGAGAAATCAGAGT/AJGCTCCTTGTGAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149	G A	---			CACATTTTGAATGCAACTGAGAAANTGGTTTNTAGGCTACCTTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGNTCCCAAGCCCA TTAGCAATATCTTA/GAJTCAAATTTTAAAAAGAGAACACAGGAAATAAGGAAGGCCTAACAGAGGAG TTAAATAATTGTGCAAAACTTATCAGTTCTTC
WI-6564b	54	G A	---			TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCACTGTTCCTATGC/GAJCACTGGCTTTG TAGGCATTCACATCATATGTCTGTCTGCTGAAATCTCAATTAATTTCTCCTNCTATTCCTTTCCAT GCTCTGCTCATTTNCTCAGAAATGAAGGCATTTGATTATNATTTTGTGTTGGGTCTGTGTAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAATAAAGACCAACA
WI-6564	54	G A	---			TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCACTGTTCCTATGC/GAJCACTGGCTTTG TAGGCATTCACATCATATGTCTGTCTGCTGAAATCTCAATTAATTTCTCCTNCTATTCCTTTCCAT GCTCTGCTCATTTNCTCAGAAATGAAGGCATTTGATTATNATTTTGTGTTGGGTCTGTGTAAG GTTCTTGGCAGGAGAACATGCATATGACTTTAAATAAAGACCAACA



WI-6608b	46 C ---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCCTCAGT[C/- JAGTTCAGGCAGCTAAAGGGAGGGGATTTCTCCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAAGAACTGAATCCAGCACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCCAGGCACCTAGTACAAAGGCCACACAGAAAAAGGAA AGC
WI-6608	46 C ---	---	CTAATCACAGTAGCACTGAACATGGCTCTAGTGAGTGGGCCTCAGT[C/- JAGTTCAGGCAGCTAAAGGGAGGGGATTTCTCCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGTATTTTCTAGAGGAAAAAGAACTGAATCCAGCACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCCAGGCACCTAGTACAAAGGCCACACAGAAAAAGGAA AGC
WI-6666	68 C A ---	---	GTTAGACAGTATCCAGCAAAAAAGGTTATTTTATACCTCTACTTTTCCAAAAACGAGGAAACCTCCCC A/C/AJAAATCCCATCAACACACAGTCATGCTGGAAGGCATCTGTCTTACTCTGTGGTTTCATGTAA ATGTTGGGGTGACTCATTCGGCTCTCTNTTCTCAAGTTCAGGCTTCTGGGTAGACCAAACTA ATACACAATGTTAGGCACACAAGAGA
WI-6670b	120 A G ---	---	AGATTAAACATAATTATCTAGGGGCCATTTAGGGTNGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATAGTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACAACATGAAC[A/GTTGTAGCCA GCATTGCCATTCAGGGCCGAGTCAGGTTTGTGGGCCAGAGTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAA TTGTAAACACAGACACAGAA TCTTAGAAGGGAT
WI-6670	120 A G ---	---	AGATTAAACATAATTATCTAGGGGCCATTTAGGGTNGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATAGTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACAACATGAAC[A/GTTGTAGCCA GCATTGCCATTCAGGGCCGAGTCAGGTTTGTGGGCCAGAGTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAA TTGTAAACACAGACACAGAA TCTTAGAAGGGAT
WI-6704c	33 T C ---	---	TTTGAAAATAAATTCATGCACCAATGTTTAACT/CJACACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCTATTAATCGATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAAGTAGGCAGACATG
WI-6704b	33 T C ---	---	TTTGAAAATAAATTCATGCACCAATGTTTAACT/CJACACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCTATTAATCGATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAAGTAGGCAGACATG
WI-6704	28 T C ---	---	TTTGAAAATAAATTCATGCACCAATGTTTAACT/CJAACTCACAATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAGTTTTTCATGACACACCGNCA CTATTGCTCTTTAAATATGGTTGTACATGTCTATTAATCGATTGTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAAGTAGGCAGACATG



WI-6710	106 G A ---	---	CCATGGACAGTTTAATTAGGAAGCTTCGACTTGTTAGATAACAGAGGAAGTCCCAGTTATCTACCT ATTCCTTAAACACACATTTGTGACGGCTGGAATGATCCC[G/AT]AGTAAACTCAACATCCACACCT GCATAAACATCGCTCCCAAGTGACTATTTACTGAGTCGACACAGGATGTCACCAAGTGAGCCTC ATCTCCAGTCCAAATGGAGGAGTTGACTTAGACCTTCCTTGACAGGAAGGGTC
WI-6766b	148 G C ---	---	AAACAAATGGTGCAATTGCATAATATTTGGGTACAGTATAAACAAATACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTTCTTTGTCTACGGAAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACACAGTGGAGGGAACCTACCCAAATCCCAGTTCCTCTTC
WI-6766	148 G C ---	---	AAACAAATGGTGCAATTGCATAATATTTGGGTACAGTATAAACAAATACAATTAGTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTTCTTTGTCTACGGAAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACACAGTGGAGGGAACCTACCCAAATCCCAGTTCCTCTTC
WI-6787b	97 A G ---	---	ACAGATAAAGTCTTTATCCCTGTATGTTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACCTGTGCAGCAATGTTCAAAATTCAC[G/AT]TTTACTGCATAAGATATCTTCATGTACAAGT ATGCTTTGCTCTCTGGGAAGGACGCGTTAAAGACCTATGATAACACACATCCACATGACAAAGGA GAGTCAATAGGGCAGAGTAGANTACTCACAGGAAGAGATAATTTCAGGT
WI-6793	105 C G ---	---	GAACCCACAGGTCCTGTTATTTTAAAGGAGCAATTTACATATGATAGCAAGTTTCAACACATTCA TCAACAAGGCGGCTTCAAAATCAATCAGTCAACCC[G/AT]GAGTTAGAAAGTAGAGTCATGAGGAA GAGCTGCTGGCTGTAGGAAGTAGGTTAATGCCCTCTAATCCCCGAAAGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAAGTTTCTCATCACAGGTAAAAAGGCAAC
WI-6810b	37 T C ---	---	CACAATAATAAATCACTCCCTACCTTGAAACCTTTAT/CJAGAAGCAATTTTAAATTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTACGNGCCCAAGGATAAGGCTGAACAATA AATTAACCTTTTAAATGCTATGNACAAAGTACAATTTCTTTTGTAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAATCCAGCGCAATGAAGTTAAT
WI-6810	37 T C ---	---	CACAATAATAAATCACTCCCTACCTTGAAACCTTTAT/CJAGAAGCAATTTTAAATTTACAACACA AAGCTCAACGNACCTACAATAAGTCTAGTAGTCTGTACGNGCCCAAGGATAAGGCTGAACAATA AATTAACCTTTTAAATGCTATGNACAAAGTACAATTTCTTTTGTAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAATCCAGCGCAATGAAGTTAAT
WI-6817b	145 C A ---	---	GCATGATTAAACAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGTGTCTTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAATCAACAATGTAGCT GCAGGGTAAC[C/AT]GTGGATACCCCTGTGTGCTCTACTNGCCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTGGACACCTTGTTCAATCTGGTTCAGGTGCGGCTGTGCAG



WI-6817	145 C A ---	---	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATAGCTAGCTGTCTAGTA TTTGCTTTTTGTAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACAAATGTAGCT GCAGGGTAAC[C/A]GTGGATACCCGTGTGCTCTACTINGCCTCCAAAGGCATTAGGGGATCATCA AAGATGTTGGACACCTTGTTCAAATCTGGTTCAGGTGCGGCTGTGCAG
WI-6819b	221 C ---	---	GATGGAAGCCATTTATTTCTCTAAATTTAAATAGAGACTTTAATGGAAAAACATTTAGTAC CATCATGTCACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTT[G/T]CATATACAAAATTTCTGCTATTTG CTTAGCAACACAGCAATAACTTTTGTTTCTCTATATGACACCTAATAICAG
WI-6819a	175 G T ---	---	GATGGAAGCCATTTATTTCTCTAAATTTAAATAGAGACTTTAATGGAAAAACATTTAGTAC CATCATGTCACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTT[G/T]CATATACAAAATTTCTGCTATT TTGCTTTAGCAACACAGCAATAACTTTTGTTTCTCTATATGACACCTAATAAT
WI-6826b	154 A G ---	---	GCAAAAGCTTTATTGGCTCCAAACAAATATCCCTTTTAAACCTCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTTCCCTAAGAACCATAATAATAC ATGCAAAACCTTGACAT[G/G]GAGCTTAAATAATCAAAATGCAAAATATAGATTGGGTGCACTGT TAAGCTGAATTGCAAAATATGCAACACACACTGGACTGGGTATACGTTG
WI-6826	154 A G ---	---	GCAAAAGCTTTATTGGCTCCAAACAAATATCCCTTTTAAACCTCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTTCCCTAAGAACCATAATAATAC ATGCAAAACCTTGACAT[G/G]GAGCTTAAATAATCAAAATGCAAAATATAGATTGGGTGCACTGT TAAGCTGAATTGCAAAATATGCAACACACACTGGACTGGGTATACGTTG
WI-6857a	122 T C ---	---	AGTGCAAACTATTTGAACAAAAGTAACTATGAGTCACAGCATTCAGCAAGACATCAGACACGGA AGAGTGAACAATATTCACTAAGTAAATACAGCAGATGAGATGCTCTCACATGTAT[C/J]ATTTAAT TATTCATGCTTTTCAATAGTCTCTTAGTCAACTTTCAAGTAAATTTCCACAATATATAGCAGCTCA AACACAAATGCAGGAGCACAAATGGCAAAGTTTGGCAACTGTTTGGGCTAATT
WI-6865	153 G A ---	---	TTATGAATACTTATGGGCATACGNGTAAATGAAGTGTCAACCTTAAATCTAAACAAACAGCTTG TTTGTTGTTGCTCCTGAAATCCTCCCTGCTCACAAAACAGCCAGCTACTNGGTTTCTAAAGACGTA ATTTGCAGGCAAACTT[C/G/A]TAGAGCCATTCTGTGCAGAAAGGGAAGGAGAGCTGTTTGT TTACCTGTAGTATGAAGATATCTTTGGGCTGTAGAACTGAGCTCATTAA
WI-6909	73 C T ---	---	ATTGAAAACCTGTTAGCAACAGATAAATACAATAGAGCCTGGATATAAAAATGAGAGAAGAATGC AGACTT[C/J]AAGCTTATAGAGAAAGTCAAAAAGGAGCAAGTTTTGAAATCAGATTTTATGATAC GGAAAAAAATTTCTTTTTTGCCAACAGGATTATTTCGAATAATAAATCTGCCAGTGCCCAATCAG AAACACCATTTCCACAATATTGTCATGCCCTAGTGGCTATTTTATACATATC



WI-6910b	163	G T	---	CACTCAAAAACCTTTATTTCATTGATTACAAAACGTGTACAATAATTTACAAAAGTTTAGGCATTAAATCCCA TATTGACATGAATGCTGTGGAGAGTCTAAAAATAAATATGTGGCACATAGCTTAATATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATA[G/J]TGAGATGTAATGGAGAAATTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAGTCCCGGACCTTCCATGTGAATGACTCTTCCTTGGC
WI-6915	144	A	---	GCCTGTTTTTTTGTGTTTTTAAAGTGACACCTTGGCCTTGTGGCAATTTCTTCACCTTATCTTACCC AAAAGTGCCTTTGGGCCAGCCACTGACTGATTTAAAACCCAGAAATGTGGTTTTAAACAATGTGGT CGTGGTGAATTCAGGTGATTTTATTTCTATTTGGTAGTATTTTCAGATTTCCACAAAGAACATG TATTGCTTTGTAAATTTGAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175	T C	---	CAATCAAAAAGTTCCAAAGTTTCAAAGCTGGGATGAAAAGCCAGGTCTTCTGACTTGCACCTGTGCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCTCCCATAGAAAGTTCACTCTTAAATTCATGTCCCATG CTTTGCTTGGTCCCTGTGAGGAAAGGGTCAGCTAAAGGTC/AAAGTTC/AACTGTTCTATAAGGATGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175	T C	---	CAATCAAAAAGTTCCAAAGTTTCAAAGCTGGGATGAAAAGCCAGGTCTTCTGACTTGCACCTGTGCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCTCCCATAGAAAGTTCACTCTTAAATTCATGTCCCATG CTTTGCTTGGTCCCTGTGAGGAAAGGGTCAGCTAAAGGTC/AAAGTTC/AACTGTTCTATAAGGATGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79	G A	---	TTTTATGAAACATTTCCAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATCCCAATCCTAGGTAAGATATCAAGTTACAAANTAC AAGTCCCGNTAATTAACCTATAGGTAGTATATAANCAAAAATGNGTTTTNGCAATTTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6955	79	G A	---	TTTTATGAAACATTTCCAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAATCCCAATCCTAGGTAAGATATCAAGTTACAAANTAC AAGTCCCGNTAATTAACCTATAGGTAGTATATAANCAAAAATGNGTTTTNGCAATTTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6957	47	C G	---	AAACTAAAAACCCCTTATTGTCTCCAAGTGTGGCAAAATAGAAAATC/GJTTTCAATTACATTAGG AAATCGGGTGGATAACGGAGTATAGTTATTCACCTTAAGAAGCATTCAGTCAAAATAATCACAAAA ACAAATTCAGATTCGTTGGATCTTGGTCATTTATGGCTGAAGAAGTGGATTTGAAACCACTTTAGG CTAAATAAATGTATATGAATAATGCATAGACTGTGTATCTAGAAAATCATGC
WI-6996c	242	G T	---	ACTTCTAGTGCCTCTGTACCACCACTCTAATGCCCTCTGGTCCCGCACTTCTGATGTCGGTAGGCCT TAAATCTGCCTGGCTCCCTCCCTCTGCTTCAGACCCAGAGGAGAGCCGGCAGTTCCCTG CAGGAGAGAGAGGGGCTGTGGACCCCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCTCGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTCTCTCTCCG/GJTGCGGATC



WI-6996b	242	G T	---		ACTCTAGTGCCTCTGTTACCAACCACTCTAATGCCTCTGTGTCGCCGACCTTCTGATGTCCGTAGGCTTAAATCTGCCTGGCTCCCTCCCTCTGTCTTACGACCCAGAGGAGAGAGAGCCGGCAGTTCCCTGCAGGAGAGAGAGGGCTGCTGGACCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCTCTGACTCTCTCTGATGTGGGCCCTCTGTGCTCTCTCTCCGCTGCTGGGATC
WI-6996	228	T G	---		ACTCTAGTGCCTCTGTTACCAACCACTCTAATGCCTCTGTGTCGCCGACCTTCTGATGTCCGTAGGCTTAAATCTGCCTGGCTCCCTCCCTCTGTCTTACGACCCAGAGGAGAGAGAGCCGGCAGTTCCCTGCAGGAGAGAGGGCTGCTGGACCAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCTCTGACTCTCTGATGTGGGCCCTCTGTGCTCTCTCTCCGCTGGATC
WI-7021b	112	G A	---		TGGGAGGACAGGGAGATGCTGCAGTTCCTCCAAAGAGAGAGGTTCTCCAGAGTCATCTACCTGAGTCTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGTGCCAAATG/AJCCGACTGCACCTTCTGTGCTTCAGCTCTTTCGACATCAAGGCTCTCCGTTCCACATCCACACAGCCAATCCAATTATCAAAACCCTGTTAATACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A G	---		TGGGAGGACAGGGAGATGCTGCAGTTCCTCCAAAGAGAGAGGTTCTCCAGAGTCATCTACCTGAGTCTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGTGCCAAATG/AJCCGACTGCACCTTCTGTGCTTCAGCTCTTTCGACATCAAGGCTCTCCGTTCCACATCCACAGCCAATCCAATTATCAAAACCCTGTTAATACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	C T	---		GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGGACCTTGAGAGCCTGCATCCAGGATCGGGTGGCCCTGCAGCCTCTCCACCTCACCCTCCATGACAGCGCTAAACGTTGGTGA/CJGGTGGGAGCCTCTGGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTCCAAACAACAGAAAGTCATTCCTCTTTTAAATGGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCCATTTGATA
WI-7056b	118	C T	---		GGCAGTAGGACCAACAGTGTGGGTTCTGCTGGGACCTTGAGAGCCTGCATCCAGGATCGGGTGGCCCTGCAGCCTCTCCACCTCACCCTCCATGACAGCGCTAAACGTTGGTGA/CJGGTGGGAGCCTCTGGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTCCAAACAACAGAAAGTCATTCCTCTTTTAAATGGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCCATTTGATA
WI-7091b	153	A C	---		AATTCGCTGAAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCTCTTAACATCTTAGAGGTCCATGGAGAAGGCATATGGAGAACATGTTTATCTGCTCTATAAATAGTATTCCAATCACTGTGCTTAATTTAAATAGCATT/AJCTTATCATTTATCAGCCTTTATGTATTTCCAAAGTAAATATTAACATATTATTCATTGGTCTCTTTTATCTGTTCTATATGAATGCTAT
WI-7091	153	A C	---		AATTCGCTGAAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCTCTTAACATCTTAGAGGTCCATGGAGAAGGCATATGGAGAACATGTTTATCTGCTCTATAAATAGTATTCCAATCACTGTGCTTAATTTAAATAGCATT/AJCTTATCATTTATCAGCCTTTTATGTATTTCCAAAGTAAATATTAACATATTATTCATTGGTCTCTTTTATCTGTTCTATATGAATGCTAT



[illegible]



WI-7175	194 C T ---			CTCCTAGACTAGTGCCTTTACCTTTTATTAATGAACCTGTGACAGGAAGCCCAAGGCAGTGTTCCTCAACCA ATAACTTCAGAGAAGTCAGTTGGAGAAAATGAAGAAAAGGCTGGCTGAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATATAATGGTTTACTGCTGTCATTTGTCCATGCCTA/C/TAJGAT AATTTATTTTGTATTTTGAATAAAAAACATTTGTACATTCCTGATACTGGG
WI-7178b	273 G A ---			TGTATCAGGTCAGGGAAGTGGACAGGAGTCAGTGTCTGGCTTTTTCCTGTAGCCAGCTGCCTGGAG AGGGTCTCGCTGTCACTGGCTGGCTCTAGGGGAACAGACAGTGAACCCAGAAAAGCATACACCA ATCCAGGGCTGGCTCTGCACTAAGAGAAAATTCACATAAATGAATCTGTTCCCAAGAACTACCC CCTTTCAGCTAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGAA
WI-7178	273 G A ---			TGTATCAGGTCAGGGAAGTGGACAGGAGTCAGTGTCTGGCTTTTTCCTGTAGCCAGCTGCCTGGAG AGGGTCTCGCTGTCACTGGCTGGCTCTAGGGGAACAGACAGTGAACCCAGAAAAGCATACACCA ATCCAGGGCTGGCTCTGCACTAAGAGAAAATTCACATAAATGAATCTGTTCCCAAGAACTACCC CCTTTCAGCTAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGAA
WI-7182b	116 A C ---			GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCCTCTGCAACCCACTCTGAGCCTT/C/JTCTCCTCCTATTT TACTTGAGGCTGCCAATTACAGCCCCACGTTTCAGCTCAAGAGATGCCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCTGAAGCCTAGTACCCCAATT
WI-7182	106 C A ---			GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCCTCTGCAACCCACTCTGAGCCTATCTCCTCCTATTT TACTTGAGGCTGCCAATTACAGCCCCACGTTTCAGCTCAAGAGATGCCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCTGAAGCCTAGTACCCCAATT
WI-7191b	273 T A ---			ATAATTGCTGTGTTTCTAGCCTGGCAAGATATTTTCATAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAATATTTAGATAAATGCACAGCACCACATCTAAGCATTAGTGATGGGTAGC TGATGTCAGCTTCATGTGGATTTAAGCACTCTAGAAACAATGAAGCTTCTTGGCATAATTTAAGGAG CTCCAAAATGTTACCTATTAAATTTGTAACCTAGCAAGTAGAAGACCATTT
WI-7199c	112 T C ---			CCCAGTGGTGAACAGAACCTCCAAAATTTGAGTTGCACCCCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGCTCTGTCAGCTCCTTGAACCTATGAGCT/C/JGGGCCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAAATTAGCATTCCTTAATGTTTGTGTTTGGTGTCTGAATTTCTTTTATTAT AGTCTATAGTTTTACTCCTCAGTTCCTCACCATCATCTTGTCTAA
WI-7199b	112 T C ---			CCCAGTGGTGAACAGAACCTCCAAAATTTGAGTTGCACCCCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGCTCTGTCAGCTCCTTGAACCTATGAGCT/C/JGGGCCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAAATTAGCATTCCTTAATGTTTGTGTTTGGTGTCTGAATTTCTTTTATTAT AGTCTATAGTTTTACTCCTCAGTTCCTCACCATCATCTTGTCTAA



WI-7216c	237	T C ---	---	TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCCTCCAGAAAATACGTATGT TTAAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAAATTGACTGTACTGTTTAA CTGTCAATTCTCTGAGGCTAAACACAGTTTGTITTTTTCCTTGTAAATCACTT
WI-7216b	237	T C ---	---	TGACACTAACACTCTAATTCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTTCTCCCC AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCCTCCAGAAAATACGTATGT TTAAAAACCCCTTCTGCTATACATAGGAAAAGACACACATCCACCTAAAATTGACTGTACTGTTTAA CTGTCAATTCTCTGAGGCTAAACACAGTTTGTITTTTTCCTTGTAAATCACTT
WI-7220b	147	A T ---	---	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCACTATTGTCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCAGTAGAAATATCTTTGAGCACAGTGAATGACCTATCTCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAAATCTGGCTTACTGCACATATTAGTGTTT
WI-7220	140	A T ---	---	AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCACTATTGTCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCAGTAGAAATCTTTGAGCACAGTGAATGACCTATCTCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAAATCTGGCTTACTGCACATATTAGTGTTT
WI-7226	232	C ---	---	GATCGAATTTTCAGATGATTCGGAAATTTTCATTCAGGATTGTGTAATAGTGACATATATGATATA TACATATACCTCTTCTTAAATTTTGTAAATGTTAACTGGCAGTAAGCTCTTTTGTATCATTT CCCTTTTCCATATAGGAACATAATTTGAAGTGGCCAGATGAGTTTATCATGTCAGTGAAAAATAA TTACCCACAATGCCACCAGTAACITTAACGATTCTTCACTTCTTGGGGTTT
WI-7228b	254	GA ---	---	ATAGCTTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATTGGCTCCAATTCATAA TATGTTCAACAGGAGATTACAATTTTGTCTCTTCTTGTCTTTGTATCTATTTAGTTGATTTTAAATTA CTTCTGAATAACGGAAGGGATCAGAAAGATATCTTTTGTGCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTTAAAATAAGAAATGTTATCCAACTATTAAAGATATCTCAATGT
WI-7228a	163	GA ---	---	ATAGCTTCCAGATTACAAAGGCCAAGGGTAATAGAAATGCATACCAGTAATTGGCTCCAATTCATAA TATGTTCAACAGGAGATTACAATTTTGTCTCTTCTTGTCTTTGTATCTATTTAGTTGATTTTAAATTA CTTCTGAATAACGGAAGGGATCAGAAAGATATCTTTTGTGCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTTAAAATAAGAAATGTTATCCAACTATTAAAGATATCTCAA
WI-7233c	213	C T ---	---	CGATCGTACTGCCAGTAGCATTTGCTGTCTGCTCCGGCTTGTGTTGTACATTTTCAATTGTTTACA GATGTGAACCTTATCTCTTGTCACTAATTAATTAATTAATTAATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTAGCCCTCTACTTCTCTTCTGCCACCTTTTGTGGCAATATTAAAGTGAAGTCTGCTAATA GTGTAAGTATCTTGTGCACAAAACCACTGCCAGATAACAGAGGGGCTG



WI-7233b	213	C T	---			CGATCGTACTGCCAGTAGCATTTGTCTGTCCGGTCTGTTGTACATTCATTTCAATTGTTACA GATGTGAACITTTATTCCTTGTCACTAATATATTTAAATTAATTTCTAGGAAGTCAAAAAATATAA TAAAGGTTGAGCCCTCTACTTCTCTTGCCACCTTTTGTGGCAATATTAAAGTGAAGTACTGCTAATA GTGTAAGTATC/TJGTGCACAAAACCACTGCCAGATAACCCAGAGGGGCTG
WI-7233	211	T C	---			CGATCGTACTGCCAGTAGCATTTGTCTGTCTGTCGGTCTGTTGTACATTCATTTCAATTGTTACA GATGTGAACITTTATTCCTTGTCACTAATATATTTAAATTAATTTCTAGGAAGTCAAAAAATATAA TAAAGGTTGAGCCCTCTACTTCTCTTGCCACCTTTTGTGGCAATATTAAAGTGAAGTACTGCTAATA GTGTAAGT/CJACGTGCACAAAACCACTGCCAGATAACCCAGAGGGGCTG
WI-7238	128	T C	---			GGGTCTAGACAGCTCACCATTTTGTCTGTATCTGTAAACACTTTTGTCTTAGTCTTTTCTTG TAAATTGATGTTCTTTAAATCGTTAATGTATAACAGGCTTATGTTTCAAGTTTGTJ/CJCCGTT CTGTTTAAACAGAAAATAAAGGAGTGAAGCTCTTTCTCATTTCAAAGTTGCTACCAGTGAT GCAGTAATTAGAACAAAGAAACATTTCAGTAGAACATTTTATTCCTA
WI-7252f	520	T C	---			CCACAGGATCCAGCCCAAGCGGCCCTCCGGCCCTTCCACTGCAGCAGACGCCGGGACAGAG GCCTGCCGGGCGCGCCAGCCCGGCCCTGGCTGGAGGCTGCCCGGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCCTCCA
WI-7252e	552	T C	---			CCACAGGATCCAGCCCAAGCGGCCCTCCGGCCCTTCCACTGCAGCAGACGCCGGGACAGAG GCCTGCCGGGCGCGCCAGCCCGGCCCTGGCTGGAGGCTGCCCGGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCCTCCA
WI-7252d	540	T C	---			CCACAGGATCCAGCCCAAGCGGCCCTCCGGCCCTTCCACTGCAGCAGACGCCGGGACAGAG GCCTGCCGGGCGCGCCAGCCCGGCCCTGGCTGGAGGCTGCCCGGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCCTCCA
WI-7252c	552	T C	---			CCACAGGATCCAGCCCAAGCGGCCCTCCGGCCCTTCCACTGCAGCAGACGCCGGGACAGAG GCCTGCCGGGCGCGCCAGCCCGGCCCTGGCTGGAGGCTGCCCGGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCCTCCA
WI-7252b	540	T C	---			CCACAGGATCCAGCCCAAGCGGCCCTCCGGCCCTTCCACTGCAGCAGACGCCGGGACAGAG GCCTGCCGGGCGCGCCAGCCCGGCCCTGGCTGGAGGCTGCCCGGCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCAGCCCTAGAGCCTGCCTGGAGCTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGTGGAACTCAGTCAATTAGACTCCTCCTCCA



WI-7252a	520 T C ---	---	CCACGAGATCCACAGCCCAAGCGGCCCTCCCGCCCTTCCCACCTCGCAGCAGACGCCGGGGACAGAG GCTGCCCGGGCGCCAGCCCGGCCCTGGCTCGGAGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCTAGAGAACGCAGCCCTAGAGCTGCCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCCTCCA
WI-7265m	252 T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAAAAATATAACGATCTCT AAAAATACCAACAGTTGTATTTTCTTTAAGGAGTAAAGATTGCGCTT/
WI-7265l	231 T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAAAAATATAACGATCTCT AAAAATACCAACAGTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265k	121 T G ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAAAAATATAACGATCT CTTAAAAATACCAACAGTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265j	174 T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAAAAATATAACGATCT CTTAAAAATACCAACAGTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265i	227 T C ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAAAAATATAACGATCTCT AAAAATACCAACAGTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265h	80 T A ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAAAAATATAACGATCT CTTAAAAATACCAACAGTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265g	170 T G ---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTATTTTGTATATATGTAAAAATATAACGATCT CTTAAAAATACCAACAGTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT



WI-7265f	231	T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGATGTT TAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTTATATTATGTAATAATAACGATCTCT AAAAATACCACAGTTTGATTTTCTTTT/AJ/AGGAGTAAAGATTGCGT
WI-7265e	227	T C ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGATGTT TAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTTATATTATGTAATAATAACGATCTCT AAAAATACCACAGTTTGATTTTCTTTT/CJCTTAAGGAGTAAAGATTGCGT
WI-7265d	174	T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGATGTT TAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTT/AJ/TATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGT
WI-7265c	170	T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGATGTT TAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGT
WI-7265b	121	T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCAGTATGTTTATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTA GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGT
WI-7265a	80	T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTTACGTGTTT TTTCAGTATGTTT/AJ/TATTTGCCACCAAAAGTAAATGCATTTTACCCATTCTGTGGTTCAATTGTA GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGAATTTGTTTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTTAAAGGAGTAAAGATTGCGT
WI-7281b	183	C ---	---	GATACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCAAAGC ATCTTCCCTGGGAAGTCTTTCTGGCCAAAGTCTGGCCAGCCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTTGCCAAAAAACGGAGTCCGAGGCCGCGAG GTGTTGTGAAGACCACCTGTTCTGTGTTGGGTCTCTGCAAGAAGGCGCTCTC
WI-7281	171	C A ---	---	GATACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCAAAGC ATCTTCCCTGGGAAGTCTTTCTGGCCAAAGTCTGGCCAGCCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTC/AJ/TTGGCAAAAAACGGAGTCCGAGGCCGCG CAGGTGTTGTGAAGACCACCTGTTCTGTGTTGGGTCTCTGCAAGAAGGCGCT



WI-7282b	159	G C ---	---	TGTCACCTGGCACATTCATTTCTCAGTTGAAGAAGAGAAAAATTTGAAAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGGTGAGTGTTCCACTCAAAATATGTCAACTTNNNNNNNT AGGCCCTTTCATAAAAACCAAAC[TG/C]TAGCAAGATGCAATGCATGGCAATCTGTGGTCTCCA GTTGGTTATCTGAATAGTGTACCAATTCACCAAGACAGTCTGAGATTGG
WI-7292	92	T C ---	---	CTTGATTACTCCACTGAGGTGGGAGCATCTCCAGTGCTCCCCAATTATATCTCCCCACTCCACTAC TCTCTCTCCACTTCATTTTC[C]/C]TTGTCCTTCTCTCTAATTCAGTGTTTGGAGGCCTGACTTG GGGACAACGATATTGATATTATGTCGTCTTTCTCTTCCCAATAGAAATAAGTCATGGAGCC TGAAGGGTGCCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGCTGA
WI-7301f	133	A G ---	---	AACATATGGCAGTGGTCTGTTATAGTAGAGGGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTG[ A/G]CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCA ATCAAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301e	94	T G ---	---	AACATATGGCAGTGGTCTGTTATAGTAGAGGGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTG/TG]TGGAGGATATGATGGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301d	138	A G ---	---	AACATATGGCAGTGGTCTGTTATAGTAGAGGGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGT[A/G]GTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301c	211	A C ---	---	AACATATGGCAGTGGTCTGTTATAGTAGAGGGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATTATGGAC[A/C]CATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301b	182	C T ---	---	AACATATGGCAGTGGTCTGTTATAGTAGAGGGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301	88	G T ---	---	AACATATGGCAGTGGTCTGTTATAGTAGAGGGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTG/TG]CGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAATTATGGACACATGAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG



WI-7301	205	A C ---	---	---	AACATATGCAGTGGTCTGGTTATAGTAGAGAGCGGGTATGGTGGTGGACCGAGGATATGGAA ACCAAGTGGTGGATATGGTGGCGGTGGAGGATATGATGTTACAAATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGGAACATAATGATTTTGGAAATTACAGTGGACAAACAGCAATCA AATTACITGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7314c	49	G A ---	---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA[G/A]TTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCCTTTTCAGCAGTGAATAAAGTCAATTAAAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAAACTTGTTTTT
WI-7314b	49	G A ---	---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA[G/A]TTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCCTTTTCAGCAGTGAATAAAGTCAATTAAAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAAACTTGTTTTT
WI-7314	36	A G ---	---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAA[G/J]TTGGGAGGTGAGTTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCCTTTTCAGCAGTGAATAAAGTCAATTAAAACTTCCCAGG ATTTCTTTGGACCCAGGAACAGCCATGTGGTCTTCTGTGCACATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTATTAAACAAAACTTGTTTTT
WI-7321b	199	C T ---	---	---	ACTCAGGGAAGGATGCCCCATTAAAGTGACAAAAGGGTGGGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGGACTGCTTTGGCATCCAGGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATC[C /T]GTTTGTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199	C T ---	---	---	ACTCAGGGAAGGATGCCCCATTAAAGTGACAAAAGGGTGGGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGGACTGCTTTGGCATCCAGGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGGTGGCACACCCATC[C /T]GTTTGTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248	A C ---	---	---	AGACATTCTCGTTCCTGAAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCCCTGGC TCCAGTGAACCTTGGGCACATGCTCAGGCTACTATAGGTCCAGAAGTCTTATGTTAAGCCCTGGCAG GCAGGTGTTTATTAATTTCTGAATTTTGGGATTTTCAAAAGATAATATTTACATACACTGTATGT TATAGAACTTCATGGATCAGATCTGGGGCAGCAACCTATAAATCA[A/C]CA
WI-7338c	221	A G ---	---	---	CTCTTCTCAGCACATTGATGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTGCTTACCTTGAGC CATTATTTGTGTCAGAGAAACAAAAGAAACAGAAATCAATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTTCTCTTTACACAC[A/G]TATACACACAGACATCAGAAATTTCTGTT



WI-7338b	125 A C ---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTGCTTTACJCCTTG AGCCATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTCTTCTCTTACACACATATACACAGACATCAGAAAATTCGTGTT
WI-7338	125 A C ---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTTCTCTCTTACACACATATACACAGACATCAGAAAATTCGTGTT
WI-7338	221 A G ---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTTCTCTCTTACACACATATACACAGACATCAGAAAATTCGTGTT
WI-7384c	146 T A ---	---	CCTATGTCATGAAATGCTAGGGGCCAGGGAAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAATACCATTAATACATTTGTATTTTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTTT/AJAAAAATCTTAATGATTATTTTACTTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384b	146 T A ---	---	CCTATGTCATGAAATGCTAGGGGCCAGGGAAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAATACCATTAATACATTTGTATTTTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTTT/AJAAAAATCTTAATGATTATTTTACTTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7384	145 T A ---	---	CCTATGTCATGAAATGCTAGGGGCCAGGGAAACAAAATTTTAAAAATAATAAAATTCACCATAG CAATACAGAAATAACTTTAAATACCATTAATACATTTGTATTTTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTTT/AJAAAAATCTTAATGATTATTTTACTTACTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAAATTTGAGCAGAAATTTAAAAAAGAA
WI-7388c	106 A T ---	---	TGAAATCCTGGGTCTCTGGCCTGCTGTAGCTGGTTATTTTACTTTGCCCTCCCTCCCTCTTTT TGAGATCCATCCTTTATCAAGAAAGTCTGAAGCGACT/AJTTAAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAGGTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGTGCTGTCCCAAGAACTTTTCCCCCAAGATGTGTATAGTTATGG
WI-7388b	106 A T ---	---	TGAAATCCTGGGTCTCTGGCCTGCTGTAGCTGGTTATTTTACTTTGCCCTCCCTCCCTCTTTT TGAGATCCATCCTTTATCAAGAAAGTCTGAAGCGACT/AJTTAAAGGTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAGGTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTTGTGCTGTCCCAAGAACTTTTCCCCCAAGATGTGTATAGTTATGG



WI-7388	94 T A ---	---	TGAAATCCTGGGTCTCTGGCCTGCTCCTGTAGCTGGTTATTTTACITTTGCCCCCTCCCCACITTTTT TGAGATCCATCCTTTATCAAGAAAGTT/AJCTGAAGCGACTATAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCAATTGCAACAAGGTTACCTCTATTTGCCACAAGCGCTCGGGATTGTGTTGA CTTGCTGCTGTCCAAAGAACTTTTCCCCCAAAGATGTGTATAGTTAATGG
WI-7438	64 A G ---	---	TTAGATTTTAATTGGCAACCAGCAACTCACTGCCACCATTCCACTGCAGATCTNCTATTCTCTGGI/G GTTGATATGACAAGGAACCCCTATTGGAACCAAGCTCTCAGATTGNCATGTGCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTACTGTTCTACTGTAACATAGTTTGNTGCTGATTTTGTTA TTGGAATGAATATCGCTTCCACTGACTTTTACCA
WI-7454b	152 T C ---	---	CCATGATCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATTTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCAATTTGTCTACTTCTCAAAATGTTTTTGACA
WI-7454	152 T C ---	---	CCATGATCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCCCTGATAGCACTGTCTGAATTTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCAATTTGTCTACTTCTCAAAATGTTTTTGACA
WI-7464c	177 G C ---	---	AATTTGAAAATCTGAAAAAAGTGCATAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCAGTCCATCTTAACCATGTACATGCAGTAAATGACATAATTTTAAATTTCCCTATGTA CAACAGAGCCACAGCACAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCAGGAGGAAGCAACGTTCCACCAACATTTAT
WI-7464b	168 C A ---	---	AATTTGAAAATCTGAAAAAAGTGCATAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCAGTCCATCTTAACCATGTACATGCAGTAAATGACATAATTTTAAATTTCCCTATGTA CAACAGAGCCACAGCACAGAGGGTGGGCATAAGCAGTTGCCAAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCAGGAGGAAGCAACGTTCCACCAACATTTAT
WI-7464a	103 C A ---	---	AATTTGAAAATCTGAAAAAAGTGCATAGCAGAGAAATGACACTTATTCCAAATAAATAAATTGT CCATTTTTCAGTCCATCTTAACCATGTACATGCAGTAAATGACATAATTTTAAATTTCCCTAT GTACAACAGAGCCACAGCACAGAGGGTGGGCATAAGCAGTTGCCAAGAGAGCTTTCACATCAT GAAAGAAAGCCCTACAAATAGGCCAGGAGGAAGCAACGTTCCACCAACATTTAT
WI-7499b	134 T G ---	---	CAATTCTCAATCCCAACCTAGTCTGNTGCTTAACCATTCAGACACAACCTCCACTTCGAAGGTTTTA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCACGTTCTTTGAATGCTTCAIT /GJTATAGTCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGA ACTCTGTACAAAATTCCTTTGAAAATATAAATTTGGAAATGAGTGATGA



WI-7499a	33 A G ---			CAATTCTCAATCCAACCTAGTCTGNTGCCTAA[A]GJCATTCCAGACAAACTTCCACTTCGAAGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCGAGAGGCACATCAGCTTCTTTGAATGCTTC ATTATAGTCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTTTAGGAA CTCTGTACAAAATTCCTTTGAAAATATAAATTTGGAAATGAGTGATGA
WI-7506b	118 A C ---			TGGGAATAGTAAGAGAAAGATGGGAAGGTGACCAAAAACAATATAGAGGCCAGAGGCCAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGTAGTCTGGTCTGATTGCCTAGC[A]CJGGAGAGTTGAG TGCCACAGGTAAAGATGAGTGAAGAGGAAAAAATCATGATGTCATGTATGCAGTAATTAATGTCA GAAGAAAATATTTAAAAATATTGGACCACCTTGTCTACCATCCCTACCCACT
WI-7506	118 A C ---			TGGGAATAGTAAGAGAAAGATGGGAAGGTGACCAAAAACAATATAGAGGCCAGAGGCCAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGTAGTCTGGTCTGATTGCCTAGC[A]CJGGAGAGTTGAG TGCCACAGGTAAAGATGAGTGAAGAGGAAAAAATCATGATGTCATGTATGCAGTAATTAATGTCA GAAGAAAATATTTAAAAATATTGGACCACCTTGTCTACCATCCCTACCCACT
WI-7534b	143 C T ---			TGTGAATCTTAGCTCTGAAGGTGTTTATGCCTTTGGGGTTCTTGATGTGTCGCAGTGTCAACCA AGAGTCAGAACTGTACATCCCAAAATTTGGTGGCCGTGGAACACATTCCTGGTGATAGAATTGCT AAATTGT[C]TGTGAAATAGTTAGAAATTTCTTTAAATATGTTTCTTATTCGTGAAAAATTCGG AGAGTGTCTGCTAAAAATGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135 T C ---			TGTGAATCTTAGCTCTGAAGGTGTTTATGCCTTTGGGGTTCTTGATGTGTCGCAGTGTCAACCA AGAGTCAGAACTGTACATCCCAAAATTTGGTGGCCGTGGAACACATTCCTGGTGATAGAATTGCT [C]AAATTGTCGTGAAATAGGTAGAAATTTCTTTAAATATGTTTCTTATTCGTGAAAAATTCGG AGAGTGTCTGCTAAAAATGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162 G A ---			GGGAAAGAATAAAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCCTGTTTGAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTTGAAC TAGATTGCATGCTTCCTCTTGTCTT[G]A]GGAAGACCAGCTTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7543	162 G A ---			GGGAAAGAATAAAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCCTGTTTGAGGGAAGCCCCACTTGAAGGAAGAAGTCTAAGAGTGAAGTAGGTGACTTTGAAC TAGATTGCATGCTTCCTCTTGTCTT[G]A]GGAAGACCAGCTTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7555c	60 T C ---			GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGT[C]JCTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCTTCTGTTAAAGCCACTTGGGTC ATAAGAAAGGGAAGTAAAAAATGAAGTCTGACTAGAAATTTCTATTGCAGAGGCCAAGTACATTTAGT ATGGCAATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTTGAATTTTCAG



WI-7555b	60	T C ---	---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTTCTCTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCAATCTCTGTTAAAGCCACTGGGTG ATAAGAAGGGAAAGTAAATAAGAGTCTGACTAGAAATTTCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTGATGTGCAATTTTGAATTTTCAG
WI-7555	60	T C ---	---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTTCTCTA AAAAGAAAGTGGTATGTTGTGATGATCAGCACTAAGTCTGCAATCTCTGTTAAAGCCACTGGGTG ATAAGAAGGGAAAGTAAATAAGAGTCTGACTAGAAATTTCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTGATGTGCAATTTTGAATTTTCAG
WI-7567b	290	G T ---	---	---	TGAGCCATCACTAGAAAGAAAGCCATTTTCAACTGCTTTGAAACTTGCTGGGGTCTGAGCATGAT GGGAATAGGGAGACAGGGTAGGAAAGGGCGCTACTCTTCAGGGTCTAAAGATCAAGTGGGCCCTTGG ATGCTAAGCTGGCTCTGTTTGTATGCTATTATGCAAGTAGGGTCTATGTATTAGGATGGGCCTAC TCTTCAGGGTCTAAAGATCAAGTGGGCCTTGGATCGCTAAGCTGGCTCTGTT
WI-7569b	63	T C ---	---	---	AATGTATCCCCTTTCGGTCCAAACAACAGGAAACCTGACTGGGCAGTGAAGGAGGGATGGCATTC AGCGTTATGTGTAAAAACAAGTATCTGTATGACAACCGGGATCGTTTGCAAGTAAGTGAATCCAT TGCGACATTGTGAAGGCTTAAATGAGTTTAGATGGGAAATAGCGTTGTTATCGCCTTGGGTTTTAAAT ATTGTAGATTCCACTTGATCATGGCCTACCCGAGGAGAGAGGAGTTTG
WI-7574c	216	A G ---	---	---	GCACAGCAAGATGGAGCGGTGTAGGAAGTCCCTTTTCTCTGTTTGTGTTGCGCAAGGCCAAAC TCCCACCTCTGCCCCCTTTAATCCCCTTTCTACAGTGAGTCCACTACCCCTACTGAAAATCATTTTG TACCATTACATTTTAGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCACAGGGCAGTCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574b	216	A G ---	---	---	GCACAGCAAGATGGAGCGGTGTAGGAAGTCCCTTTTCTCTGTTTGTGTTGCGCAAGGCCAAAC TCCCACCTCTGCCCCCTTTAATCCCCTTTCTACAGTGAGTCCACTACCCCTACTGAAAATCATTTTG TACCATTACATTTTAGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCACAGGGCAGTCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574	216	A G ---	---	---	GCACAGCAAGATGGAGCGGTGTAGGAAGTCCCTTTTCTCTGTTTGTGTTGCGCAAGGCCAAAC TCCCACCTCTGCCCCCTTTAATCCCCCTTTCTACAGTGAGTCCACTACCCCTACTGAAAATCATTTTG TACCATTACATTTTAGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCACAGGGCAGTCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7576c	168	A T ---	---	---	AATGATGATGATAATGATGATGACGACGACAACGATGCTGTAAACAAGAAAAACATAAGAGAGC CTTGGTTCATCAGTGTAAAAATTTTGAAGGGCGGTACTAGTTCAGACACTTTGGAAGTTTGTGT TCTGTTTGTAAACTGGCATCTGACACAAAAAAATGTGTTGAAGGCCTATTCTACATTTCAACCTAC TTTGTAAGTGAGAGACAAAGCAAGCAANNNNNNNNNNNNAAGAAAAATAAAC



WI-7576b	168 A T ---				AATGATGATGATAATGATGATGACGACGACAAACGATGATGCTTGTAAACAAACATAAGAGAGC CTTGGTTTCATCAGTGTAAATAATTTTGAAGGCGGTACTAGTTTCAGACACACTTTGGAAGTTTGTGT TCTGTTTGTAAACCTGGCATCTGACACAAAAAA[A/T]GTGAAGGCCCTTATTTACATTTTCACTAC TTTGTAAAGTGAGAGAGACAAGAACAAANNNNNNNNAAGAAAAATAAAC
WI-7577g	77 T C ---				AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]TGTTCCTTTTAA AAATATGCA[T/C]CAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAAT AAAGAAAGTTTCATTTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50 G C ---				AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]TGTTCCTTTTAA TAAAAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAAT AAAGAAAGTTTCATTTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157 G A ---				AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAAAGTGTTCCTTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAAT AGAAAGTTTCATTTTGGTTTACAC[G/A]TAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48 A G ---				AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAAAGTGTTCCTTTTAA TAAAAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAAT AAAGAAAGTTTCATTTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84 G A ---				AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAAAGTGTTCCTTTTAA AAATATGCATCAAAATC[G/A]TCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAAT AAAGAAAGTTTCATTTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93 T C ---				AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAAAGTGTTCCTTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAAT AAAGAAAGTTTCATTTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154 C A ---				AACCATGTTCCCTTCTTTAGCACCACAAATAATCAAAACCCCAACATAAAGTGTTCCTTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAAT AGAAAGTTTCATTTTGGTTTACACGTAGGAAGAAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC



WI-7577j	117 A G ---			AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577i	77 T C ---			AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577h	50 G C ---			AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA TAAAAATATGCATCAAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577g	157 G A ---			AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTTACAC/GAJTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577f	48 A G ---			AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA TAAAAATATGCATCAAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577e	84 G A ---			AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATC/GAJCTCTCATTACTTTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577d	93 T C ---			AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATT/CJACTTTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577c	154 C A ---			AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTTCTCTGAGGGTTTAGTAACACAGTAGGAGTTAAT AGAAAGTTCAATTTGGTTTAC/JACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC



WI-7577b	117	A G ---			AAACATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTCCCTTAA AAATATGCATCAAAATCGTCTCATCTTTCTCTGAGGGTTTGTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGATCAAGAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGATTTTC
WI-7577	107	G A ---			AAACATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTCCCTTAA AAATATGCATCAAAATCGTCTCATCTTTCTCTGAG[G/G]TGTAGTAAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAGAAGAGAGATCAAGAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTCTGAAATTGACTGATTTTC
WI-7619q	106	C G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAGGGCCCAATGGGTCTATCCCTCCCTAACGAGACTCTCTGTCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGCCTCTAAGGGGAGTGTGGGTCTGTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150	T C ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAGGGCCCAATGGGTCTATCCCTCCCTAACGAGACTCTCTGTCTGGGGTGCTAATTACATGG CAGGAAGAATGGGCCTCTAAGGGGAGTGTGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCTCT CGCTTTCTTTTACACAGAAACAT/GJACATACCGAGAAACCTATTTC
WI-7619o	228	A G ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAGGGCCCAATGGGTCTATCCCTCCCTAACGAGACTCTCTGTCTGGGGTGCTAATTACATGG CAGGAAGAATGGGCCTCTAAGGGGAGTGTGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCTCT CGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619n	237	G C ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAGGGCCCAATGGGTCTATCCCTCCCTAACGAGACTCTCTGTCTGGGGTGCTAATTACATGG CAGGAAGAATGGGCCTCTAAGGGGAGTGTGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCTCT CGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99	C T ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAGGGCCCAATGGGTCTATCCCTCCCTAACGAGACTCTCTGTCTGGGGTGCTAATTACATGG TGGCAGGAAGAATGGGCCTCTAAGGGGAGTGTGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189	T A ---			ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAAGAC AGAGAAGGGCCCAATGGGTCTATCCCTCCCTAACGAGACTCTCTGTCTGGGGTGCTAATTACATGG CAGGAAGAATGGGCCTCTAAGGGGAGTGTGGGTCTGTCTCCCTTTTTCATCTTTTCCCTCTCT TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC



WI-7619k	90 C G ---	---	ACAAAGCGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCAATGGGGTCATCC[C/G]CTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGAGTGTGGGCTGTCTCCCTTTTTCATCTTTTCCT CTCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619j	206 T G ---	---	ACAAAGCGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCT[G]TTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619i	106 C G ---	---	ACAAAGCGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG ATGGCAGGAAGAATGGGGCTCTAAGGGAGTGTGGGCTGTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150 T C ---	---	ACAAAGCGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT TCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619g	228 A G ---	---	ACAAAGCGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTTTCTTTTACACAGAAACAT[A/G]ACATACCGAGAAACCTATTTC
WI-7619f	237 G C ---	---	ACAAAGCGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99 C T ---	---	ACAAAGCGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG TGGCAGGAAGAATGGGGCTCTAAGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT TCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189 T A ---	---	ACAAAGCGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGAGTGTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT TCTCGCTTTCTTTTACACAGAAACATACACATACCGAGAAACCTATTTC



WI-7619c	90 C G ---				ACAAGGGGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCC/C/GCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGGAGTGGGGTCTGCTCTCCCTTTTCCATCTTTTTCCT CTCTCGCTTCTTCTTACAGAAACATACATACCGGAGAAACCTATTTC
WI-7619b	206 T G ---				ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGATGGGGCTCTAAGGGGAGTGGGGTCTGCTCTCCCTTTTCCATCTTTTTCCTCTCT CGCT/GTTCCTTCTTACAGAAACATACATACCGGAGAAACCTATTTC
WI-7619	189 T A ---				ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGATGGGGCTCTAAGGGGAGTGGGGTCTGCTCTCCCTTTTCCATCTTTTTCCTCTCT TCTCGCTTCTTCTTACAGAAACATACATACCGGAGAAACCTATTTC
WI-7626d	105 A G ---				CCTTTGATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTCTCTGTAAACAAATGGGATCTGTCTGGC/GTAAACCAACATCATGGACCAATGTG CCATACTAATGATGAGCAATAGCACAAATGGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCCCTGCTGATTTATAGTAACCAATTTCCCTTTGGACTGTTC
WI-7626c	155 C T ---				CCTTTGATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTCTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAACATCATGGACCAATGTG TACTAATGATGAGCAATAGC/TAACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCCCTGCTGATTTATAGTAACCAATTTCCCTTTGGACTGTTC
WI-7626b	28 T A ---				CCTTTGATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAG TAATCTATGTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAACATCATGGACCAATGTG CCATACTAATGATGAGCAATAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCCCTGCTGATTTATAGTAACCAATTTCCCTTTGGACTGTTC
WI-7626	144 T C ---				CCTTTGATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTCTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCAACATCATGGACCAATGTG TACTAATGATGAGCAATAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTGCCCTGCTGATTTATAGTAACCAATTTCCCTTTGGACTGTTC
WI-7689c	134 A G ---				TCCATAACCGCTGATCTCAGGGTCTCTGCTGCCGCCCAACCCAGATGGGGGAAAGCAGGTGGC TCCCAGTGGCTGCTGCCAGGCCAGACCTCTAGGACGCCACCCAGCAAAAGTTGTTCCCTAAAJA /GJTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGAAAAAGAGAGCTTAAT GATAATATTGIGGIGGCCACAAATAAATGGATTTATAGAAATTCATATGAC



WI-7689b	134 A G ---	---	TCCATAACCGCTGATTCAGGGTCTCTGCTGCGGCCCAACCCAGATGGGGAAAGACACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTCTAGGACGCCACCCAGCAAAAGGTTGCTCTAA[A] /GJTAAGGCGAGATCACACTGGGCGAGCTGATACAAATTGCAGACTGTGTAAAGAGAGGCTTAAT GATAATATTGGTGCCACAATAAAATGGATTATTAGAAATTCATATGAC
WI-7689	121 G A ---	---	TCCATAACCGCTGATTCAGGGTCTCTGCTGCGGCCCAACCCAGATGGGGAAAGACACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTCTAGGACGCCACCCAGCAAAAGGTTGCTCTAA AATAAGGCGAGATCACACTGGGCGAGCTGATACAAATTGCAGACTGTGTAAAGAGAGGCTTAAT GATAATATTGGTGCCACAATAAAATGGATTATTAGAAATTCATATGAC
WI-7690	45 G A ---	---	TGGAGAACATTCAATCTTGCCTCACTATTCAATCAATGAAGATT[A/G]CACTGAGATCCAGAGAGG CTGGATGACTTGTCAAGTTCACAGCATGGTAGTGGCAAGAGAGGTCAGAGTCTGGCCCTTGAT GCCAGCTCAGTCCACAAGCTCAGTAGGAGGATGTTCCAGTGATAGGGCCACCCAGGAAGCAC AGGTCCAAAGGCTGTCACACTTATCAGCAGCAACAACCTGCAGTTCATCC
WI-7703b	164 T C ---	---	ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTGGAACAAGTCAGTCATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTAAAGTAAAT[C/J]GGTCTCTCACTTGTTTATTAACTCTAAATTCT TTCATTTAGGGGTAGCATTTGTTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7703	156 T C ---	---	ACAGAAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTGGAACAAGTCAGTCATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTAAAGTAAAT[C/J]GGTCTCTCACTTGTTTATTAACTCTAAATTCT TTCATTTAGGGGTAGCATTTGTTGTTGAAGAGGTTTAAAGCTTCCATTGT
WI-7743e	106 C A ---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGTACTACTGCGGCTCTGGGCTCGGAGCCCTATCCGAGGCGAGGTCAGGA GAGGGCGAGAACAAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275 C T ---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGTACTACTGCGGCTCTGGGCTCGGAGCCCTATCCGAGGCGAGGTCAGGAGAG GGGCAGAACAGCCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743e	106 C A ---	---	TTAAATGAGTGTGTTTGTACCGTTGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATCTGTACTACTGCGGCTCTGGGCTCGGAGCCCTATCCGAGGCGAGGTCAGGA GAGGGCGAGAACAAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC



WI-7743d	275	C T	---	TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTACTGGGTCTCTGGGCTCGGAGCCTATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743e	106	C A	---	TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATTCGTACCTACTGGGTCTCTGGGCTCGGAGCCTATCCGAGGCAGGGTCAGGAG GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743d	275	C T	---	TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTACTGGGTCTCTGGGCTCGGAGCCTATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743c	106	C A	---	TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATTCGTACCTACTGGGTCTCTGGGCTCGGAGCCTATCCGAGGCAGGGTCAGGAG GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743b	275	C T	---	TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTACTGGGTCTCTGGGCTCGGAGCCTATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7743	106	C A	---	TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAAGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATTCGTACCTACTGGGTCTCTGGGCTCGGAGCCTATCCGAGGCAGGGTCAGGAG GAGGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCC
WI-7743	275	C T	---	TTAAATGAGTGTGTTGTACACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCCAAGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTACTGGGTCTCTGGGCTCGGAGCCTATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCCGCTCCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAAG
WI-7758	144	A G	---	TGACATTTATTCAAAGTTAAAGCAAACACTTACAGAAATTAAGAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTCAGAGTCTTCAGAGACTTCGTAATTAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATCjA/GjTAGTTTAAACTGCATTATAAATTTTATAACAGAAATTAAGTAGATTTTAAAA GATAAAATGTGTAATTTTGTTTAAATTTTCCCATTTGGACTGTAACTGACTGCC



WI-7765b	126 G C ---	---	---	ACAGGGCCTTTGGCAGGTGCAGCCCCCACTGCCCTTTGACCTGCCCTCCCTTCATGCATGGAATTCCTCTCATCTGGAAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTATGG[G/C]TTAGGGAACATTCCTCCTTGGAGTCAAAAATCTCAATCTCCCTATCTTTGCCACCCCTCATGCTGTGTGACTCAAACCAATCACTGAACCTTGTCTGAGCCTGTAAATAAAAGGTCGGA
WI-7773b	237 C G ---	---	---	TTAATTTACTGATTCAGCAAGCAACCAATCATGTATCAGATTATTTTAAAGTTTATCCGTAGTTTTGATAAAAGATTTCCTATTCCCTGGTTCTGTCCAGAACCTTAATAAGTCTACTTTGCCATTAAAGGCACTAGGGTTCATGCTTTTACCTTTNNNNNNNNNTGTAAAGTCTAGTTACCTACTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCAAC[G/C]TTTCGACGTTTGA
WI-7774b	170 T C ---	---	---	TGCAACCTCTTTTCGTGATGGCAGCCTGCTGGTCAGCACTCCAGTAGCGAGAGAGCGCACCCAGAATCAGATCCCAGCTTCGGCATTTGATCAGACCAACAGTCTGTTCCCGGGGAGGAAACACTTTTAAATTACCTTTTGAGGCACCACTTAACTCTGTTT[C/J]ATACCTTGCTTATTAAATGAGCGACTTAAATGATGAAAATAATGCTGCTTTAGTAGCAAGTAAATGTGCTTGCT
WI-7785c	165 G ---	---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATATTTATTGTCTGTAATACTGTAATGCATTGGATAAACTGCTCCCCCATTTGCTCTATGAAACTGCACTGGTCAATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAAATTATTATCACATTTACCAATAATTTTGTCATTGATGATTTATTTTGIAAATGATCTTGGTGTGC
WI-7785b	165 G ---	---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATATTTATTGTCTGTAATACTGTAATGCATTGGATAAACTGCTCCCCCATTTGCTCTATGAAACTGCACTGGTCAATTGTGAATANNNNNNNNNGCCAAAGGCTAATCCAAATTATTATCACATTTACCAATAATTTATTTGTCCATTGATGATTTATTTTGTAATGATCTTGGTGTGC
WI-7785	156 - T ---	---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATCTGTAATAGTGAACATATGGAAGTATTAGAAATATTTATTGTCTGTAATACTGTAATGCATTGGATAAACTGCTCCCCCATTTGCTCTATGAAACTGCACTGGTCAATTGTGAATANNNNNNNGCCAAAGGCTAATCCAAATTATTATCACATTTACCATAATTTATTTTGTCCATTGATGATTTATTTTGIAAATGATCTTGGTG
WI-7789c	84 G A ---	---	---	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCAAAGGAGGGCACCATCTTACAGAGACTCTCCCTGACGGTGGAAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGACCCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATATGCCCTCTGTGTGACTCGGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7789b	84 G A ---	---	---	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCAAAGGAGGGCACCATCTTACAGAGACTCTCCCTGACGGTGGAAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGACCCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATATGCCCTCTGTGTGACTCGGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT



WI-7789	73	GA ---	---	<p>TCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCAAAGGAGGACCACATCTTACAGAGACTCTCCG TGACG[G/A]TGGAATTTAAGTTTAGGGTCCCTAAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGAAGTCCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT</p>
WI-7790b	190	CT ---	---	<p>AATTGTCAGTCACCTTCTCAAAACCTTACAGTCTTCTCAAGGTACTCTTCATGAGATTCAATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTGAGCTTTTACTTTTATGG TGTGATTAAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAATC[G/A]TTCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAG</p>
WI-7790	190	CT ---	---	<p>AATTGTCAGTCACCTTCTCAAAACCTTACAGTCTTCTCAAGGTACTCTTCATGAGATTCAATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTATGTGAGCTTTTACTTTTATGG TGTGATTAAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAATC[G/A]TTCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAG</p>
WI-7795b	81	CA ---	---	<p>CAGATGTTCTGGTAACTGATTGCTGGCAACACAGAGATCTCTGGCTCATATTTCTTTCTCTCAT CTTGATGATGAT[G/A]GTCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACACATATAAATGATCTTTTCTCCAGAAAATTTCTCTTGAGGAAAATGTCCAAAA TAAGATGAATCATTAAATACCGTATCTTCTAAATTTGAAATATAATCTG</p>
WI-7795	81	CA ---	---	<p>CAGATGTTCTGGTAACTGATTGCTGGCAACACAGAGATCTCTGGCTCATATTTCTTTCTCTCAT CTTGATGATGAT[G/A]GTCATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACACATATAAATGATCTTTTCTCCAGAAAATTTCTCTTGAGGAAAATGTCCAAAA TAAGATGAATCATTAAATACCGTATCTTCTAAATTTGAAATATAATCTG</p>
WI-7814c	41	GA ---	---	<p>TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG[G/A]TTTCATTTAGTCATGTGACCACCTC TGCTTGTTGTTCCACAGCCTGCAAGTTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA</p>
WI-7814b	41	GA ---	---	<p>TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCG[G/A]TTTCATTTAGTCATGTGACCACCTC TGCTTGTTGTTCCACAGCCTGCAAGTTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA</p>
WI-7814	28	GA ---	---	<p>TTCTCTCATTTTATCCCTCACCTGT[G/A]CATGCCAGTCCCGTTTCATTTAGTCATGTGACCACCTC TGCTTGTTGTTCCACAGCCTGCAAGTTTCAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAAAATATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA</p>



WI-7830d	150	C T ---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/TT]TAATGTACACATTGCATTTGATAAAATTAATTTGTTGTTTCCCTTG AGGTGATCGTTGTGTTGTTGCTGCACATTTTACTTTTTGCGTGTGGA
WI-7830c	54	G A ---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTTCCCTTG AGGTGATCGTTGTGTTGTTGCTGCACATTTTACTTTTTGCGTGTGGA
WI-7830b	134	G A ---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC G/AJATCCATAACTTTAGTCTTAATGTACACATTGCATTTGATAAAATTAATTTGTTGTTTCCCTTG AGGTGATCGTTGTGTTGTTGCTGCACATTTTACTTTTTGCGTGTGGA
WI-7830	44	A G ---			GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATAAAATTAATTTGTTGTTTCCCTTG AGGTGATCGTTGTGTTGTTGCTGCACATTTTACTTTTTGCGTGTGGA
WI-7865e	25	C T ---			CCACTTCCTATCTGATTTTCCCAG[C/TT]AATGAGGAGGCAATTCAGTCTCCACAAAACATCTA GCCATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTCAGGGTGTCTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865d	191	C T ---			CCACTTCCTATCTGATTTTCCCAG[C/TT]AATGAGGAGGCAATTCAGTCTCCACAAAACATCTA ATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTCAGGGTGTCTCCAACTGAAATCTCAATGTTCTCAGT[C/TT]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865c	25	C T ---			CCACTTCCTATCTGATTTTCCCAG[C/TT]AATGAGGAGGCAATTCAGTCTCCACAAAACATCTA GCCATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTCAGGGTGTCTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865b	191	C T ---			CCACTTCCTATCTGATTTTCCCAG[C/TT]AATGAGGAGGCAATTCAGTCTCCACAAAACATCTA ATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTCAGGGTGTCTCCAACTGAAATCTCAATGTTCTCAGT[C/TT]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA



WI-7865	25 C T ---	---	CCACTTCCTATCTGATTTTCCAG[C/T]AAATGAGGAGGCAATCTAGTCTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTACATAAGATTTCAAGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCTATGTAAGGAAAGTGCTATTACCCAGTAACCCAAA
WI-7865	191 C T ---	---	CCACTTCCTATCTGATTTTCCAGCAATGAGGAGGCAATCTAGTCTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTTACCTATACAAACAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTCATAAGATTTCAAGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTA[C/T]GAAAAAC CTGAAATCACATGCTATGTAAGGAAAGTGCTATTACCCAGTAACCCAAA
WI-7867c	92 A C ---	---	TTCAACACCTGCTTCCACCTCCACCATCTGTGCAATCACTTCACCTTCAGCCTCACTAGTCCCO CTAACAATTACCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTAAATGTGGGTTTAAATATGGC CTGTTGAGTTTAAATGTTAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7867b	92 A C ---	---	TTCAACACCTGCTTCCACCTCCACCATCTGTGCAATCACTTCACCTTCAGCCTCACTAGTCCCO CTAACAATTACCTGTCAAGAGG[A/C]GAGTGCAGCTCAGGTGGATTAAATGTGGGTTTAAATATGGC CTGTTGAGTTTAAATGTTAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7868c	173 C T ---	---	TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGGCTTT CACCAACCTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGCTTACCCCTATTCAAGCA[C/T]TAGAGGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCAATCTAATGCCTAGAT
WI-7868b	173 C T ---	---	TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGGCTTT CACCAACCTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGCTTACCCCTATTCAAGCA[C/T]TAGAGGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCAATCTAATGCCTAGAT
WI-7868	66 T C ---	---	TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGGCTTT /CTCACCCAACTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACAC AATCATTTAATATTTCCCTGCTTACCCCTATTCAAGCAACTAGAGGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTGACTCAGGTTCCAGTAGTTCAATCTAATGCCTAGAT
WI-7870b	85 T C ---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAGAAAGCACTATTAACTCTGCAGTATTAGAAGGG GTGGGGTGGCGGGAATCCT[C/T]ATTATCAGACTCTGTAATTGAATATAAATGTTTACTCAGAGGA GCTGCAAAATTCCTGCAAAAAATGAAATCCAATGAGCACTAGAAATTTAAACATCATTAAGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGAGACCCACCTAATATCAATTG



WI-7870	76 C T ---	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTACTCTGCAGTGATTAGAAGGG GTGGGGTG[C]TGGGAATCCTATTATCAGACTCTGTAATTGAATATAAATGTTTACTCAGAGGAG CTGCAAAATTGCCTGCAAAATGAAATCCAATGAGCACTAGAATATTTAAACATCATTTACTGCCATC TTATCATGAAGACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54 C ---	---	---	TTAGGTCATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCTGGGGGGCGCTCTCCCCCTG CAGCGTGCAAGACTCTAGCTCATGAGTGGAAGTCACTACAGACTGGCGCGCCAGGGCCTCT GGCTCCCTGCCAATCCTCCCTGGAGAAGGACATGGGAATGAATTGAATGGGGGGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAAGGCTGTCTTCTCCAGAGCAAGAAG
WI-7889b	54 C ---	---	---	TTAGGTCATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCTGGGGGGCGCTCTCCCCCTG CAGCGTGCAAGACTCTAGCTCATGAGTGGAAGTCACTACAGACTGGCGCGCCAGGGCCTCT GGCTCCCTGCCAATCCTCCCTGGAGAAGGACATGGGAATGAATTGAATGGGGGGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAAGGCTGTCTTCTCCAGAGCAAGAAG
WI-7894c	142 A G ---	---	---	AGCCACCCCCAAATATACTGTTATCCAGAAGCTGTTATGTCCTGTTTCCATACATGTTTTGTACT TTTACTATATCATACATCAATTAACCTTATGTCCTATTGTTTGTGAATTTATATTGCGTATAC ATTATC[A/G]ATGTAAATTTGCATTTTATTGAAATTTATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA
WI-7894b	142 A G ---	---	---	AGCCACCCCCAAATATACTGTTATCCAGAAGCTGTTATGTCCTGTTTCCATACATGTTTTGTACT TTTACTATATCATACATCAATTAACCTTATGTCCTATTGTTTGTGAATTTATATTGCGTATAC ATTATC[A/G]ATGTAAATTTGCATTTTATTGAAATTTATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA
WI-7900e	84 C T ---	---	---	GCTCACTGTACCCATCCTTACTCTACTTGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C]TCCCTGCCATTGAACAGTGATTAAAGTTTGAAGCCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCAGATTTGAACCCAGTGAAA TATGATGATTCTTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T ---	---	---	GCTCACTGTACCCATCCTTACTCTACTTGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C]TCCCTGCCATTGAACAGTGATTAAAGTTTGAAGCCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCAGATTTGAACCCAGTGAAA TATGATGATTCTTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T ---	---	---	GCTCACTGTACCCATCCTTACTCTACTTGCCAGGCCACAGTAAACAAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C]TCCCTGCCATTGAACAGTGATTAAAGTTTGAAGCCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCAGATTTGAACCCAGTGAAA TATGATGATTCTTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC







WI-7901	33 C T ---	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATACTAGACACACACAGGACACATATATTAACAG ATTGTTTCATCATGTCATCTATTTCCATATAGTCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACCTCAGGCCCTGGTGGGGTGGGTATTTGGGCGAGCGCGGTGGTCT CACTCAGTCGCTGTCATGCTCTGTCATACAGACAGGTAACCTAGTTC!
WI-7901	271 T G ---	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATACAGACACACAGGACACATATATTAACAGATT GTTTCATCATGTCATCTATTTCCATATAGTCAAGAGACCATTTTATAAACATGGTAAGACCT TTTAAACAACCTCAGGCCCTGGTGGGGTGGTGGGCGAGCGCGGTGGTGGTGCAC TCAGTCGCTGTCATGCTCTGTCATACAGACAGGTAACCTAGTTCGTGT
WI-7926c	150 C A ---	---	---	CATTCGGCATCTGTCACCCAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCAT TTGGAGATCAGAAATTCATATTTAAGCAAGTGATACAAACACAGTGATTTGGGAATGCCCTCAT TACAATGCAATACCTTACATCTTTAATCTCTTTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAAATACACTGTGGGAA
WI-7926b	28 A T ---	---	---	CATTCGGCATCTGTCACCCAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCAT TTGGAGATCAGAAATTCATATTTAAGCAAGTGATACAAACACAGTGATTTGGGAATGCCCTCAT TACAATGCAATACCTTACATCTTTAATCTCTTTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAAATACACTGTGGGAA
WI-7926	150 C A ---	---	---	CATTCGGCATCTGTCACCCAGGACAGAAAGCATGGACAAGGATGAGCTTTACAAAGATGATGCAT TTGGAGATCAGAAATTCATATTTAAGCAAGTGATACAAACACAGTGATTTGGGAATGCCCTCAT TACAATGCAATACCTTACATCTTTAATCTCTTTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAAATACACTGTGGGAA
WI-7947b	203 G T ---	---	---	AAGAGCCAGCAGGTCAAAGGCCAACACACACCAATAGCAGCCAGCCACAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTACAGTTAGAAACACAGCCAGGCCACAGATCCCATCCCTTTCC TGAGTCATGGCTCAAAATCAGGGCCACCATTTGCTCAATTCAAATCCATAGATTTTGAAGCCACA GAGTTCTCTCCCTGGAGCAGCAGACTATGGGCGAGCCAGTGTGCCACCTG
WI-7947	203 G T ---	---	---	AAGAGCCAGCAGGTCAAAGGCCAACACACACCAATAGCAGCCAGCCACAGGCCAGGTCCTGT GCTATCACAGGGTCACCTCTTTACAGTTAGAAACACAGCCAGGCCACAGATCCCATCCCTTTCC TGAGTCATGGCTCAAAATCAGGGCCACCATTTGCTCAATTCAAATCCATAGATTTTGAAGCCACA GAGTTCTCTCCCTGGAGCAGCAGACTATGGGCGAGCCAGTGTGCCACCTG
WI-7963b	145 T C ---	---	---	CATGTGCTGCATGAAGAGCTAAATTTAAAGCAAGTAAGACTAATTTTAAATAAAAATGCC ACAAATTCATTTCTCCTCTAAGTATTACAATGGAGTTATTCTCTGCCTAAAAAGTGAAGAAAT TGAGTGAATGATTCJAAATTTTGAATTTAGGATAGATCCCAAGTTATTTCCCAACTCTTGTTCCTC CCATAAAGTTAGGCATGAGGAGGAGCACTATTAAAGCAGAAAGACGGAAAA



[illegible]



WI-8021b	57	C T	---			ACAACTCAGAAAGGACTGTGCAAGTCAATGAGTCGCTTGTAATCTCATCTGGAA[C/T]GATCCC ACGCTTAGAACCTTCACCAAGGAGTTTCTTGAGTAGATTCTCAAAGCTTGGTAGGCATTGGA ACTGGTCCCTTACATTTGAGATTTCTTTTGGCCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAGGGGTGATTGCAATTCGGTGAATTGCCA
WI-8021	57	C T	---			ACAATCTCAGAAAGGACTGTGCAAGTCAATGAGTCGCTTGTAATCTCATCTGGAA[C/T]GATCCC ACGCTTAGAACCTTCACCAAGGAGTTTCTTGAGTAGATTCTCAAAGCTTGGTAGGCATTGGA ACTGGTCCCTTACATTTGAGATTTCTTTTGGCCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAGGGGTGATTGCAATTCGGTGAATTGCCA
WI-8024c	206	A G	---			CTGAAATTTACTATGCTCTCCACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTTAGGAGGACAGGCGAGGGATCCAGTGGCACTTCCATGGGAAGACAGAGAGAGT GGCCCCAGAGATGGAAGGACCCAGTGTATCACCACCAACACCATTTTCAGCCGCTTAGCCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCTGTCAGTACACAGGAAGAGC
WI-8024b	206	A G	---			CTGAAATTTACTATGCTCTCCACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTTAGGAGGACAGGCGAGGGATCCAGTGGCACTTCCATGGGAAGACAGAGAGAGT GGCCCCAGAGATGGAAGGACCCAGTGTATCACCACCAACACCATTTTCAGCCGCTTAGCCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCTGTCAGTACACAGGAAGAGC
WI-8077	167	A G	---			GAATGAGCTTCTAGCGCGAGGGACCTGCTGCTGTTGTTGGCCCTGCACATGCTATGGAATGC TTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTGCCCAAACCTCTTCT AAGGAGTCTGGGGTGTATGCCCTACAAAC[C/A/G]TAAATTTCTCATCAGATGGATTTTATTAAAGTT GTGATTGTGACTTACTTTCCAATCTGACTCTGGCATAACAAGGGAAAA
WI-8118f	114	G C	---			TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGAGCTTGTG[C/T]TTCTTAGCCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A G	---			TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGAGCTTGTGTTTGTGTTTCTTAGCCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T G	---			TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACTGGCAATACAGAATGAGCTTGTGTTTGTGTTTCTTAGCCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA



WI-8118c	44 C T ---			TCTAGGTTTAAATCAAAGCAATTGCANTTTGGATTTTGAATGAIC/TCACCTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAACTGGCAAAATACAGAATGTAGCTTGTTGTTCTTAGCCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCGTATTCCTGCTCCTCTATTCCTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---			TCTAGGTTTAAATCAAAGCAATTGCANTTTGGATTTTGAATGACCCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAAC/T/CGGCAAAATACAGAATGTAGCTTGTTGTTCTTAGCCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTCGTATTCCTGCTCCTCTATTCCTCT AAAAATCAGACTCATTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---			TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGGCCTCGGGAAG AGGGTAGGAGACCGAGCAGCATCTCTGTAGAGGAAGACAGAAAGGAGACCCCTCTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAAGGC ACCAGTGGGCAAAAGAGCACAAATGAAGGATGATGATAAAAACAATCACGGCA
WI-8171c	46 A G ---			TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/AGTGGCAGCAGGGCCTCGGG AAGAGGGTAGGAGACCGAGCAGCATCTCTGTAGAGGAAGACAGGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAA GGCACCAGTGGGCAAAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171a	46 A G ---			TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAAC/AGTGGCAGCAGGGCCTCGGG AAGAGGGTAGGAGACCGAGCAGCATCTCTGTAGAGGAAGACAGGAAAGGAGACCCCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAA GGCACCAGTGGGCAAAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171b	298 T C ---			TTTTCTCTCTCCGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCAGGGCCTCGGGAAG AGGGTAGGAGACCGAGCAGCATCTCTGTAGAGGAAGACAGGAAAGGAGACCCCTCTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAAGGGCAGGTGGGAGAGGTTCCCTGTACTTAAGAGAAGGC ACCAGTGGGCAAAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8314b	85 G C ---			GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGG/GC/JAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACTGTCCAATAGAACTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT
WI-8314	78 C G ---			GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCCATTCGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAGAGCACTGTCCAATAGAACTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT



WI-8321	178 G A ---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCTGTATATACTAGTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTGAGATG/AJAGTATCTTAGTATTTCTTCTA TTTTGCTATGGTTCTAGTTATCAACCTACTTTATTAGCTGAACGTGTTGGC
WI-8321	178 G A ---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTTGGTACTTTCAAGAGCTGCTGTATATACTAGTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTGAGATG/AJAGTATCTTAGTATTTCTTCTA TTTTGCTATGGTTCTAGTTATCAACCTACTTTATTAGCTGAACGTGTTGGC
WI-8332b	123 A C ---	---	TATGTACTACATTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTTCCCTGTGC/AJAGTATCTTAGTATTTCTTCTA CAGTACTGTTGGTGTGTTTCTTCCCGAGCAATGCCTACTGCAGCTACTTAGTAACAACACTAG AGGTGGAGGGTNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114 A C ---	---	TATGTACTACATTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGGGGATATA AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTTCCCTGTGC/AJAGTATCTTAGTATTTCTTCTA CAGTACTGTTGGTGTGTTTCTTCCCGAGCAATGCCTACTGCAGCTACTTAGTAACAACACTAG AGGTGGAGGGTNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311 T C ---	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATCATGGCAGAAGGGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAGGAGGAGTCTACACACTTTT AAACAACAGATCTCATGAGANTTCCATCGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCTNTCACCAGGCCCTCTCCACACAGTGGGG
WI-8378	308 T C ---	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCCTCAGGAAGCTTATAATCATGGCAGAAGGGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAGGAGGAGTCTACACACTTTT AAACAACAGATCTCATGAGANTTCCATCGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACCTNTCACCAGGCCCTCTCCACACAGTGGGG
WI-8426	184 T G ---	---	TTTAGCACATATTTAGCATTAAAGCCTCAAACGATACAGCAATATGTTACATTTCTTTGTGAAAACAG TTGTTGTAGACTGTTAANNNNNNNAATGTAACCTCCGACTTGTGCCTAATAGGATTTGACCNITAA GAGNTTCTTTTGTGTGGANGGGTGGCTTGTGTAACCTCCATCTGT/GJGCTTGTAGCTGGTG AGGCTGGGAGTATGGANGNCCCGGGGCCCTTGGCNATGNATTCAGTGAG
WI-8450h	61 C A ---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTACATACACTC/AJCA TCTTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTTGTTATTTAAGA AAAAACCTTCCCAGTTATGTGCAAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAAATGCAATTCAT



WI-8450g	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTC/JACACTCCAT CTTCTATCTTAGTTCCTCAAGTTTAGTTTCAATCCCAATATACCAATTCATTTGTTATTTTAAAGA AAAACTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCTCAAGTTTAGTTTCAATCCCAATATACCAATTCATTTGTTATTTTAAAGA AAAACTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCTCAAGTTTAGTTTCAATCCCAATATACCAATTCATTTGTTATTTTAAAGA AAAACTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCTCAAGTTTAGTTTCAATCCCAATATACCAATTCATTTGTTATTTTAAAGA AAAACTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCTCAAGTTTAGTTTCAATCCCAATATACCAATTCATTTGTTATTTTAAAGA AAAACTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61 C A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCC/JCA TCTTCTATCTTAGTTCCTCAAGTTTAGTTTCAATCCCAATATACCAATTCATTTGTTATTTTAAAGA AAAACTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTC/JACACTCCAT CTTCTATCTTAGTTCCTCAAGTTTAGTTTCAATCCCAATATACCAATTCATTTGTTATTTTAAAGA AAAACTTCCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60 A G ---			CAAGGAAAGCTGTCAGTCTTCATAAACCTTCAAGAGGTTACAAAAATACGTTATTTTAA/JGJCTA CAATTCAGATTAGCATCCAACTACAAACATGATGATACATTCGTCACACACCATACAACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATGTTTATACCTTGTGAAAACTTTATTGTGCACAGT GACATCCATCCGCCAGACTTAATGTTATAAAGCAGCTGAGCAGAGTTCTCA



WI-8461c	105 A T ---			CTTCCTCCTCCAAAATCTACATGAATACCTTGAAGACAATAATACTACAACCTTACAATGCCAATTA GACAAAGAGANTAAATGATATAATATAAATCATTTT[A/T]NNNNNNNNCCCTGTCTTATTCACAT TCAGGGAAGTCTAGCAACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAAANTCAAGGATTGCAAAAAGGGGG
WI-8461b	38 T C ---			CTTCCTCCTCCAAAATCTACATGAATACCTTGAAGACAAT[C/J]ATAACTACAACCTTACAATGCCAA TTAGACAAAGAGANTAAATGATATAATATAAATCATTTTNNNNNNNNCCCTGTCTTATTCACAT TCAGGGAAGTCTAGCAACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAAANTCAAGGATTGCAAAAAGGGGG
WI-8461	38 T C ---			CTTCCTCCTCCAAAATCTACATGAATACCTTGAAGACAAT[C/J]ATAACTACAACCTTACAATGCCAA TTAGACAAAGAGANTAAATGATATAATATAAATCATTTTNNNNNNNNCCCTGTCTTATTCACAT TCAGGGAAGTCTAGCAACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAAANTCAAGGATTGCAAAAAGGGGG
WI-8461	105 A T ---			CTTCCTCCTCCAAAATCTACATGAATACCTTGAAGACAATAATACTACAACCTTACAATGCCAATTA GACAAAGAGANTAAATGATATAATATAAATCATTTT[A/T]NNNNNNNNCCCTGTCTTATTCACAT TCAGGGAAGTCTAGCAACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAAANTCAAGGATTGCAAAAAGGGGG
WI-9438	77 A G ---			AATAACATGTTATGAACAAGCTGTTACAAGTAGTAGGTAGTGACCTTAATTTTGATAAAAAAT TAAAAAGCAT[G/A]ACATGCATATAAAAAATTAGATTATGTACAAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAAATATTCCTCCCTTGTGTTTGTCTTTTAAAAAACATTATTTCTGAAAAAAA ATCAGAAAAACATGATCGTGGAGAGAAATTATTA
WI-9439b	101 C T ---			ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAAGTAACATTTTAGTA CAGAAAAATCCCAGTCTGCAGCTCAGTACCTG[C/T]GTGCACACTGTACCATCTCAGTCCCACCTCT GCCTGTAACCTTAGAAAAACAGCCCTACCCCGAGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACTGTACCTGTAAAAACAAAG
WI-9439a	76 C T ---			ACAGAAATTGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAAGTAACATTTTAGTA CAGAAAAAT[C/T]CCAGTCTGCAGCTCAGTACCTGCTGTGCACACTGTACCATCTCAGTCCCACCTCT GCCTGTAACCTTAGAAAAACAGCCCTACCCCGAGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACTGTACCTGTAAAAACAAAG
WI-9446b	75 T C ---			GAAGGCTTGATTAAAGGGAGGNTTATTTGATGTNAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAA[C/C]CCTCTAAAGNGACACATGCCCCAAATGACCANGNCATAGCAAAACCTTTTAAAT TACTCATCTTTCATATGTGTTTGTGNCCTTACTNTATCACTGTGCTCTGCTTGTGCTACCTTA TGNGAACTGCACACTATCTGTGGCAATATTGT



WI-9446	75 T C ---	---	GAAGGCTTGATTAAGGGAGGNTTATTGATGTNAACCTACCAATCCATAGACTATAAAGANCATTATAAAAAATTC/CCTCTAAAGNGACACATGCCCAATGACCANGNCATAAGCAAAACCTTTTAAAT TACTCATCTTTTATATGTGTGTTGTCNCCCTACTNNTATCACTGTGCTCTCTGCTTTTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATATGT
WI-9497b	185 A ---	---	ATTAATAATGTCAAGGTTTCATGTTTACATTTCTTATATCAAGTACAATGGTATATATACATTTTGTGA GAGATAATTAATCTAGATCCAGGCTTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAAAGTATGTTAATGTCACCTT GGAAATCTACATGGAAAAGCCCAACAAATAACTAAACCTTGACTAATGAAG
WI-9497	185 A ---	---	ATTAATAATGTCAAGGTTTCATGTTTACATTTCTTATATCAAGTACAATGGTATATATACATTTTGTGA GAGATAATTAATCTAGATCCAGGCTTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAAAGTATGTTAATGTCACCTT GGAAATCTACATGGAAAAGCCCAACAAATAACTAAACCTTGACTAATGAAG
WI-9523b	193 C A ---	---	GTGAAAAGTTTCTATTCATTCATCATACAATAGATTGTGCTAAGGATCATTTTGGAAAGATGTG CAGCATTGAGAAAGTTGTATCTCATCATGAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCACA GACTCAGACAATTACAACTATTTCCAGCCATGATCTATGGTGATTTTCCACACATTTGTA/C/AJAGTG AAAGCTCTTCAGCTTGGAAACAACCTTGCAAGGCAGACTGCATGCACATATAT
WI-9523a	47 G A ---	---	GTGAAAAGTTTCTATTCATTCATCATACAATAGATTGTGCTAAGTATGTAAGTATTTTGGAAAGAT GTGCAGCATTCAGAAAGTTGTATCTCATCATGAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCA CAGACTCAGACAATTACAACTATTTCCAGCCATGATCTATGGTGATTTTCCACACATTTGTACAGTGA AAGCTCTTCAGCTTGGAAACAACCTTGCAAGGCAGACTGCATGCACATATAT
WI-9554	202 T C ---	---	AAAAACACAAGTTTCATACATCACAAAAAACCTTCCATTATAACACAGAAGTGATTATTACCAGAC AAGCATCAGTGATGTATCTGCTTTCAGTCTTCTAGTGTGTTATGTACAATGCTGTAGATAATGCAGCCCATG CAATACACCCCAAGAACACTAGAGTCTACACCCCAAGTACAATATGATAAGCAGCCCTCTGCAAGTG GT/C/GCTGGATACCACTAAGAAGTCTACTGCAGCCATGTTGGTTATGATTTT
WI-9555	97 G A ---	---	CCAAAAGCCAAACCATTCATATGTATGGATTTCATAAACATTTTATGATCCTTTTGTAGGTAAGTAT AAATACCTTTTACATGGCTAACCTTCTAACIG/AJCTTGAAAAATCAATTTCAAGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAGGCACAAATGATCATCTCAGATTAAATACAGGTAAGTATTCAG GGNTAAATGGTACAAAAAAGGCTGTAACTCTTTTNCITTCACATTGATCACA
WI-9625b	172 A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCCTGGGAAAAACITTTGGAAAAAACAACGCACACA TAAGTATCATAACTGAGGGTTGGGACAAGTTACTTCT/ATGTTTACCATTTTATATTGACATAA AGTAGCACAGACTAGTATTTCATTTAAAAAACAACACTGACAAATCTTTTC



WI-9625	172 A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCCCTGGGAAAAAATCTTGGAAAAAATCAACGACACA TAAGTATCATAACTGAGGGTTGGGACAAGTTACTTCTATGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTTCATTTAAAAAACAACACTGACAAATCTTTTC
WI-9647	144 C T ---	---	TTTTCTGAGATTCAAAGAGCTACATTTTGGTAGTGTACTATACCTTTTTCATCCTTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTTTAAACAGTGTATGCTAGACCTAAAAATCCAGCT TACAACTCTGTGCTTTACCTGATACATTTATCCATTTACTTTTCAATTTTAAAAATGTTA ACTTAATACGTCTCTTCAGATGCCCTGCTTTTGTAGTTAATTGTTTT
WI-9676n	114 A G ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGTGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTTGT
WI-9676m	184 G T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGTGTGGCTTTCTCTGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTTGT
WI-9676l	84 A C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGTGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCAATGTTTGT
WI-9676k	202 C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGTGTGGCTTTCTCTGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA C/TTCAGGGTCTCTCAGCTTTAAGCCTTGGAAATCCTATGCAATGTTTGT
WI-9676j	92 C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGTGTGGCTTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAGCCTTGGAAATCCTATGCAATGTTTGT
WI-9676i	173 T C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAAATGCAGAGCAAGTGTGGCTTTCTCTGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAGCCTTGGAAATCCTATGCAATGTTTGT



WI-9676h	134	C A ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGCCCCC C/AJATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676g	202	C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGCCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGG C/TJAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676f	184	G T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGCCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676e	173	T C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGCCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676d	134	C A ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGCCCCC C/AJATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676c	114	A G ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGCCCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676b	92	C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGCCCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676a	84	A C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCTGCCCCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT



WI-9738b	40 C A ---	---	TGGACCAACACAGACAGATGATTCCCTGGTGGCTGTGTA/C/A/JATTACAACCTCATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAACACACAGTAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACTTGCCTGGAGCGGGTGGTTTTCACTATGTGAGTATCTA TCITTTATTCTGTCCTTATGTTGGTGGGCACATGCTGTATTGCTGCC
WI-9738	40 C A ---	---	TGGACCAACACAGACAGATGATTCCCTGGTGGCTGTGTA/C/A/JATTACAACCTCATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAACACACAGTAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACTTGCCTGGAGCGGGTGGTTTTCACTATGTGAGTATCTA TCITTTATTCTGTCCTTATGTTGGTGGGCACATGCTGTATTGCTGCC
WI-9756	47 A ---	---	ACTGAAATGTAATGGCCAAAGGCCACCCAGGACCTTAAAAATCATAAGAAGTTAATCTGTGGGAAAA GAGTAACATAAAAAGCATCTAAACAAGAGCAGGATGTGATGTAATGTGTCCTCCCTTATCAGCTTAGTC AGTAAAGATAAGAAAGCCCTGGTGAGTATCCACTTCCACAAACACACAGAAATATACACATTTTGGAAAG ATTCCACTTAACCACTTGATTCTTCACITTTTATGATTTAAACCTCCCGTGG
WI-9758	135 A G ---	---	GATGTCCTTAAGGATTGCAATGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATGGAATAAT TAGGAACTGGGAGAAATCAATCAAAGAAGAAATCTTGTTCGCAAGGTCAATTTTATACATATTTA A/JGJTAATAAATCTGCTGGTAGGTTCTATAGCAATGCTAAGTAAAGTAACCGCTGGTTCTAAAT ATTACG
WI-9778	127 G A ---	---	ATTTAAATCAGGCAGCGGGGAAAAATGGATACTTTTCATATGTCTGTACCCCACTATAAATCTTTTG GTTCTCATGCACCAATTTTCATTTGCTCTCTCACTCCAGTACCAGTATTTACCAATTTG/AJCTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTAGAATGTTGGAATTTCTCTATTACACACITTTGCTCA AAGAATGTGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116 C A ---	---	TCCTCCCTTGGCTCCTCATGCCCACTCCCTCAGCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGTGACAAATGCAGTTTC/AJTGATCCCAAGGAGGAG CTCAAAAAAAGTGGAAATGGGAGAGAGGACCTGGAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAGTGGACTAAAGTTTGAGGACCAGACATGGAAGTTGGCTTTGGC
WI-9841	101 A G ---	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGCTATGGAGAAATGCAGAAATGGCATGA TATGAAATCCCATTTTGAATGAATAAAATATAC/AJGTGTATGTATATATCTTATTAACTTT AGGATTATATACACACAATAAACGCTGTGAAGATAAAGTCTATCAGTGGGAAATGAGA TTGAAAGAGGGGATGTGTTACTTGTATGCTGTTG
WI-9880c	222 G A ---	---	GAACATAACACCTTTCTGCATGGATTTTCTGATTATTGGCAGTTAACAATAAAATGTTATTAGATC ACTGGTCTCTGTGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATTTTATATAAGCACATGAA AATGGAATGAAATAATGA/GAJTTGACATAGGAAATTACCTACATATTTTG



WI-9880b	157	C A	---			GAACAAACACCTTTCTTGCATGGATTTTCTTGATTATTGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGGAC/AJTATATAAGATCCTCTTTTAAATATATATTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T	---			GAACAAACACCTTTCTTGCATGGATTTTCTTGATTATTGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGCTTCTGTGGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTG TGAGTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATATTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T	---			ACACTGAGGGACTCCAAATCCTNACAGACATATGCACCTCGGAATCAACTCAGGGATGCACAGCAT CCCTGTGCTGGAGTTTATTTTAAACAAACACGCCCGAGTTATCACAGTTCTNTTTTGTCT/CACCC ATTTCCATAACAAAGAAGCTACACAAAATNGGGGGGAGANACTCTCTTTGGAGACTGACACACATT TGCAGAGGGGTCATGAATAATGATTCCAAA
FB25G10b	109	A G	---			TCCCTCAATGACAGATGAACATAATTTCTCTTGGGTAAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGAA/A/GJTGATTTTAGATCCTCCCCCAG TGACAAAGTAAACTGAACTGACCATAATTTATACATAAAATGGAATGTAAGAACCCTATTTTGGATATCC CGGAC
FB25G10	109	A G	---			TCCCTCAATGACAGATGAACATAATTTCTCTTGGGTAAGAAATACTTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGAA/A/GJTGATTTTAGATCCTCCCCCAG TGACAAAGTAAACTGAACTGACCATAATTTATACATAAAATGGAATGTAAGAACCCTATTTTGGATATCC CGGAC
IB3071	102	C A	---			ACAACGCTGAACCTCCATAACAGTCAATGGTACAGTCAACATCACATGTACAGAACACACAATTTA GATGAACCTGAAATTAAGNTAAATAAAATAAAAT/C/AJCAATTTTCAGNAAACAAAAATCAAAAC ATTAAGGNTCCCTGNNATAATCTTAACCCCTAATGAGATTTCACTGGNCTCAAGTCATTTTGTAGTGA GGCATTCAACAATATGACCCCTATTACCCAGTCTAGGGATTCTG
NIB551	161	C T	---			CGTCCTTTCTTTTGGAGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAATTGGGTTGTCCC TACTGAGCTTGGGGCCAGGTGTGACTTAGGAACCCCAATCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGTCT/TTGACCACATACATCGGGCCATTGGTTGATTTTCAGCTTT GCAAGCAGCGTAGTGAGAAAACCAAAAGCTTGTC
S72904	51	G T	---			AGCATAGAAAGTGATTATATTTTAAATGGTTTTCAAGTGAAGTCTCTT/GTJAATTTGTCAGTTC ATTCTGGAAAATCTTTGAGTTAAATAAGGATCTAGGACAGCACTCGAAGTACAGGCCCTAAA GAGAAATGGCTCAAAACCACAAAGTGTGTAACCTCTCCCTCTCTGTCAATTGGTTGCTCTTAAATA TTGCAAAAGTCTGATGCTAAACAGTATTTGGAGTGTTCAGTGTCTGTA



UTR-00481	115	CT	---	---	TATCTTTTATCCTGGGCCACAGTCTTGATTATTCCTCTTGTTAAAGACTGAATTTGTAAACC CATTAGATAAATGGCAGTACTTTAGGACACACACAAACACACAGAC/TJACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTTAGCATTTCAGATTGAGC
ESTC1	33	---	---	---	CCCTGTAGCAGTCTCAGCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTTCTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAATTTCCCTTACANTCAATACTGTTGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGGCTCACTTCTCACANGCTGTATTACCTTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	AAACCAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCCACAGTGAOC
ESTC110	23	---	---	---	AACTCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGACACAGTGTGCTGACAAGGTGACACTGAACANACAGTTTTCCTTTAATTGTAAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCTATCACAATTTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34	---	---	---	GACAAATAACACAGCTAAGCTACTGACATAAAATATNCAATAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACACTGAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCCTCAGAAAAGCCAGGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGTGGAACCTGG
ESTC129	20	---	---	---	AGTCACCATGCCAGCCTAGNATGAGTTTAGTAAGATTGGTTATGCTGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAA
ESTC130	49	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAATGAACANGAGAAGCTGAAACAAT CTACACCTGAATG



ESTC132	30	---	---	---	GGTAAAGTCTAAATTACTGCTTAGCAACNCTATGTTGTCAGGTTTTTCTGCTGCA
ESTC137	21	---	---	---	CCAGTTGGCTTCTGCTCCTCANAGTCTCTCTCCATGTGGCAAACA
ESTC139	45	---	---	---	AGGAGCACAGCCTAAGGACATGAAGGTACAGATTCTCAGAGAGNGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	CCCATTGTGGTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTCCCTTGCGTGGTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATAATCTATTTTATTCATTTTAAATC AAAGANACCATTCCTTAACAAACA
ESTC143	29	---	---	---	GTTTACGAAAAGTACTGAAAATGCTATTANTAGCTGAATTTGTGATTCCTTTTG
ESTC144	26	---	---	---	AAATCCATATTTCTTGACATGAGGTNGCTTTTATAGCAGCATTTTCGG
ESTC146	20	---	---	---	CATGTCAGGATAAGGAGCANACACCAGGATTATACACGGTGGCAGCG
ESTC148	42	---	---	---	TCCTTGGTTGTCTACACAGACACTTAAGTACTGTATCGTGTNATGCAGCGGCTGTGGAGGCCCCCTG GGGGTGGCTGGGCTGTGCTCTGAG
ESTC149	28	---	---	---	TCAGTTCATTTATTTGCTTTAAGAGTTANATACCATGAGACACAGTTCTGG
ESTC15	28	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCAITTAAGCAGAAGTTTCTTCAGTGATCTT
ESTC150	20	---	---	---	CCAGGAAAACAAAAGCACACANACTTATAGAATACTTTGGTTTAAAAATTATTCATAATATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	GAAGCTAAGGCCCAATTTTTTTCTTTTAAATACAAATCTACTGGTGTCTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	TTTTTAATTGACAACTCAATCTCTACATACATACAGTNTTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAACTCATGAGCAATTTACA
ESTC156	32	---	---	---	GCAGCATTTGTGACAGGAGAGCGCAAAACAAANCCTGGCTGGGATGGAGCGGGGGCGGCTCA CCACCACTGCAT
ESTC158	35	---	---	---	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	AGCTGGCAAGAGACTTCTCTGAGGCACATCAGNTACGTTGGTCAATTTAGGGCACGGTCTGGTTCTGCA GCTTTGAAAGG



ESTC16	23	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCCCCACAAGGACAGGTT
ESTC160	38	---	---	---	TTTAGCATTGCTGGTGCAGTGGGGGCTGAGCTGGGNGCAGTGGCAGTGTCAGTGGGCCGCTTG GGACTGGGTGA
ESTC162	36	---	---	---	CTCTCGTCCGTTTGCAGTTGCTGTTGTTTCCAGNTACACCAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	TCATTCTCCATAGAAATATTGTTTTGTAAACANGAATAACAATCCAATATATAACATTAAAAACAATCC GATACATACCA
ESTC169	22	---	---	---	GTCTCTGGTGTGCAGGGAATCANTTTGTCTGGATTAGAGGAAGGTGCCCGCTCTGTTCCATGACTT
ESTC176	23	---	---	---	CACCTCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	---	---	---	TGGGTGGCTCTTTAAATACCTTCCATTATATTTTCAAAATTTTNCCTTATTCTATTAAAAATACCTTTTAT TCTCTTTATCCCATAAAAAGGCAACCAA
ESTC18	29	---	---	---	TCAGACACTGCCGACATCAGCATTGTCTCNTGTACAGCTCCCTTCCCTGCAGGGGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	TAGGGATTCCAAGTTGCCTGGNTTTAATATAATACATATTCACAAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	GCTTGACTAGCGAGGCTACATCACAAATTTATAAAGTGCCAGATNAGTGCTAATTGTCATTCAAGCTTG ATTTTTCACCTCA
ESTC187	24	---	---	---	ACCATGATTGCCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGATGGCTGG
ESTC188	25	---	---	---	TCTATTACAGGGTTATGTCACACCNTGTCAACCTCAAAACAGATGATACTCATCATCTGCTTCCAT CTTGC
ESTC189	27	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGGATCACACTCGTGATCA
ESTC196	42	---	---	---	TCCTCAAATACCACCTTCCCTAACTTATCAGTCTAGTAGCNTTTCAAAGGAGGAAATGGGTAC CTTTCAGGGG
ESTC197	26	---	---	---	ATCTCCAGTGTCTGCTGCCCTCCCNCGCAAAGTCTCCACAAGCACA
ESTC20	33	---	---	---	AAGATTAGGACAGACCGGTATAGTAGCTCTGNGGAACCTCCAAAGAAATCTAGAGGGGGCTGTGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	TTTGGTGAAATCCCAATATATGAGTTTAAAAAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTTGCCTGCAACAG



ESTC201	35	---	---	---	TCTTACTTGGGTAGTTTACAAACAATTTTAAANCCACATCCAACAGATTGGTT
ESTC202	22	---	---	---	CTGCTGGAGGGAGGACAGACGNCAGCGGCTGGTGCGGCCCCAGAAAGGCTGGCGTGGATGTT CGAGATGAGCC
ESTC203	27	---	---	---	ACACTTAACAGGTTAAATATCCAAATNAATTTACTGCAACTTTTGTAGAAATTTTATTGTGCTAC AAGACAGTTGCA
ESTC208	43	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATAACTATTGTTTAAAGC CTAAGAGTGAAAA
ESTC210	29	---	---	---	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAGAGTGAGTGACGGTGACCTGTG
ESTC212	27	---	---	---	GGGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGGT TCAAGTC
ESTC214	21	---	---	---	CTCCAGAGTCCCTCCTCANACCAGGGGAGGAGGTTAGGGAAT
ESTC216	49	---	---	---	TGGCAAGAAATTTATTACACTAACAAATTTAAATTAATCACAGGTATNTTAGATTGGTCAGAAAA CAAAAGACCA
ESTC217	28	---	---	---	TTTTGTCAATAATGAGCAATACACTGANTGGAAATCTGCATGATTAATAACATTAAACAAGTTTCA AAACACACCCCA
ESTC219	32	---	---	---	GTACACATCCTGGGGTGAGCACACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAAAGGAAGC
ESTC22	41	---	---	---	TCATTGAAGAAAAATTATGGGTTTTATTCTTAATTGNGAGAATGCTTAATGTCACAGGCTACA TAAGGGCC
ESTC223	27	---	---	---	CTTCTGAAGCCCAAGAGAGGGGCGAGAANGTAGTCTTGATTTAAAAAACAGAAAGGGGAGGAGGA
ESTC224	37	---	---	---	CGAAGGTAGATTTCCCTCACATATTACAAAATACACANAACACACACACACACACACA
ESTC225	20	---	---	---	TGCACTGTTACTCCCGACACNGAGAGCTTACATACCATATAGAAAGAGCATAGTGCTTCAGAAAGGA ATGTGTAGGATCG
ESTC23	27	---	---	---	TTCTACTTTTATTCATATTCCCACCACNATAACGACTCCTTTAATTTAACTAAAAACCATACAGGGT TCCTGAAAGGG
ESTC230	43	---	---	---	GCTTCTCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA
ESTC231	24	---	---	---	CAAAAGGGTAGTCATATTCGCCCANCAACAGCATGATAAAATAATTC AAC



ESTC28	23	---	---	---	GAAGAGCTGGGCACGCATCTGACNTTTCTTCTCTATTCCTATAAAAAATAAAGGAAGCAGAAATCT GC
ESTC3	20	---	---	---	CAGACATGACCTACCGTCCNGCCCTCAATTCATATTTATCTTGAGCCGCTTGGTCAGGTTTGAT TCGCACACTCC
ESTC31	32	---	---	---	ACAGCCCCACAGAACTATTGTAAACAATATNTCAGTCGGTGATCATTGTAATATACATAACAAAG CAATTTCTCTAGA
ESTC33	25	---	---	---	AGCACTCCAGCTCCTTGACGTTGTNGGACCAGGGAACCTCCGGAA
ESTC39	26	---	---	---	AAGGAAGGGAACCCACCTGGGCTTNGGTCACAGAACTCAGAGCCTGGGCATTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAAAATCATTTATGCTGATGGAAGAAACCAATT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTGAAGATCTTTTAAAAATATTTTGACTTTGCCCTTCAC
ESTC45	37	---	---	---	TTTGAGGTTTGTGCTGGAGTTTGTCTTTGTAACNCTCTCATCGAGGCTATATAATAA
ESTC50	56	---	---	---	CTGTCCGTGGTGAGCCCTGCCCTGTCCCATGGGCCAGGAGCCACTGGTGGGANCOCGGCAGATG TTACCCCTGT
ESTC56	45	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTTGGCAGGAAGNAGTGGAGGAAAGGACACCA AGT
ESTC57	20	---	---	---	AAGTGGGCCCTCCAGTCCCTCTCTGGGCACAGATCCCACAGTCTGCTC
ESTC59	38	---	---	---	GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATTTGTTCCAGACTTCAGGAAAAATGATTTCC ACATGGTAAGGCC
ESTC6	27	---	---	---	TCGTCAGCACTTCACTACCAATGAGCNTTAGCTACTTTTCAGAAATTGAAGGAGAAAAATGCATTATG TGGACTGAACCG
ESTC61	57	---	---	---	AGTGATTTGGCTAGGGTGTCTCATCTGTGAAATTCACAGCGCAATGACAGCANCCTCTCTCCC ACCCACTCAAG
ESTC63	20	---	---	---	ACAGACACAGCATCACACCANAGGCCCCACGGGAGGTCTGGGAGACGACACTTTTCCCTGGGAAA GGCAGCTCTAATC
ESTC69	20	---	---	---	GAGAGGCTAGTCAGGAGGGANACCCTCAAGTTTAAATCCACACACTTACTTACTGCTCATCCGT CACTTTCGCTAA
ESTC7	45	---	---	---	AGTTTCCCTAGAGCTGTGGGCCAGATAGCTTCTCTGAGTTGCANGCAGCATGGAGATTTGGACACT G



ESTC72	37	---	---	---	GGGCTTCACAAATGGGTATTGGGGCCAGGAGGCTGGCNITTTGGGTGACGCCTAAAGAGTGTGAOC
ESTC74	49	---	---	---	AACAAATTCACAGCTACAGGAAATCTAGAACAAAAATCAAAATATTCACACNTTGGGTGAAAAAGTTG
ESTC77	40	---	---	---	GAAGA ATGACTTTCTGTCCCATCGGAAACAGAGTTTCCCCAGGNGAGCCCTTCCTATCTGCGGTTA
ESTC81	20	---	---	---	GGCTCAGCACAGGGATAAGANCCCCACTCCGCATGTCCCCAGAGGGCAGCACCTCCAG
ESTC82	25	---	---	---	TTTCAGATGATGGGTCTGAGATGNTCCTCAGGCTGCATCAGCTGTCTTCAGTCTCCAGAACAGAAA GAGCCTGACCCA
ESTC83	53	---	---	---	CAAAATCAAAATACACAGATCCAGATATGTGAACCATATATACATATCTATACANCCATTATTTAGAC TTTCACAAACCT
ESTC85	28	---	---	---	TTTAGCTGCTATACCAAGTTTCCATAAANCTGTCTGCTGTTGGGGAGGCTACAGCCTGACCACATTG TTTGC
ESTC89	22	---	---	---	ATTGCAAGGAAGTGGAAACGTGNTCAAAACAGAAAATGGTGACAATGA
ESTC90	33	---	---	---	CTGGTCTCTCGTCTGGCATTCGTCTCCTCNGGCCAGTGTCCACCCAAAGTGTCTTCCCGATGAT
ESTC93	29	---	---	---	CTCCCTCCTCAGTTCACAGTGAGACTANGGAGATTACGGCAGGATCC
ESTC95	32	---	---	---	GCACGTCTTTGTCTCCTCTTCAGAAAGTTGNAGACGTCTATTTAGTTGATTATCTGTGCG
DWU-100	127	C T	---	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCCTAATTCA GTGGATCTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTTGACTGTCTCCA(C/T)GCCAG ATCTTATCAATGATCTTTCACCTAAGAAACAGCAAAAGATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATTGCGATTTTCACAAAAATCAAAAGAAAGAAAGGCTTAGCTG
DWU-177	77	A G	---	---	TTCCATCCTAGATATCTACTCAAAATAATTGAGACAAGTTTCAACAGAAAGACGCTTGTGCTGAA TGTTTCATGGC(A/G)GCCCTATTTCACAGTAGCCAAACGATGAAAAACAAACCCAAAGCTATATTAACA GATGAAAGGATAAACAAAAATGTGGTCCATCCATACAATGGAGTATTACACAGCCATAAAAAAGGAAT GAAGCAGTGTATCCCTACTACACTGTGGAT
DWU-286	213	A C	---	---	CAAAATCCTGGACTATCAACCTTGTGCTTAATCCCTGCAGCATCAAGGTTATCCATCTAAGTGAC ATTTTGAATTCAGCGGTGCCACCCCAATCATGCCAGCTTCTGTATATGAATGAGATATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTTCATGTCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGG(A/CT)GGGAAACCCAGCCCTATCTGAGTCTCGGCTCCCTCC



DWU-252	94 A G ---	---	AGTATACAACATTTAAGCTGTGGTCAAGGCTACAGATGTGCTGACAAGGCACTTCATGTAAAGTGT CAGAAAGGAGCTACAAAACCTACCCTCA/GJTGAGCATGGTACTTGGCCCTTTGGAGCAACATCGGC TGCAATTGAAGATCCAGCTGCCTATTGATTTAAGCTTTCCTGTTGAATGACAAAGTATGTGGTTTTGTA AT
DWU-330	85 C T ---	---	GAACATTCTCTGCAGCACTTCACTACCAATAGCATTAGCTACTTTTCAGAAATGAAGGAGAAAA TGCAATTATGTGGAGTGAAC/JTCGACTTTTCTAAAGCTCTGAACAAAAGCTTTTCTCTTTTGCAA CAAGACAAAGCAAGGCCACATTTGCATTAGACAGATGACGGCTGCTCGAAGAACAAATGTCAGAAA CTCGATGAATGTGTGATTGAGAAATTTTACTGACAGAAATGCAATCTCCCT
DWU-370	231 A G ---	---	GAAATGTTAATTGGCAGGTGAAAAGGTACAGATGTGCTGAGCAGACCCTTGGTTTTAAAGAG AAGCATCATTTCCCAACAGGCAACTGTAGAAGCCAGCTGAAGAGTAAAGGAAAGGTCTGAGG ACTGAGCCTGTGGCTGGCTGGAAGGTAATGTTGAGGCCCCCTTCACTCCATCACAAGAAAGTC ATTAGCGGTACCAATTCAGTGTCTGTTCTT/GJGCACTATTTCCTCTGTGC
DWU-1537b	89 A G ---	---	CTCTTAACCTCAGTCCCTCATCTATAAGATAAGGGATTGATGTGATCACATAGCTCAGGTAATC CAGGACCAGAAACCCAGAGC/GJTGAGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAACACACAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52 C T ---	---	CTCTTAACCTCAGTCCCTCATCTATAAGATAAGGGATTGATGTGATCA/C/JTAGCTCAGGTA ATCCAGGACCAGAAACCCAGGAGCATGGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAACACACAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196 C G ---	---	ACCATCTTACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGCCCCCTGGGGAATTCAGGGTCACTGTTCCCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAGTGGGACTGTGAGGACATGGAGCCCTCGGCACTGAGCTG/C/GJAGA CCCGCAGACCAACTCTGAGCTTTCTGGCCCTCTGAGTCTTGCTCTC
ESTD-ADAa	184 G A ---	---	ACCATCTTACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGCCCCCTGGGGAATTCAGGGTCACTGTTCCCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAGTGGGACTGTGAGGACATGGAGGCCCTC/GA/JGCACTGAGCTGCAGA CCCGCAGACCAACTCTGAGCTTTCTGGCCCTCTGAGTCTTGCTCTC
ESTD-ANT1	160 T C ---	---	TCTCTGTCACTTCTACTCCATTAGTCAAGGTCAAGTGAAGAACTGGGGCAATTAACCAAGTAATCA TGGACTGCCCAACTCGGAACAAGAGGGCGCAGTGGAGCAGGAGTATGCTACGCGGTACCTT TTTTATGGAGGACCGAACTGAGGCT/C/JGAGCTCAGATGATCTGT
EST10398 2b	168 A G ---	---	TGCCTGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGAGGCTTTTATGAAGCGGGCCCATGGTA AGATGCTGCCACCTCTTACTACTGATGATGTTTACATTTTGGGGCTTGACTTTCCACACGGAAG CATTGTTTTCTCGGGCCAAGAGGTATCTACC/GJATAGTGTCTATTAGGCATTG



EST10398 2a	147 C T ---			TGCCTGGGTGGCAGGCTGCAACAAGGAGGGAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTATCTACTTGATGATGTTTACATTTGGGGCTTGACTTTCCACACGGAGAAG CATGTTTCTTTC/TGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTG
ESTD-C7	14 G C ---			ATATCGTGGCCTTA/GC/TTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90 T C ---			CTTTCATGCAGATAGGCTTCTCTACTAATCACAGAAATTTGAGAAGAGCAAAACAACATTTCAAGG ATAATGGGCAATCATTCTTTT/C/TCTCTTTAGAGTCTACCGG
ESTD- GPPK2L	38 G A ---			AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTTTACAC/GA/CCGAGAACTGCTCGATATC
ESTD- HRASb	82 A G ---			CTGGGCTGCGCCGACAGCTGCTGGCACCTGGACGGCGGCCAGGCTCACCTCTATAGTGGGTCG TATTCTGTCACAAA/G/TGCATCTGGATCAGCT
ESTD- HRASa	37 C T ---			CTGGGCTGCGCCGACAGCTGCTGGCACCTGGACGGC/TGGCGCCAGGCTCACCTCTATAGTGGG TCGTATTCTGCCACAAAATGCATCTGGATCAGCT
ESTD- NRAMP	81 A G ---			GGAGCAGGAGGTGGGAGGGGTCTGTCTGCTCCAGGTCACAGACACAGAGCGGCTCAGTG TATCCACACCCCA/G/TGTGGCGCTGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-OTC	18 A G ---			GTGACCTTCTCATTAA/G/AAACCTTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGC AGATCTGAATTTAGGATAAAACAGAAAGGAGAGTATGTAACA
EST36751 7	36 C T ---			CCAAGTCGTTCATTTTAGCTTTGCAGGTTTAACT/C/TGATTACTTTTTCTATTCAAATCTCTGTA AAATTGAATATGAACCTTAGTTTCTGATCTATGTTTCAAGTTAAACAG
EST40562	109 A G ---			CACGTGGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTGTCCCCAACTTGTGGCTGAC TTTATGGCTAAGAAAGTTTCACTGGATGCATTAAAGAAAT/G/TTTTACCCTTTTGAAGAAATAA ATGAAGGATTTGACCTGCTTCGCTCTGGAAGAGATCCGTACCGTCTGACGTTTGAACAATACA GATGCTTCCCTTGTAGCAGTTTTCAGCCTCCTCTACCCCTA
EST18288 3	121 C T ---			GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGA/C/TGGGAGCCAGT GTGGACAGCACCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAAGGCAAAACCTCTCTGCTGGCTC TGGCCCTAGGACTTAGTATOC
ESTD-AK- 168	31 C T ---			GGGAGTGACAGCTAGACACCAAGGGGGCT/C/TTACAGCTGTGTTCTCATGGAGGACAGGCTTCT GCTCATTCTGG
ESTD-ALB	180 A G ---			AATCCAGCACTTTAGGAGGCTGAGGCAAGGCATATCACAGAGTCAGGAGTTTGAGACAGTCTGA CCAAACATGGTGAACCCCATCTCTACTAAAAATACAAAATAGCCAGGCATGGTGGTGCATGCCTGT AATCCAGGAGGCTGAGGCAAGGAGATCGCTTGAACCTGGAGGCG/G/JAGGTTTGGTGGAGCCGA GATGGCAACATTGCACTCCAGCCTGGGCAACAAGAGTAAACCTCTGTCTTC



EST70523 3	182 G T ---			TTCCGCCAGCCCCCATCTTGGCACCCCTGGTCCOCCTAGGGGCCACCCCGCGCACTCAACGCTCT CGCTCTCGGTAACATCCGGCCGGCGCGTCCCTTGAGCACATAGCCTGGACCGTTCCGTATAGGAGG ACCGTGAGGCCCTTCTGTCCGGGCTTCCAGGGGCCAGCCCTG/TCAGAGAGAGGGGTCCTGT GGTGAGCTGAACACAGCTGTGGAGTGCTCCACAGTG
ESTD- APOA2	101 C T ---			CCAGGTGTTGTGGCAGCTGCTGTATCCAGCTACTCGGAGACTGAGGCATGAGAACTTTTGAAC CGGGAGGCGGAGGTTGCAGTGAGCTGACATGCTG/TCGCACTGCACTCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112 C T ---			CAGTGATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTACAGATCTTTGGCTCACATGAAGGCCAAATTCGAGAGAC/CTAGAGATACACGAGAC CGAATGTATCAATGGACATTCAGCAGGAACCTCAACGATACCTGTCTCTGGTAGGCCAGGTTTATA GCACCTGTACCTACATTTCTGATTGGTGACTCTTGCTGCTAAGAACCTT
EST74167 6	137 C ---			AGACCATGAAGGAGTTGAAGGCCCTACAAATCGAACTGGAGGAACAACCTGACCCGGTGGCGGAGG AGACGCGGCACGGCTGTCCAAGGAGCTGCAGGCGCGGCGAGGCCGCTGGCGCGGACATGGAGGA CGTCCGCGCGCGCTGGTGCAAGTACCGCGGCGAGGTGCAAGCCATGCTCGCCAGAGCAACCGAGGAGC TGCGGGTGCGCTCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTC
EST43211 8	132 C ---			CGCTGGTGCACTACCGCGGAGGTGCAAGCCATGCTCGCCAGAGCAACCGAGGAGCTGCGGGTGGC CCTCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTCCGATGCCGATGACCTGCAGAAAGCGCC TGCGAGTGACAGCGCGCGCGCGAGGCGCGCGCGCTCAGCGCCATCCGCGAGCGCGCTG GGCGCGCTGGTGAACAGGCGCGCTGCGGGCGCGCACTGTGGGCTC
ESTD- ARSB	126 A ---			GGAAGAAATGGAGCCTGTGGAGAGGCGCTCCGAGGGGTGGGCTTGTGGCAAGCCCTTGCTGA AGCAGAGGGCGTGAAGAACCGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAACCAATCAGTGAA GGAAGCCCATCCCCAGAATTGAGCTGCTGCATAATTGACCCAAAC
EST36770 4	144 C ---			TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGCTGGCAGGCTTGGCCAGTTTGCAGCTATAATCC ATCGAAATGATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTCCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGCTGGGCTGACCAAAATATAGTGGTTTCCCTTTCTCTGATCAT TCTTACAAGTTACTCTTATTGGAAGGCCCTAAAGAAGGCTTATG
EST26021 1	137 A ---			TAATGTAAGCTCATCCACCAAGAGCCTGCACCATGTTTGGAGTTGAGTGACATGTTGAAACCTGT CCATAAAGTAATTTGTGAAGAAGGAGCAAGAGAACATTCTCTGCAGCACTTCACTACCAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCAATTATGTGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTCTTTCCCTTTGCAACAAGACAAAGCAAGCC
ESTD- BA511	29 A G ---			GGGCAACATAGTGAACCCCATCTCTACA/G/AAATACAAAATTAGCCAGGTGTGTAGCAAG TGCTGTAGTCCAGCTACTTGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG CAGTGAGCCAAAGATGGTCCACTGCA



ESTD- BCL2	116 A G ---			AGGTGATTAACTCTCTTCTTCTGGGGCCGTTGGGTGGAGCTGGGGCGAGAGGTGCCGTT GGCCCCGTTGCTTTTCTCTGGGAAGGATGGCGGACGCTGGGAGAAQ[A/G]GGGTACGACAAACCGGG AGATAGTGATGAAGTACATCCATTATAAGCTGTGCGAGAGGGGCTACGAGTGGATGCGGGAGATGT GGCGCGCGCGCCCGGGGGCGGCGGCAACGGGCATCTTCTCTCCCA
ESTD-BCR	69 C T ---			CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCGGAGACTCATCATCTGCGCAAGA GA[C/T]CAAGAGAGGTCAGCTTCTGTTGCCGGAAAGGAGGCGAGGTACAAAGCTAACTCTGCTTC AAATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCCCTGGCACA
ESTD- BRCA1aa	119 C T ---			AAGAAGAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCAC[C/T]TGGTACCTGG TACTGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACA GAACCAAAATAAAT
ESTD- BRCA1bb	139 A G ---			ACTAAATGTAAGAAAAATCTGTAGAGGAAAACTTTGAGGAACATTCAATGTCACCTGAAAGAGAA ATGGGAAATGAGAACATTCGAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAAATGTT TTTAAAG[A/G]AGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCA GTATTAATGAAA
ESTD- BRCA1cc	126 A G ---			ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTAGATGATGGTGAATAAAGGAAGATAC TAGTTTGTGCTGAAATGACATTAAAGGAAAGTTCTGCTGTTTATAGCAAAAGCGTCCAGA[A/G]AGGA GAGCTTAGCAGGAGTCTAGCCCTTCACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCA AGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
EST51212 0	122 A C ---			ATCTGAGCTCGCAATAGCTTCTGTTCTACTCTCTCTCCACAAGCCCCAAATTCACCTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCCTTTGTGCTCCCACTCAATACA[A/C]AAAGGCCCT CTCTACATCT
ESTD-C1R	40 A G ---			ACACAGTGTGCTGGCACTGGGGTGGGATCCTCCTCCCT[A/G]ATTGCTCCGGGAAGCACATTCTAT CAA
ESTD-C1R	40 A G ---			ACACAGTGTGCTGGCACTGGGGTGGGATCCTCCTCCCT[A/G]ATTGCTCCGGGAAGCACATTCTAT CAA
ESTD-C6	31 A C ---			CCCAGTCAGTTGGGGACAGCCATGCACCTG[A/C]GCTCTGTGTAGCCCTTCAACCATGCATTCCATC TAAGCTCTGCAAAAT
EST20118 2	119 C ---			GTCCGAATCCTCCTCTGAAAGTGCCCGGTTTAACTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTAGGGGCTTGAAGCTGGAGTGGGGTTAGGGACGGGCTCTCTCGTGCATCCTAAGCTCT GAGAGCAACCTCCCTTGAAGCTGGAGTGGGGTTTAGGGACGCGGGTCTCTGCGTGCATCCTAAGCT CTGAGA
EST53018 6	67 A G ---			ACAATCCAGGTCACACATTCAGAAAGAGGAGGGGTGGTCACTGAGCCTGGGTAGGTCAGTAATCCA [A/G]GGATTCAAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC



ESTD- CB22	119	C T	---			GGCAAGTTTTATTGATAGAGAGGAAATCAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGGAGTGGCAACCCATAGGGC/TGGATACAAAAG ACAGGCAAGGAAGGGTAGAACCATCAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCT AGTAAACATAATTGCTTCATTAGTCCCTTCCCGGCCCTCTCTC/CACACAC
ESTD- CB23	136	C	---			TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCTTTCCCGGCCCTCTCTCTCACACATACAGAGCCCTACCAGGACCAGACAGCT CTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAAAAAGTGTTCCCAACCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD- CB24	145	A	---			ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTCCCTTTCAGAGGACCTGAA AAACGTGTCCCAACCCGAGGTGCTGTGTTGAGCCATCAGAGCAGAGATCTCCACACCCAAAAAG GCCACACTGTATGCTTGCACACAGGCTTACCCCGACACGCTGAGCTGAGCTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTGACACAGACCCGACGCCCTCAAGGAG
ESTD- CB25	146	A G	---			GTTTTCTTCAGACTGTGGCTTCACTCCGGTAAGTAGTCTCTCTTTCTCTCTATCTTCGCCGCT TCTGCTCTGAACCCAGGCAATGGAGATCCACGGACACAGGGCGTGAGGAGGCCAGAGCCACCTG TGCACAGGTAG/CCTACATGCTCTGTTCTTGTCACAGAGCTTACCAGCAAGGGTCTCTGTCTGCC ACCATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGATGCGCGTG
ESTD- CB27	125	C T	---			TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTTGTTGGGCGTGGTGCATTTGAGGAGTGCTGTGGAGTCTGCTCATCACTGAC/C/TATCTTC TGATTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCCAATGCT GCTTCTCTGTTTCATCTGATGGAAGTCTCAAAACACCATTTCCATACC
ESTD- D4S338	59	A T	---			TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGA/TATGTA TTTTCTTAAACAATAAATTTGAAGTCCAAAATTTACTCTTGATCCATGGACTGCAGAAATAATGTTA TTTTAGCTGTGAGAAAAACAATACTAATCTTGATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGTA TTGCCAATAAGCAGTAATTTTGAGAGGAATCTTGTTTTCATGCAGTAG
ESTD- CYP2D6	61	A G	---			CAGGCCAGCGTGGTCGAGGTGGTCACCATCCCGGACAGAGAACAGGTGACCCACCCTATGCI/AGJCA GGTCTCATATTGAAGCTGCTCTCAGGGTCCCTTGGCTGAGCAGGGCCGAGAGCATCTCGG
ESTD- D11S1873	40	A C	---			AAAAAACATTTTAAACACCTTTTCAATCATATACACCATA/C/JATTTCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTTCCAATTACTTGCAATCTAAAAATGTCATAACTGATTAATGCAAGTTCAACAG ACAACITTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATTTATGCCCA TATCTGCATGTG
ESTD- D17S33b	169	C T	---			CATCCCAAGCCCATCTCTTAGCCACTGGCATTTTTTGGCGCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGCGCCCTACCTTTGTAGTCCATGGGAAGGCTCTCTGGGCGGTG GGGTGTGGTGTGTTGTTGTGTAG/C/TGGGGGCTTTGGTTTCAGTTGCACACTATTGGCTT ATTGCAGATTGCTTGTCTTCCACCTGAGCGAGCCTC



ESTD- D17S33a	75 C T ---	---	CATCCCAAGCCCATCCTTAGCCACTGGGATTTTGGCCCTCTGACAGATACACTCAGGGCCGT CATGCTG/CJACACATCCAGGGGGCCCTACCCCTTGTAGTCCATGGGAAGGCTCCTCTGGGGCG GTGGGTTGTGGCTATGTGGTGTCTGTGTAGACGGGGCTTGGTTTCAGTTGCATATTGCGTT ATTGAGATTGCTTTGCTTTCCACCTGAGCGGCCTC
ESTD- D18S8	133 A G ---	---	TTTGAGACCACCTGGCCAACATGGCGAAATCACATCTCTACCAAAATTACAAAATTAGCTGGGTG GGTGGTACATGCCTATCGTAATCCAGCTACATCGGAGGCTGAGCAGGAGAAATGCTTGAACCCJA /GJGGAGGCGAGGCTTGCAGTGAGCCCAAGATCACACCCTGACCTACAGCCTGGGTGACACAGTGGA GACTCTGCTCAA
ESTD- D3S11	44 G ---	---	AACTGATTAGAACCTGAAAATACATAATTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AAATTTTGCATCAATTAATAAATCCAATAAAGTACACTGTAAATAAGAAATTTAACAGAAATATCATGT TTATTCAAACTATTTATCACCTATTTTATTTGTTAAGCCATACTAAATCTTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G ---	---	AGGTTCCACATATTGCTGATGTTTGTGATGTTTCQJ/GJGGAGCCTTGATGTCATTCGTATCTCCT CAGGTATCCACCTTGAGACGTACTTTTCAAAAACCTCTCTACAGCCGTTGTTGTTAATTAATCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTCCTCC AGAAGTGAACATACCTGCTCCTAGAGCCAGAGTACATCTGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTATTGGAAGGATGCTC/JJGGT
ESTD- D3S2a	248 G ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAACTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTCCTCC AGAAGTGAACATACCTGCTCCTAGAGCCAGAGTACATCTGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTATTGGAAGGATGCTC/JJGGT
ESTD- D7S399	83 A G ---	---	TGAATCTTAATTGCTATCTACAAATGTATAATCTGAACTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCJ/GJGCTCCTACATCATCCTTTTCAAAACATTTTCATCCATGGACTCCATAC TAGAATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DMb	146 A C ---	---	GTGGGACACCGAGGGCTCCAGGCTGGGCGCTTGACGCTGAGCTCAAGCAGCTGCTCGGCCCTCCACT TCCATGGGTGGGGCTGGGACCTCACTGCTCCCTGGGAGAGGAGGAGGGAGGGAGGAGACA GAATGCTGATTJ/CJCTGTGGTGAGAACCAAGAACTCTGGCCTGTGGGTAGGGGCAGCTGCTTCCAAAG ACCTCCTGATTGTAGGAAGGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD-DMa	66 C G ---	---	GTGGGACACCGAGGGCTCCAGGCTGGGCGCTTGACGCTGAGCTCAAGCAGCTGCTCGGCCCTCCAJC GJTTCCATGGGTGGGGCTGGGACCTCACTGCTCCCTGGGAGAGGAGGAGGGAGGGAGGAGAGA CAGAACTGCTGATTATCTGGTGAGAACCAAGAACTTCTGGCCTGTGGGTAGGGGCAGCTGCTTCCAAAGA CCTCCTGATTGTAGGAAGGGGAGCAGCAGAGCGAAGAGAACAGAGT



ESTD- DRD1	154 C T ---	---	---	TCCCCAGCCCTATCGGTATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCCATCAC ACAAACGGTCAGCACCCCAACCTGAATCGCAGATGAATCCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGG[C/T]TCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	144 C ---	---	---	TCTGCCTTTGGTGACGAGGCTGCCCGCGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGGACCCGGTACAGCCCATCCACCCAGCCACCACTGACTCTCCCGACCCG TCCCACACGGTCTCCACAGCACTCCCGACAGCCCGCCCAACACAGAGAAGAAATGGGCATGCCAAAG ACCAACCCAAAGATTGCCAAGATCTTTGAGATCCAGACATGCCCAATG
ESTD- DRD3	109 C T ---	---	---	AAGAGATGGCCAGGATGAGCGCGAGTAGGAGAGGGCATAGTAGGCATGTGGCGGGGCTGGCTGG CACCTGTGGAGTTCTCTGCCACAGGTGTAGTTCAAGTGG[C/T]ACTCAGCTGGCTCAGAGATGCC ATAGCCAGAGGGAGGTGGTGATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ERB2	93 C T ---	---	---	TCTTCAGGATCCGCATCTCGCCTGGTTGGGCATCGCTCCGCTAGGTGTACGGCTCCACAGCTGG GGTGAGGGGGTGGTGGTCAAGTGC[C/T]GGGGGGCGGTGCAGACCCACGGGCTGGGAGACTTCA CCCCGCTCACCTCCGTTTCTCGCAGCAGTCTCCGCATCGTACT
ESTD- ETS2	43 A G ---	---	---	ACTCACAGTGTCTTTAAGTGAATGGTCGAGAAAGAGGCAC[C/T]GGAAGCCGCTCCTGGCGCTG GCAGTCGTGGACGGATGTTCTGGCTGTTGAGATTCTCAAAGAGCGAGCATGTCGTGGACACA CACAGACTATTTTAGATTTCTTTGCCCTTTGCAACCAAGAACAGCAAAATGCAAAAACCTCTTTGAG AGGGTAGGAGGGTGGGAAGGAACAACCATGTCATTTCAGAAATTAGTTG
ESTD-F9	111 A G ---	---	---	AGATCCTGATGATTTTTCTCTATTTTTCTAAATGTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTGAGTTAATTTGTGTAAGTATGATGTTTAA/GJGTCAAACCTCATTTTTTTTTCC ATAGGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAAC
EST68787 5	144 A ---	---	---	CTTCCTATGGGATTGACTTTATTCTCCATTGCTTACCTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGACGCTCATGACAAATTTGAAGCTGACAAATTACACAAGAAAGGAAATAAATTCACAGTCAA AGAAATCAAGCACTTTTCGAACATTTGAAGTTGTTTTGAACTTGGTGTACCTTTAATTACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
ESTD- GCH	200 C G ---	---	---	CGCAGACCGTCAAGTGTGGGTGGGAGTGTGGAGGAAGGAGGAACTGGGGTTTAGGGACT TTCCGGGGTACTTTCCCGTTCTGTCTTGCAAGAAAGGGGGAGAACACAGAGCCAACTGGCTAA GTGTAGGGGACCTCTGGTGCACCGTGTCTGTCTGCTGCCCTGTTACAGTGCTGTCTGTGCGCGAGT[C/
ESTD-GCK	88 A G ---	---	---	G/GACTCTGTCCCGAAATCCGAGAGCT GTTTTATGCATGGCAGCTCTAATACAGGATGGTCAGCCCTGCTGAGGCCACTCTCTGGTCACCATGAC AACCACAGGCCCTCTCAGGA[A/G]CAGAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAATGCCGAGCGCGCTGAGCCCGAGGAGCAGGCTAGGATGTGAGAGACACAGTCTC ACCTGCAGCCTAATTACTCAAAAGCTGTCCCCAGGGTCACAG



EST34088 2	62 A T ---	---	GTGGGGCAACAGTGGGAGAGAAGGGGCCAGGGTATAAAGGGGGCCCAAGAGACCGGCTC(AVT) AGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G ---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCAAC(A/G)GGCATCA TTGAAACCAAGTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTTCCTAGG
ESTD-HT2	154 G ---	---	GGGCTAAATTTCCGAGCAACTTTGCATAGACTGTTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAAGATGTGTACAGTTTGTACAGAGATAAAGGATAAACCTGGGTTTTCTGTGC TTTGCTTCTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGAGTCGTGAAGTTTCAACAAAGACACCTT
ESTD-HT5	149 C ---	---	AACACAAAGCCCCAGCGAGAAATTGAACTCGGACCCCTGGTTTACAAGACCAGTGTCTAACCCCT GAGCTATGGAGCCCTGCTGCTGTTGTTTTCTTCTTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCGGGCTACCGAATAGGATGTAGCTTGAGTAAATTCAGGATATTCTCTACAAAATGAAA ACATTTCTGCTCTGTAAATCCCTCGAAAAGGTTCT
EST37382 5	124 A G ---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCTCTTCTCTCTCCCTTGGGA CTTTGAGTCAAAATGGCCTGGACTTGAGTCCCTGAACCAAGCAAGAGAAAAGAG(A/G)CCCCAGA AATCAGGTGGGCACGCTCGGCTACCGCATCTCCCTTCTCACGGGAATTTTCAGGGTAAACT
ESTD- IGFBP1	43 C T ---	---	ACCCAGTGGAGCCGCTCATTCACCGTCTTGGCAGGAGTGC(T)CTGGGAGAGAAGGAAGATG TCCAGGGCACACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120 C ---	---	TTTACTATTTCAATGGATACAGAAATTGTGGGAGTCACATATATTCCTATGAACAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCCACATTGTGTGAGTGACGGGCGAGTGGGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCAAAAATACTAATAAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	110 A G ---	---	CAAAGTAGCACCCCAATAAATGTTAGCTATTACTATCATTTATTTATTTATTTATTTTGT AGATGGAGTCTGGCTGTCAACCCAGGCTGGAGTGCAGTGGC(A/G)CAATCTCGGCTCACTGCAAGCT CTGCCTCCTGGGTTTCATGCCATTCTCTGCCCTCAGCCTCCGAGTAGTGGGAATACAGGCAACCCGCC ACTGTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTACCCGT
ESTD-IL1B	99 A G ---	---	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTTCTCTGCCCTC(A/G)GGAGCTCTCTGTCAATTGCAGG
EST74082	134 A T ---	---	TCCAGGGTGGCTGGACCCACAGGCCCAAGCTCTGCAGCAGGAGGACGTGGCTGGGCTCGTGAAGCATG TGGGGTGAGCCCAAGGGCCCAAGGCAGGGCACCTGGCCTTCAGCCTCAGCCCTGCCTGCCTGT(A/ T)CCAGATCACTGTCTTCTGCCATGGCCCTGTGGATGGCCTCCTGCCCTGCTGGCGCTGCTGGCC CTCTGGGGACCTGACCCAGCCGACGCTTTGTGAACCAACACCTGTGGC



EST45311 0	151 C T ---	---	---	GGCCTCCTCTCTCCAAATCTGTCCTATAGTTTTCTCTATTAAAGTGAACATACATGCATTCTTTTAGT GGATAGATGCACACAAACACAAAGCCATTATGGGAAGGATCCACGTGTGTGGCCATATTGTAACA CATTCTCTGCAATC/TJACCTCTTTTCATTTAACAGCCCTTATTCAATGGCCCTTTTCTTTTTCAGTA GTACATACACATCTGTGCATTTGTTGAAT
EST65258 8	80 A G ---	---	---	TGCCCCATCAGCGGCCGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACAGAAAT CCAGTTATTTTC/TJGJCCTCAAATGACAGCCATGGCCGGCGGGTCTCTGGGGCTCGTGGG GGGACAGCTCCACTGACTGGCACAGTCTTGATGGAGACTTGAGGAGGGGCTTGAGGTTGGT GAGGTTAGGTGGTGTCTCTGTGAAGTCAGGACATCAGTCTGATTAA
EST38216 3	26 A T ---	---	---	ATGCAGGATGAAGGTGGACAGGGAGG/TJGAGGGCCAACTGTCTCCAGGGCCTGCAGATGTCG CTGGACTATGGGTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 KRT10b	149 G T ---	---	---	ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATTTAGCATTTGTTTAGCATTAACCTAA TTTTTTCCTGCTCCATGCAGACTGTTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGGAAG TTTTTTTCTCTC/TJJAAGTGCCAGTATCCAGAGTTTTGGTTTTTGAAGTACCAATGCCTGTGAA AAAGAACTGAATACCTAAGATTCTGTCTGGGGTTTTTGGTGCAATGCA
ESTD- KRT10b	183 C T ---	---	---	CCAAAGTTAAATAGTATTGGAGTTAICTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATTT AAAGGAAGAAATGCATTTTAAAGTAAGTCTAAGGTTTTTCCATTAAACCCTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGC/TJTGCTTTTTAAATAGT CTCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT10a	133 A G ---	---	---	CCAAAGTTAAATAGTATTGGAGTTAICTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATTT AAAGGAAGAAATGCATTTTAAAGTAAGTCTAAGGTTTTTCCATTAAACCCTATTACTTCTA/TJ GAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTGTCTTTTAAATAGTC TCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8b	231 C T ---	---	---	ACCTCACCCCTCCCTTAGCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGTCTCAGGTTTACCA/TJGTCAACATTGACACA
ESTD- KRT8a	21 C T ---	---	---	ACCTCACCCCTCCCTTAGCC/TJGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAGTGAGGCCCAT GGCTGCCTATCTCTCCGTCTCAGGTTTACCACGTCAACATTGACACA
EST75099 6	82 C T ---	---	---	CACCTGTGTGTCTAGATCTCCTCAGTGGCGGCTCTACTGGGTTGACTCCAACTTCACTCCATCTCA AGCATCGATGTCAA/TJGGGGGCAACCGGAAGACCATCTTGGAGGATGAAAGAGGCTGGCCCCACC CCTTCTCCTTGGCCGTCTTGAGGTGGG



ESTD-LF79	142 A G ---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATTTGTAACCGTAGCAAAACATGCGATTGGTATTTAGA AAATAAAAAATTTCCAATATGATGCTGTGTATACCTGCGCTCTGCCATGCAGCATCATAGCCTGT GGGAACCAAGGGGCTCCCTTACCACCCAGA
EST35879 9	142 A C ---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACTGTGATCTCCCAATCTTGTGCGTCCACCCGATG GAACTGCCGGCAATCTGACAGCTGTGCACCCAGGCTGTACCCAATTAGGTGAACATGGCTTCGAG AGAGTTG/CJACAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGA A
ESTD-LMP2	35 C G ---	---	TACACACTTCTTACCCATTCACTGAAAACGACT/C/G]GCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGCCCTAGGGCACTCAACACTCCAGCTTCTCAGCTCTGGCTGTCTGCTGCTGCA AGGTTTTCGTTAATCTCAATCAATGCTCTCTCATCTTTTAG/C]TAGCTGTGGGTTTGTGTTG TTCTTGTGTTTTCGTTAGTATCTGACTACTTTTAAATTAATAAAGAGATGATCTAAACAAAATAG AGATTGTTATCAGAAGTTCACAACATTTATTAAAAATTTTTCACCTG
ESTD-MCC	45 C T ---	---	TTGTCAGGAGTGTGCTGATGCTGCTGCCCTCCAGCTCTGTCCTAGC/C]TAGAACTTCAGGACAACGTGC AG
ESTD-METH	118 C T ---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAACACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGTCTTTCCAAAGGTTTGGTCTAAGTGTGCTAATACCTGATTAAC/C]TGGATTTTCTGACG ATCTTCAACTGCTAGAGCATCTGGTCTCTGTTTAGCATGG
ESTD-NF1	25 A G ---	---	ATTATCCAGATGAATTTACAAAACCTA/G]TACCAGATCCACAGACTGATATGGCTGGT AACATGGACTGTATATTTGTACAAAAAAAGTTTATTTTCTAAAAAAGAAAAAAGAAAA AAATTTAAAGGGGTACTTATATCCACACTGCACACTGCC/C]A/G]GCCCAAAACGCTTATTGTGGT AGGATCAGCCCTCATTTGTTGCTTTGTGAACCTTTTGTAGGGGACGAGAAAGATCATTTGAAATTC GAGAAACCTCTTTAAACCTCACCTTTGTGGGGTTTGTGGAGAAGGTTATCA
ESTD-NFB1	107 A G ---	---	TGTCCTAGGCCAGCCCTGCTTGTCTCCCTGGCTGTATCT/C]A/G]GTACTGCAAAGAGAAACACA GACAT
ESTD-NPPA	45 A G ---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTTCTGCAGGCATATAGAATTTGGT GGGTTTCTTTATGAGGTGATATTGGATCTTTTGTGTTGATTATATATAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTAGTGTATTAACTTGGCAATAGCATTTG C/T]ATCCCTGIGGTTTAAATAAAAT
ESTD-NRAS	202 C T ---	---	GGCACCAACCCACCCAGCACACCTCCAACTCAGCCAGACAAAGTTGTTGACACAAGAGAGCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGG/C]A/G]GTACGCCGTGATCATCGGAGGCGCGGG CACATGGCAGGGATGAGGGAAGACCAAGAGTCTCTGTGGGCCCAAGTCTCTAGACAGACAAAACC TAGACAATCACGTGGCTGGCT
ESTD-PAI1	100 A G ---	---	



ESTD-PAR	120	A	---	---	CTCTCAGGAACCAACAGCTCTTCTACCAACACGACTTATTGCTGTCGAGAGGTACAACCCGTAGA
ESTD- Per/RDS	74	A	G	---	ACCTTCTCCTAACTGTAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT
EST68308	5	29	C	T	AATCGACTGGCTTTCATTAGCTCTGTGAGTGTCTTCTTCTCACTTCTGTGTTCTAGAACGTTTCTAG
EST54045	6	39	A	G	GACTGGCAGTTTAAAGCTTTCACCTAGGCTTCTGTATACCCATGCC
ESTD-PXMP1	88	A	G	---	ACCTACAGACGTCGCTGGATGGTGTCTCCAAACCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTG
ESTD-RDS	127	A	---	---	CTGGAGA/GAG/GAGCGTCCGCGAGACCTGGAAGGCCT
ESTD-s14544	94	G	T	---	GGAAGAGATTTAAGAAGCTGATTTGGAC/TAATCTGGTCTTTGAGTGTGAAGAGTTTCATGTC
EST52908	0	45	A	C	TCTGCCTGAGTTACACAGAAATCCTTTAGTACGCGAGTAATAGATATAATCGACACAGATGGGAAT
EST19590	55	C	T	---	GGAGAAGTAGACTTTAAAGTAAGAAAGTAGTTATTTTTTA
EST76136	39	C	T	---	GGAATATTAATAATATTTAAATACCTCCATTTTGCTT/A/GTCTTTTAGTGAAGATGATACCTGC
ESTD-SPTB	176	C	T	---	AAAAGACATGGCTAAAGTTATGATGTCATGTGGCAATTTGTTCTTACAAAATCGGATGGAAA
				---	TCTGTTAAGTAAGTACTGTTTTGCCCTTGGAAITGGATTTTAAATGTTGACTTTATCAT
				---	ATGAAACATGGTCTTTAATTTATGATATGTTTGTATAGCTATCTTAAAAGGGCTTCTTTTTTTA
				---	ATGCAGAAAAGAGGGGAAAAA/GAGCGAGCTGTGGTGACAAAGGTGTTTTCTCAAGGCTCATAC
				---	AGATCTGAAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAAGTCTTATGAAAATTATAATCTT
				---	CCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTGTCTGGAGAAGAGCGTCCCGGAGACCTGGAAGG
				---	CTTTCTGGAGAGTGTGAAGAGCTGGCAAGGCAACCAAGGTGGAAGCCGAGGCGCAGACGCGAGG
				---	CCAGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAAATAGTGCACT
				---	CCAAGAAACGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA
				---	TTGGGAAGTTAGAGCCTATATTAATTAACGGAATTAAGGCAAGGACACAGAGGCTTAATTGAAAA
				---	TATCCCAAAGTTGAAATGTCTCAGTTTC/GTCTGTGGTTAGATGCAGGATTTATATGATCCGTTA
				---	ACCTCT
				---	ATCACAGGTCTCTGGTCTCTGGCCATCATTTCTTGGGAGAGATGG/A/CJTGGTGGTCTGCAAGCCCTT
				---	TGGCAATGTGAGATTGATG
				---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAATGACATTGATGAGTGAAGATGT/C/JTGGCTCAG
				---	GATGCCGGAAAATGAC
				---	TGAAGCTTCTGCCACGCTTGCATTGTTTCTAGGAGAACC/C/JTGGCTCATACCTTTATCTATAGCCTT
				---	CCCCTAGTCTT
				---	TGAACACCCCTGTGGTCCGGAGCCAGTTGTGTTCTCTCTGGAGCCCTGAGGAGTTTGTGTGTGTG
				---	CAGTCCCCCGGCCCACTGCTGTTGAGCTGGACATACACCTTCACCTCTTGGCCCGGAGAAAGAC
				---	ATTTACCCACCTGGCCATGTCCCTGGCCTGTGTGCACAC/C/JTCCCTCTGTGAAGACCCCAACCCCTGC
				---	CTCCCCACCCCAAGCCAGTTTCTTAGCAAGGGCAGGAC



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ESTD-TAT	224	C	---	---	AAATGGTCAGGACCCCTGATCCACAAGAGTGGTACCATTTTCATCAGGGCCATCAGTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCAATCATTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTTCACAACCTTTCTCCAGTATGGATGGATTTATGATGGGGG GAGAAGCAAAATTTTAAATAGGACCCATGAGACACATCA
ESTD- THRB	125	A	C	---	TGCGGCCTTCTCCGGCAGGGTAGACTTCITACTTGGCTGTGATTTCCAAAGAGAAAGAGTCCCAAG CACAGAAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATCACACAGGATC[A/C]CTTCAT CCACTGGATTGGCCCAACAAGCTGAGTGCAGCCAGGACTCAACGGTCCCCCTGTAGATGGG
ESTD-TYR	122	G	T	---	TAGTGAAGTTTTCATCTCCTGTCAAGTCTCTGGATTCTTGTCCACCACAAGAGAGTCTATGC CAAGGCAGAAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCAGTATCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAGAGGTCATAAATATTGATGTCGTTAA CATGGGTGTGATCCATTTTTCATTTGGCCATAGTCCCTATGGGGATGACA
ESTD- TYRP1	222	A	C	---	AGTAGTGGATGAAGCTAACCGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGCTAACAAATGCCCTACTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTTCTTTCACCTTATTACCTTCTTCT AATACAAGCATATGTTAG[A/C]ATTAAAGTTCTAGGCATACTT
ESTD- TYRP1	222	A	C	---	AGTAGTGGATGAAGCTAACCGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGCTAACAAATGCCCTACTCTTATGCATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTTCTTTCACCTTATTACCTTCTTCT AATACAAGCATATGTTAG[A/C]ATTAAAGTTCTAGGCATACTT
ESTD- VB12	148	C	T	---	TTCCCAAGGCCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAGGTACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCCCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148	C	T	---	TTCCCAAGGCCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAGGTACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCA[C/T]CAGACTGAGAACCCCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74	A	G	---	TTCCCAAGGCCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACAC[A/G]TGGATGCTGGAATCACCCAGAGCCCAAGACACAAGGTACAGAGACAGGAACACCA GTGACTCTGAGATGTCAACCAAGACTGAGAACCCCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT



EST58607	0	105	A	G	---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAAGCCAGTCCATCCTGTAGTCAATCATAGTTGTGGCTCC CAAGTTGCTCTCCTCACTGAGCAACAAGGACAGCCAC A GTGGCGGGATGGCCGGGAGGTTG TGGTTGCGGCCACGGCTGTGGCTGTGTGAACGGTAGCCTTTGGCGTTGCGATGCGCTAAACCTTTGT TTCTTGGCCAAAGGAGGGGGGTGCCATGCTGAGATGTAGATGCGGCC
ESTD-VWF		36	G	---	---	---	AGGTAGGAAAGCAAAAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTTCCACACTGTCCTTTGG TCCCTAGAGTCTG
EST71770	6	189	C	G	---	---	AGCACCACTCTCAGCTCAAGCCTCAGCACCAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGAGTTATTTATCTCTGAAGTCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGTTGTAACAACAAGAGAAAACCCTGCAGAGTACCAG C G TGTGTGGTGGGA AGGAGTGCCAGTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAAG
ESTD-TNFab		152	A	G	---	---	TTCTGCATCCTGTCTGGAAGTTAGAAAGGAAACAGACACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGCATGAGGACGGGGTTAGCCTCCAGGTCTACACACAATCAGTCAGTG GCCAGAAGACCCCCCT A G GAATCGAGCAGGGAGGATGGGAGTGTGAGGGGTATCCTTGATG CTTGTGTGCCCAACTTTCCAAATCCCCGCCCGCGATGG
ESTD-TNFa		88	A	---	---	---	TTCTGCATCCTGTCTGGAAGTTAGAAAGGAAACAGACACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGCATGAGGACGGGGTTAGCCTCCAGGTCTACACACAATCAGTCAGTG GCCAGAAGACCCCCCTCAGAATCGAGCAGGGAGGATGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGCCCAACTTTCCAAATCCCCGCCCGCGATGG
EST52418	6	113	A	G	---	---	CAAATTACAGGGTCAACTGCTATGATGTGTTTGGAGCCCCAGTCACCCCTTTGGTGGCTACAAGATGTCG GGGAGTGGCCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACT A G AAGTGAAGAACTGTGAGTG TGG
EST13586	3	89	A	G	---	---	CCCACTCTATTTGCCAGCCCCCAGGGACAGAGCTGATCCTTGAACCTCTTAAGTTCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCC A G GGGCTGGCTTATCAGCCTCCAGCCACAGCCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGTGCCTCTGCTGCCTGCC COGGTCACTC
EST51976	7	123	A	T	---	---	AGGCAGAAACTGGGCCCCCATGGGGGGACGTGGAAGGCCACTTGAGCTTCCTGGAGAAGGACCTGA GGGACAAGGTCAACTCCTCTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAG A TCTCTC CCTCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGGAGCAGCAGGAGTGCAGATGCTG GCCCTTTGGAGAGCTGAGCTGCCCTTGGTGC
EST11458	6	140	A	G	---	---	CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGCCTCATCTTGTCTCGAGTTT CTCTGCCATGTGCTATTGACGACGGACCTGTCCAAAGCCAGATGATTTACCATTTTCCACAGTGGT CCC A G TTAAAAACATTCTATGAGCCAGGAGAAGAGATTACGTATTCTCTGAAGCCGGGCTATGTG TCCGAGGAGGATGAGAAAGTTTATCTGCCCTCTCAGGACTGTGGCC



ESTD- AT3aa	60 C T ---	---	AGACCTCAGTTTCCTCTCTGTAAAGGGAAGTTTGTCTTGGATCTCCATGGGCCAGC[C/T]AGCA CTGGTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACCAGGTGGAGAGGAAATTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAAAGAGCTGGGAAATGTGG
EST39852 8	106 C G ---	---	CGGTCTTCTCCAGGTATTGTTGCAGAGGCCGAGATGACCTCTATGTCTCAGATGCATTCOCATAAG GCATTTCTTGAAGGTAGTACACCTTCCCACTCTCTT[C/G]GIGGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAAGGCCCTGTTCCAGTGTTAAGGCATGCAAAAGGCGCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112 A G ---	---	ACCTGGTGTGCTGGTGAACCTGGTCTCTTGGCATTGCCGGCCCTCTCTGGGCCCGCTGG TCTCTCTGGTGTGGGTAGTCTCTGGAGTCAACGGTCTCTT[C/G]GTGAAGCTGGTCTGGATGGCA ACCTGGGAACGATGGTCCCCAGGTCCGATGGTCAACCCGACACAGGAGAGCGCGGTACCCC TGGCAATAT
EST36027 2	120 A C ---	---	AGTGACTTCCAAGAAATGGCTACCAACTTGCCTTCATGGCCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCCTGCAAGAACAGCATTCATACATGGATGAGGAGACTGG[C/G]AACCTGAAAA AGGCTGCTATCTACAGGCTCTAATGATGTGAACCTTGTCTGAGGGCAACAGCAGGTTTCACTTAC ACTGTTCTGTAGATGGCTGCTCTAAAAGACAAATGAATGGGAAAGACAA
ESTD- COL2A1cc	112 A G ---	---	AGAAATGTATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGAACATACGTTGCTATTATGCTCTCTTCTCTGCTACTT[C/G]GGGTGTTCAAGGTGGAAAA GGTGAACAGGGTCCGCTGCTGCTCCAGGCTTCCAGTAACTCAAGCATATAACAATACTACTGCCT TTGGTCAGCCTATTGAGCTGTAAATCACCATACCGTAACCT
ESTD- COL2A1dd	97 C T ---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGGACCTGGAAAC[C/T]TGGACTTCTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATACAATTTTATTTGACCAAACTATCATGGAACA GCATT
ESTD- CPT2	150 A G ---	---	GCCGAATGCCCGGAGTTTCTCCAATGTGTGGAGAGGCCCTTAGAAGACATGTTTGATGCCCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAGCTACCATCACCTTCTCATCATGAAAAAC TGGAGGCCGGGAT[C/G]GTGCTCATGCTGTAAATCCAGCATTTTGAGAGGCTGAGGCGGTGGAT CACTTGAGGTCAGGAGTTTGAGACCAACCTGGCCACAT
EST12274 0	135 A G ---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTCTCCAATAGAGCCTTACCAAAAGTGAT TACATAAAGAAGTCAAGTGGTTTACTCTCATGACCAAAATTTCTTCCCTCTTAGGATGAGGTG[C/G] A/GTAGTAAATGACCGATGGGTGAGAACCTGTTCTCTGTCCATGGAGGATACTATAACTGTGAAGA TAAATCAAGCCACAGAGCTTGCCAGATC
EST76807	91 G ---	---	ATGCTAAGGGGATCGGACATGAAGGACCCCTGTGACCGATTGTCTATCTCCAGGGCCCTGTCTATC CAGCTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGCTCCGGAGGACTCAACACTGCCCCCT GCTGCCATGTGGACTGTGCAAGTTGAGGACTTCTTG



ESTD-SSA1	111 C T ---	---	TTACATTTGTGGATTGTTCTTTTGTGTCGACGACCTTTTCAACATGATGTGATCCCATTTGTCCAAAG TTTGCTTTGGCTGCTGTGCTGTGGGATATTTGAAAGAGATTC/TJTTTGGCAGTCCAATGTCCCTAGA GAGTTTCCCAAAGTTTCTTGTAATAGTTTCATAGTTTGAGGCCTTAGATTTAAGTCTTTAATCCATT TTGATTTGATTTCTGTA
ESTD-RYR1	109 A G ---	---	CTTGTGACGGGAGGTACGTCTCCGCCTCTTTCATGGACATATGGATGAGTGTGACCATTTTCCC CTGCTGACAGTGATGACGAGCGAGACTTGTCTACTATGAG/GG/GGGAGCTGTGTGCACTCATGCC CGCTCCCTCTGGAGGCTGGAGCCACTGAGAATCATGAGTGGAGTGGAGCCACCTGCGCTGGGGCCAGCC ACTCGAGTCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G ---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTCTTACTCTCTGCTGCGATGATGTG CG/GJCGTGTGCTGGAGTAGCCCGACTCTTGACGGTCGGCATCTGAGACCAGTGAGAAACGCCCC CTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2 EST44438 7	100 C --- 62 C T ---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGGCTAGTAGCCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCTCCAGGCCCGTAGGGGAACCTGGGGGATCTAGGGGATGGGTGAGGAATGGCCC AGCCAGTCCCGCGGGTGGCTGGTCCCAACAGAGGAGGCCGCTGGAGGAGACAGAGGATGGGC TGGATGAG
ESTD-PBDA	103 A G ---	---	GGAGCCAGGAGCCGCTGCACCATGCCCGCATAGATCGGACCTCAAGCTCGACTTCAAGGA/C/TJG TCCTGCTCCGACCTAAGCGGAGCAGCTCAAGAGCCGAGCGAGGTGGG
EST12839 3	122 A G ---	---	CTTCTCATGCCAGATGGAAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGTGGGAGGCGGAGGACTAATCCAA/GJCTCTACCCGAGCTTGCTCGCATACAG ACGGACAGTGTGGTGCAACATTGAAAGCCTCGTACC
ESTD-CTLA-4	48 A G ---	---	TGCAAAACACACAAAATCTTCCAGATGCCCTATGGCTGTGGAGGAGCAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAATGAACACACAGCAGCTTACTCCAGAG/GJTCAGGTCCA AGGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGAACTTGAATGTTATTCAAC TGGATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGCTTAG
ESTD-ACE	96 C T ---	---	ATGGCTTGCTTGGAATTCAGCGGCACAAGGCTCAGCTGAACCTGGCTA/GJCCAGGACCTGGCCCTG CACTCTCTGTTTCTTCTTCTATCCCTGTCTTCTGCAAGCAATGCACGTGGCCAGCCTGCTGT GGTACTGGCCAGCAGCGGAGGATCGCCAGCTTTGTGTGTGAGTATGCATCTCCAGGCAAGCCAC
EST54419 8	88 A G ---	---	GATCAAGCAGTGCACACGGGTCAAGTGGACAGCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCC/C/TJGTCTCCCTGCGTGGGGGCCAACCCCGCTTCCA TGAGGCCATTGGGGACGTGCTGGCGCTCTCGGTCTCCACTCTGAAACATCTGCACAAAATCGGCCTGC CTTCTGCCTAATTTGAATGATATTGTGCTGTGGGACCTGAGCACTTTTATGGCAAAATGATCACTA TTTTCTTGACCCCTACTTAC/GJATCCTGGGAGATGATTTGGGTTAGCGTGGTGTGTTGTCTA CTATAGTCCCAAGTGAA



ESTD-PS-1	99 A G ---			GGGGAGTAAACTTGGATTGGAGATTTCATTTCTACAGTGTTCGGTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACAAACCATAGCCTA/GJTTCGTAGCCATATTAAATGGTTGTGCCCTTAC ATTATTACTCCTTGCCATTTTCAAGAAAGCATTTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGT TTTCTACTTTTGCCACAGATTATCTTGTA
ESTD- B3AR	104 C T ---			GGCTGCCAGGGTTCGGTGGAGGCGCCCTAGCCGGGGCCCTGCTGGCGCTGGCGGTGCTGGCCACC GTGGAGGCAACCTGCTGTCATCGTGGCCATCGCC/CJGGACTCCGAGACTCCAGACCATGACCAA CGTGTGCTGACTTGGCTGGCCGACGCGACCTGGTGATGGACTCCTGGTGGTGGCGCGCGGCGCA CCTTGGGCG
WI-567b	48 A G ---			TCTCACACTGACCCCTTACCTTCACTCCTCACTCTGCTGCCCTTGGTTC/GJAGCCCTCATCTCTTTA CAGGATCCGCCAGACATCCCACTGATCTGGCCTTAGGCTTCTTCTCCAATCCATCTTCAAAG GCTGCCACTGTGATCTTCCAAAGGTGATCTGATGCTACCATCTTGTCTTCAAGCC
WI-801c	58 G T ---			ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTTG/JAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTGCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGATTAA CATTTCTGCCACCCCTC
WI-801b	58 G T ---			ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTTG/JAGATGG TATTGGAGAAGTAGACAGAGAGAAATTAAGTAGGCAATGCATGTTGCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGATTAA CATTTCTGCCACCCCTC
WI-1099b	76 A G ---			GAAATTCACCTATACAAGAACTATTTCTCTAATTATTACATTAGTCTCATTATCTGAAATATTAT TTTTTACA/GJTACCCCTTGATTATTTTGTGATTCATTTGTACGAGAGATTACAATATCAGTAACGC TGTTCAATTGATAGTGTATCACAATGTCTAAAATACCTTTTGGGTCAACATCAAAATTAGAAAAGAAA CTTACAAAGTTTATTTGCTTTATGGTTA
WI-2529	71 C T ---			AGGAAATGGCTGATACTCCTGGTGGCTTCAATTAGTAAAAGGAGATGTAATTGCTTGATGAGCCTCT CAA/CJTTCCTTAACCTGCTGCCCTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAAGAGGACAACTGTGCTTT TTAAGAAATAGAAGAGTCACTTTCATTAGAAATGGCTTTGGGGATGACAAGTA
WI-10088	205 C G ---			TAAGGGCCTGTCTTCCCCAGAGGCCCCACGGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCCCTATGAGGTAACTGAGGATGAAGGA GTGAGTCATATTGGGTGGCAATTAATGAACCCAGCCTCTCTCTCAAGAAGACTTTTACATTTTAGAC AGG/C/GJAGCAGAAGCAGCAAGGAGAGAAAGGAAGT



WI-2625	98 G A	---	---	GGG CAG T C C T G G C T G T A G T G G T A G A C A G C A C T G A A G G A T G G A G A A G A G A A A C A G G C A G A A G C A C T G G T A T T A C A A G G C T A T T A G G A [G/A] C A A T T G A T A C T A C C C T G A G G A C T C G C A G A A T T A C C A G C A G T G G A C A G G G T A C T G T G G T G A A T T C A G T T A T C C A C T T G C A G G A G A A A G C C A G C C A A A G
WI-2924	54 G A	T G A C C T T C C T A G T C T T C T C T T A T A G G	G C C T A A G T G T A A T C A C A G G G	T C T G T T G C A T A T T C C C T C T T G A C T C T G A C C T T C C T A G T C T T C T C T T A T A G G [G/A] A C C C T G T G A T T A C A C T T A G G C C T A C C T G G A T T A T T A G A A C A A T C
WI-2939	72 G T	G G C T T G T C T C A G T G C C T T T	C T T G T T G A G G G A A G G T C T T G	C C A T T G T T G A G G T G G G T G C A C T T G T C A T T C C C T G C A C T C A C A A A G T G G C T T G T C A G T G C C T T [G/T] C A A G A C C T T C C C T C A C A A G A A T G T C T T C C A T G C T C C C G T G T C T T T G A A A A T T C G A C T T A T C C T G A A A A C T C A G C T G C A G T G T A T C T C C G T A T A A A G C C A C T C C T G
WI-3203	99 G A	G G T T A T G C C G C A G C A G	T C A A G T A T T G C C T T G T G T G G	C T T G C T A C C A T G C A T T T C A C A G C A T A C A A C C C T C A G T G A A T G C C G T A A A C C C C A T T A T A A A C A T C T T G C C A T C G A A G G G T T A T G C C G C A G A G [G/A] C C A C A C A A G G C A A T A C T T G A A G T G A C T T G G A G A A T A A G A T T T G G A T G A A A G C A G A A G G A G A T G C T A A A A G T G A
WI-3473	101 A G	A A G C A T T T T A G C C C T A G G G A	C C T G A T G T C A C C A A C A T T T T C T	G G A A A A G A A A C C T G A A G A T G A G T A G A A G T T A A T T G G G A G A T A G T T G G T A G G C C C T G T T T G G A G A T T G C A G A G A A G G A G C A T T T A G C C T A G G G A [G/T] A G A A A T G T T G G T G A C A T C A G G G C T A C A C A C T T T T C T G T A T G C T C T T C A T C A A A [A/G] T G C A G G C G T C A T T T C T G C A C A T G G T G A T A T T T A A G C A G G A G A C A T T G T C T T G G C T C C C
WI-1796b	29 A G	---	---	A C A C A C T T T T C T G T A T G C T C T T C A T C A A A [A/G] T G C A G G C G T C A T T T C T G C A C A T G G T G A T A T T T A A G C A G G A G A C A T T G T C T T G G C T C C C
WI-1796	29 A G	---	---	A C A C A C T T T T C T G T A T G C T C T T C A T C A A A [A/G] T G C A G G C G T C A T T T C T G C A C A T G G T G A T A T T T A A G C A G G A G A C A T T G T C T T G G C T C C C
WI-4360	93 C T	G T A G T C A C A T T A G G T A T T T C C A A A T A A	G A G A G A T A T T T T T C A G A G G C A T T T T	A G T C G T C C A T C T T C A G G G T C T A A C T C T G G A T C T G G C C T G C A G A T A G G A A A A G A A G A T G G G T G A G T A G T C A C A T T A G G T A T T T C C A A A T A A [C/T] A A A A T G C C T C T G A A A A A T A T C T C T C C C A T G T C C C T G T C T A A A T A A C A T T T T C C C
WI-1959b	87 C T	---	---	G C T G A G C T T T G T G C A G A G C C A G G A C A A T T C A G C T G C C G A T T T T A A T A G A T T C T G C A G C A C T G C A A C A G A A C C A A A A T C A G T [C/T] G G G T A A C T G A G A G T G T T T C A C A C C C A A
WI-1973b	28 A G	---	---	G T T G T C C C T G T A G C A G A C A C A G A A G G C A [A/G] A G A G A G A A A A G C C T T T T T G T C C A G G G C T T A C A C T G A A T C C C T C A A A C A A T G C A A G A T G A G C T A A T G G T C T T A G A G G T A T A T C T A A G T G T G A G A A A A C A A A G G T A T A G G G T T G
WI-1980b	140 C T	---	---	C T T G A G A T G C G T G G A T T T T G T A T A C A C A G A A A T G G A G A G C T G G A A C T A A T C C C C C A T A T A C C A A G G A C A A A T T G A T C T G T T C T A C A A T T A C A G A T A G A G A C A T T A T G T C C A T G A C A A T G G T A A T T T T T A A [C/T] G A C A G T T T T T A A T T G A G T G A A A T T A C C A T A A A A A T A A T A A T A G T A G C A G C T A A T A T T T A C T G A G C T G T T A C T A G G T G C C T A T A A T A G C



WI-2015b	190	A G ---				TGTCAGATAGTCCGTCCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAATTATGCT ATATATTATACAATATAACAATTACTTTGCAGATAGCATGACCATGCTAGTGAACCCACAGACTAT GTGTGAATCGTCTATTAGGGTTTGCTATAAATCTACATGGTGTCTTTTCCAACCTA/G/CATATACTT CTAATACCATAGAG
WI-754b	49	C T ---				GAAGGCACAGGGAGAGAAGATGGCTGTCTATCTACCAGCCAGGGAGAGAAGC/GC/TACATTTATTGGTAA TCCTATAAAGTGCATCTTTAAAAATTTGATTTACTTTAGA
WI-754	22	T C ---				GAAGGCACAGGGAGAGAAGATGGCT/GC/GTCATCTACCAGCCAGGGAGAGAAGCCACATTTATTGGTAA TCCTATAAAGTGCATCTTTAAAAATTTGATTTACTTTAGA
WIR-1b	56	A G ---				AGGCAATCAGACCTACAGAAAGGAACCCCAATAAAAACTCTGATGATCGTACATCC/A/GJTGCGCTG GAGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-1	56	A G ---				AGGCAATCAGACCTACAGAAAGGAACCCCAATAAAAACTCTGATGATCGTACATCC/A/GJTGCGCTG GAGGTGATGCTCTCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-3b	72	A G ---				TAATTTAAAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGT/A/GJCTAAAAAGTTATTAGCTCAGAGCCTCACACATTTCTCAGTGACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69	A T ---				TAATTTAAAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAT/GTATCTAAAAAGTTATTAGCTCAGAGCCTCACACATTTCTCAGTGACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47	T ---				GAGCCTTTCTAAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCTGCTCACACATGTGCA AGGCAGCAGCAAAATTTGCCAGCTGCC
WIR-5g	209	C ---				CGGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGAGCTGTGGTCCCACTGTTAGG TTTTGAAGGGAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACACAGG TTTTACGTCCAG
WIR-5f	196	C ---				CGGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGAGCTGTGGTCCCACTGTTAGG TTTTGAAGGGAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACACAGG TTTTACGTCCAG
WIR-5e	194	C ---				CGGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGAGCTGTGGTCCCACTGTTAGG TTTTGAAGGGAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACACAGG TTTTACGTCCAG



WIR-5d	191 A	---	---	---	CGGACAGAGACAGAGAGAGAGTTCTGCAGCATTACAAGAGGTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACCTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5c	177 C	---	---	---	CGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTACAAGAGGTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACCTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5b	159 A	---	---	---	CGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTACAAGAGGTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACCTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5a	37 A	G	---	---	CGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCA/GCAAGAGGTATTAGGACTCAGTTCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACCTGTT AGGTTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAAACAC AGGTTTTACGTCCAG
WIR-6	63 A	C	---	---	TAACCCGTGAAACTTTGTCTTCTCATCTCAGGGGAGAACACAGACTTCATGTTAAGACCCAGAA[A/C] CGCAGTCTTGGGGTTGGGGCAG
WIR-7	12 C	T	---	---	TTCTGTGACTATT[C/T]AAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-8	46 C	T	---	---	GGCGTCCATGACTATCCTGGTCATTGATTGACTAATGATTCCTG[C/T]GCCCTTG
WIR-2	56 C	G	---	---	AAACAGAAAAATAGAGGTTATAAGGATGGAACCTAAAAGTTGTCAGAGAGGATGA[C/G]CTGAAG AAAGAATTACTCTCTTTGACCAATAAATACAATTGGGAAACACTGGAAACCATGGCTTGATTACT GACAAC
WI-7069	93 G	A	---	---	TGTCCTTGCTTATGCTGCCTCTTTTCGCTTGGCAGGATGATGCTGTCATTAGTATTTCACAAGAAGTA GCTTCAGAGGGGTAACTTAACAGAGT[G/A]TCAGATCTATCTTGTCAATCCCAACGTTTTACATAAAA TAAGAGATCCCTTTAGTGCACCCAGTGACTGACATTAGCAGCATCTTTAACACAGCCGTGTGTTCAAAT GTACAGTGGTCCCTTTTCAGAGTGGACTCTAGACTCACCTGTTCTCACTC
WI-18694	41 A	T	---	---	GGTCATTCCCTTTTATCTGTCAGGCAGCCAGCTGACTT[A/T]CTCTCTGTTTCTGTCATCTCTCCC CCACATACCAACTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18612	37 A	G	TGC	TTGTATTGCTG CTTGCAAAAT	CACACTGTTACACACCTATATTTCAAGTTTGGAAATGC[A/G]TATTTGCAAGCAGCAATACAAAAAGTA TTTCATGAAGAATGCATAATCTCTGAAAAATTATGAAACATCCCT



WI-18517	87	C T	CAGCCTGA	CAGGAATCAG	TGTTTGGACAA GTGCAACA	TAAAAATCAACTAGGGCTCACCCCTCAACACCCCCCTCCATTTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGA/C/TJTTGTGCACTTGTCACAAACACAACTGACTGC
WI-18668	76	C T	TAGGCAAAA GC	GGCGAAAAAC CTGCACTTTT	GCTAAATTAAA CTGCACTTTT	CGATTGACAACCTTTTATTTTCAACTTAGGTAAACAGTCCAAAATCAGTGTAGATTGGCGAAAAACT AGGCAAAA/C/TJAGCAAAAAGTGCAGTTTAAATTTAGCAAAAGGCTCAAGACAGTATGTGGAAAGGAA GGTGAGATTCCCTCCTACT
WI-18680	75	T C A	AGCATCTGGA	GCTGTCACTCT AGCATCTGGA	CCTCCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAAT/CJGCTCCGTTGTATATTCAGGAGGGGA
WI-18704	99	A C	GGGTCTCCGA GGGTAC	GGTCTCCGA GGGTAC	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTTCTGTGCGAGCACACACCAAGGGCAGGTTGGGCTTGAAGGAGCC CTTGAGGAACACCGGTTCTCCGAGGGGTAC/CJCCAGCAGGGCTTTCAGCTTAAAGTCG
WI-18673	29	A G ---			---	TGTGGCAAAACCTTGTTTTAATTGCAAAAC/CJGACTTAAATTTACAGCACATTCAATAATGAACCAAC AGGAGATTGCTGACTTTGTAAACATATGAATATATAAAATCCCTTGOAATTCAGGTAGTCAAGGTA AAAGCGCATACAAGGAAG
WI-18640	121	T C	GTCTGGGTG GGG	GTCTGGGTG GGG	GCAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTTTATTTGGAGGTTAATTCCTATTAGGATATGAAAGGATTAGCAACGATTGAGATT GTGTTCTCAGGAGGGCTCGGGCCAAAGTCTGGGGTGGGGGGTGCAGAGT/CJGTGTCCTCTTC AGTGGTATTTGGGACC
WI-18533b	91	T C ---			---	GGGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAACTCCCGAGATTTCTCTTTATTT TATATTTTCATTTTTCATCCTAAT/CJTTACTGAAGCCATTTTCTTTGGTTAACTTTAGA
WI-18533a	59	T G ---			---	GGGGAGAGGAGGTAGATTGCCAAATTGAGGCATTTTTTAACTCCCGAGATTTCTCTTTGCTTTA TTTTATTTTCATTTTTCATCCTAATTTACTGAAGCCATTTTCTTTGGTTAACTTTAGA
D11734	83	A C TTC	TCATCTGATAC CTTGTTCAGAT	TCATCTGATAC CTTGTTCAGAT	AACCAGGATA AGGTACAACT ATTT	GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTCTATCTGATA CCTTGTTCAGATTTTC/CJAAATAGTTGAGCCTTATCCTGGTTTACAGATGTGAAACTTT
D49493	159	A T TCTGGGAATT				CAGGACTTGTGGTGCAGCTGCAGACACAGAGCACAGCTCATGGGCAACATCACTGGGGCCAGAGAG AGCTGTCCGCCAGTGCATCATTAGGGGCTTTTTCATTGCTAGTACTAGCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATT/AJGGCCCTGGCCTGAAAGTGGCCCATCATTCATACCCACTGTT CT
EST10030	98	T C TCTCAAGTCCC				TATTTCATAGAGGAGACCTAGGAGGAGTTGACACAGCACACTGCTCAGCAGATGACTTAAAAATTTT CCCTTAGCCATTTTGTTC/CJCAAGTCCCTT/CJTCATCCATACCACACTGCTGATTTG
EST10052	24	G A GAGGCTG				TATTTGGCTCACTTCTGGAGGCTG/AJGAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC CTGTTGAGTCAATAACCTGGTGGGAAGTCAATCATGTGGCAAGAGAGAGGGCTACAGAGCAAGAGGAA A



EST10605 2	118 C G ---	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	GCTAAATTTTC AGAAAGAATT TTGTTT	CTTGGCTAAATCACAGTTCTGTATTCTACAAAAACITTTGTTTTCTCTGACAAAACTGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTTAAATTTGTGGAGATGCCCCATGTCGTTGTGAGACTTAA AAAAAGAAAAAGATCCC
EST11048 0	61 T G	ATAAGAGGCA TAATCT	---	AGAAAGAATT TTGTTT	CATGTGTCAATCCCATGATTGAAAAACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTTTGJAA ACAAAATCTTTCTGAAAATTTAGCTTATGAACCTATTACACTGCAAAACAGAGAGGAGCAC
EST11260 8	101 G T ---	---	---	---	TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAGTCTGAAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG[G/T]GGAAATGAAGGCAATATCAGATAAA
EST11349 9	109 C T ---	---	---	---	TTTGATGGAGAAATCCGAGGCTGCCAGCATCCACAGTAGATTTCTTTGGACGAAGAAATCCT TCTGTGATTACAGCTTACCGCTTTCTCTCATCTGCTGGTGC/TCTTCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI- 16632a	71 A G TGGAGCOCT	CCAACCTACTT TGGAGCOCT	---	TCCAGCTTTCT CTAAAACTCC T	GAATTTCTGGGTATTAAATAGCGGGTGCCACAGGAGCACATAGGAAGAGCATCCAACTACTTTGGAG CCCTT[G/G]AGGAGTTTTAGAGAAAGCTGGAGCCGAGACCATAGTAGGAGGTAGCCAGACCAA AAGGGAGGAAGGAGTGGGAA
EST11772 6	74 A G ---	---	---	---	CCAGGAATAAAAGAAAAAGATCAGAGGAACAGCTTTTGATGTTATGAGGCTGAGACACTACTC TTCTTCA[G/G]GACTATTTCATCTGACTATAAGTGAATAAATACATTGAAGACTTCAGGAGCTCA
EST11795 3	82 G A ---	---	---	---	CTTGCCATTATTTTGTCATGTTGTTCTTAAAGGCTTGGAAGATAACTTGAATGTGGGAAAC ACATAGATCCCAGA[G/A]TATTAAAGGGCTGGAAAAAGTAGCCTTAAGAC
WI-16644	42 G A TAC	CAATAAGCAG CTCATTTTGAT	ACTTCATGAAT TTTACTTCATG TATACC	AGAGCAATGGTGCGATCTCAATAAGCAGCTCATTTTGATTAC[G/A]GGTATACATGAAGTAAATTC ATGAAGTAAATTCATTATACCAAAAAGCCTCCACAGAACTTTTCATGCACCTGAGCTATGTGAAC TGAAAAGTAACAGTGGGAT	
EST12005 9	56 A G CAAAGTCTGT	TTGTATAATA ACACTCAGTA	GGCTGGTCACT TCCTGGAT	GCCTAGTAATTCAAAAAGGAACATGTTTGTTATAATAACACTCAGTACAAAGTCTGT[G/A]GIATCCAGG AAGTGACCAGCCCGACGTTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTGAAATC	
EST12055 9	32 T C ---	---	---	---	GTGGAAAAATTTTATCTGTTACGCTTTCC/T/CJATTATAATTTAICTTTGCTTGAATTCAGCACCC CACCCGATTTCAGGCAGTCTTTCTAACTGTGCCCTGTGAGCTGTTAAAAAGTCTTCT
EST12492 1b	95 A G ---	---	---	---	CCCTAGCAAAATGACTTGGAGTTGTGTCCAATTACCAAGTTACATACTGTGGCCAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT[G/G]GGAAACGCACAGCAAAATTGACGATGCAGCTTTTAA CCTTTTTA
EST12492 4	25 A G ---	---	---	---	ATCTTGAGGTTTCTGGCCCTGTTCAG[G/A]AAGTGACATCTTTACTTACCACAGGTGAGGAACCCCTAT AAAGAAACTGTGTAGAAAAGATATCAGGTGAGACTTTTTAAAGGGCTTCTTATCAGCTCAATAAA



EST12502 2	52 C G ---			ATAACTAGGGAGAAACC AAACTGGAGGCAAGTCCACAGGTACACATTGTCA[C/G]CAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAAAATGCTCACGGGGAATGACCAATTTTAAAGGGCCATGTG GTCGTCGAGGCAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAAATAGAAATGATCGGTAAAAAGAAATAGGAATGCATATTTCAACTCACTGTCACAAA CAGGTGTTTATTATCCCAAATGACAGTGTGCCGTGAGATTC[GATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTTCTCTCTCCTTCATTATTCAATTTGTTCAAAACACTGTCTAGTACCAACATTGTCCACCGGGC[A /G]TTGAGAATACAATATTGAAGAAGAGTCACTGCCCTGCCCTCTGGAATAATCAGAGTATTGA
EST12817 9a	22 C A ---			TTGGGGTCTCCAGGATTCCAG[C/A]CTCGTAGCTGATGTCATGAGGTTCTCATCCATGCTCCACGG GTTCTTGGGAGTGACCGGATGGGAATCCATGTTGCTTTGGGTACTCCATCAGGTCAATTGCG
EST12941 8	23 T A ---			TCTCAGCTTCCACCTGACCTGCA[T/A]CAACAGCCCAAGTTATTTCCACAGAAATTTGTTTGGGTTTCA ATGTAGTGTTTAGCTTTAATACACTGCACCTTGTTTG
EST12949 2a	52 A G ATACTGTT	GGCTTTAATCA TAACCTAATA	TGTGTCCTGT GGGTCTC	AGGATTTTCATGAGGCTTTAATCATAACTTAATACTGTTAAAAACAACAC[A/G]TCTGTCACTTG CAGAGACCCACAGGGACACACATTCTCTCCTCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTGTGTTTCTTAAATGAAGCATATAAACAGTTAAAATCTCAGAAAAATCATCTATAGTTGA GTGTAAACTCCCTAAATCAGTCTTCTAGGGCCACA[C/T]GGAGCAGAAGCAGCTTCCCACCCCAAG CACTCTGAAT
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCTCTTTAAAAATTTAATCGCTTTATACAATTGACACCAATAAAATGCAC[A /G]TATTTAAAGTTTACAATTTGAGAAGCTGACACGTGTCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTAAAGATTCTTCATAGCTGCTTAGGTTTGTCTTCC[C/T]AGCATATTCAGCTATAATCA CCTACATTCCCTCCACAAATATTTCTGTGTGTGCCAGGCCAGTCTCCTCACTGTCCCATGAATAGCC AGTCTTATTTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTTGAGGAAATAAATTAATGAAATAGTCT GGCCATT[T/G]GACTAACAGTTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAAACATG
EST13230 6	72 G A AGAGACGC	GCTCAGATGTG ACAGAGA	CCGGTCTCTGT ACAGAGA	GCATCATCAGCGGCTTTTAACTGAACCTTACAACCACTTGCCGCTCAATATGCAGCTCAGATGTGAGAG ACGC[G/A]TCTCTGTACAGAGCGCGGTACTGTCTTCAATCCTTTGCATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C TCTCAGGCT	AACCAGATTT TGACAAAAGA	ACAAGAGGGTT TGACAAAAGA	AAAGATATAAAAAACAACCTCCCATCAGTAGCAATACAAGGTTATACATTTTAACCAGATTTTCTCAGG CCTT[C/T]TTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAACCCCTCTTGATATAACCA



EST13278 2a	51 A G	CTTCACCGAA CAATATTTTAG	CATATCTTGG GTGGTGAGAA	TTGCGAGAACGTTTTACAAGCTCCAAACCTTTACCGAACAAATATTTTAGG[A/G]ATTTGAAAAATTAT TTCTGTAGTTCTCACCAACCCCAAGAAATATGACAGCTTG
EST13282 0	99 A T	CCACACATTTT AGTCCAAGA	GATGGAAAATT TGAGGAAGGT	GCTCACTAGATGAGCATTGACCAAAATATTTAGATAATACCTGTTGGGAAAGTGCTGAATTACTAGCC TGCCTGAGAAATCCACACACATTCAGTCCAAGA[A/T]AACCTTCTCTCAAATTTTCCATCTCCCATCAGA GG
EST13290 9		CAATTTT TAGA AGTTGGGTT	AAATCAGTTCA TGGAATTTTCA	AGCTCATCTGCAAGCAATTTT TAGAAGTTTGGGTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTT TTTTCTGTGCTTAACCTCAGTTACTTAAGACCTAAAGACAAAGTGGTATCACATCACATATTTTGT ATGTGGGCTTTTIG
EST13518 2	45 C G		---	GAAACATCTCCAGTAGTATTGAGGTTAAATGATTTCAGCATT[A/C]GACTTTAAAAATTTACCTCA ATGTTCTCGGAGTCGTCATAGTTTAAATGACTTCTGCACCTTCTTTATAACCTTGATTG
EST13522 8a	66 A G		---	CAGGTTGGTGATTCTCAACTAGGAGCTATTTTGCCCCCATCCCCCAGTGGTCTGAGGAC[A/ G]TTTTGATTGTCACAACTCGGAGAGGTGGGTGCTACTGGAATCAGTGGGTAGAGGCCA
EST13568 6	69 T C		---	CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AA[T/C]GCACACAAGGAATAAGGGAGAAAGGAGGTTGGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	101 C G		---	AAGATTACGGACCATAAGAACTGCCCCCGACCCATACACACAAATTTATAGCAGGTAACCAACAA CTGAAAGGAACAAGTAATGACTTTCTTGAACAA[A/C]GTGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25 A G		---	CCTCAACCATCTGTAAACCCGAGCC[A/G]CAGTGACCCGGGACTTGCTGCTTCCCCATCCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23 A G		---	CAATGGTGTCATGTGAACATAT[A/G]ACCTATTATATAAGTTAAAAATAATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAGTCACTGCTAAATGACCGAACAGGAGGAGGTAGGAGG
EST14221 5	42 T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAAATATTTT AAAAGA	AATATCAATGCATTCTTGTGGCATGCTAGACAGAGGCATT[A/T]CTTTTGAAGATCTTTTAAAAAT ATTTTGACTTGTCCCCCTTCACACTCATTTTAAATTGT
EST14812 2	50 A G	CAAGTCAGCTT CTACATTCTGA	TAAAGATTAC TTAAATCCCAT TATGTACT	TTCACTTAGTACCAAGGATGCTTTCAAGTCAGCTTCTACATCTGAATA[A/G]AGTACATAATGGG ATTTAAGTAAATCTTTAGAAGTCCCGAGTTTGCCCTTTCTAACATTTTCATATCAGGTGAAAAACAAT TTTTTCATATGGGTGATT
EST14815 3	128 A T	CATCACCACCC ATACTGGTT	CGGGAAAAACA GTACCGGAA	TTTGCTTCGGCAATACATAGTGGCAATGCAGCGTGAGTTGCGCCGCTCCCCACTGAACACAGTAAT TCACCAGACAATGGCGCACCACTTAAATAAAGTTGCCGTCATACCCACCATACTGGTT[A/T]TTCC GGTACTGTTTCCCGTA



EST15420 6	109 C A ---			TTTAAACCCCAAGACITGTAGATGTGAGGACTCCGATCATTTTCTCTGCCTATAGCTTGGATATCTTA ATCTCTCCCTTTGTGCATATAATCATATAGCCAAGGGACTC[A]GGAATTTTGGCTGCTTCAAGTCA TTCCAAACCTCTCAGG
EST15700 6	48 G C GGA	GAAGAAGACAA AGACAACAGA	GAATAGCTGA AACAGAGATA TTATTCTC	GTCACCAGCACITTTTATTAAAGACGTGAAAGACAAAAGACAAACAGAGGA[G/C]AGCAGAGAATAATA TCTCTGTTTCAGCTATTCCAGGATGTTATGCCAATTATCCAGAGTCTTGATCTGATGTAGTA
WI-16739	57 G A CACAAGC	GGTTTGGCCAT GATAGTTGATG	TTCAATTATCC CTATAA	AAGGATTGAAAACATACCTAGATCATATAAATTTGTGAAGGTTTTGCCATCACAAAGC[G/A]TTATAG GGAATAATGAACATCAACTATCTACAGCTAAACCTAATGAAGACCAAAATGCCCTCCAAGGT
WI-16782	96 C T CACTGTAAGG TC	GGTGGGAGTCT CTGTTCTCTOCA	CTTCTATCTTT CTGTTCTCTOCA	CTTCTCTCTCTAGACGTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAAGGA[C/T]GATGGAGGAACAGAAAAGATAGAAGAAGTTTGGGGT GCTGATGAAATTGTGGGG
WI-16783	64 A G G	TOCTGAGATGT CTTTTACCTGA	CTGCTTGGTTC AATCCTTATTA	AAAAATGTAAACCTTAGAGGTTGCCCTCTTTTGTGTCACTTTTCTGTGATGTCTTTTACCTGAG[A/G] CTAATAAGGATTGAACCAAGCAGTATTTTTTAAATGGCAAAAGTCCAGATGTAACTCGAGT
EST15948 2	58 T C ---			CAGGACTTAAGGTCAATTTGCCCTGGAAGACTTTAACTAAAGGTCAAGGCAACATAGGA[T/C]GTGA CAGCACCACTCGGACCAAGGAGTGTGAAAATCGTCACACTAGCGTGCCCAAGCCCCCTTTTTTCCCTGGC TGCTCTGCCTCCAGAGC
EST16088 8	89 G C ---			GGTTTGAAGACGCAGCTTTATCTCCACCTGCCACTGGGATCTCATTTTGAGAGCTGTTTTGTACAGCC TTTTCCAGAAAGGCCGCTC[G/C]GGGTTTTCTGAACCCCTCTATGGGCATTTTTAGAAT
EST16089 9	96 C T ---			CGTCTGAAGTTTTCTTTTATCAAGTCAACATCAATCCCTCGGCCCTGCTCAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTC[T/C]TAAAGAGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24 C G ---			ATCCCAGCTGTGAAGGGACAGAGGAG[C/G]GTAAACACAGTCCATTTATAAGGGGTGTGCACATTCCCA GGGGCTCCAAATAATGCAACATTTGTTTCACTCGTCCATGCTGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTTGGCTC
EST16104 9a	83 A G ---			TTCTTTAAATAACCCACAGACACCCCATGACACTTCCAAATTTACAGAGCAAAAAAGTGATTTGCAG CTGGTTCTCCAGGGA[A/G]TTGGCCCCGAAAGCTGGCTCAGTTCACTCCAGGACCTCAGTC
EST16118 0b	119 T C ---			ATGGTATAACAAAATCAGTTCCAGGTTTTTTTCTGTAACAAATGATCCTTTTGGCTTTCCCGTGGCATG CTCCTAAAACAACCTAAAACAACCCCTCTACGTCTAATCAGTCACCTAAGATA[T/C]CGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G ---			ATGGTATAACAAAATCAGTTCCAGGTTTTTTT[C/G]TGAACAAATGATCCTTTTGGCTTTCCCGTGGC ATGCTCCTAAAACAACCTAAAACAACCCCTCTACGTCTAATCAGTCACCTAAGATAATCGAGTGGCAAGT CTTTCACA



EST16151 2	53 C T ---			AGCCAAATCAAACGAACTCTATCAAAAACACACAAAGGCCCTAGAGGAGAGATTATC/TJAATGAACGT AAATAAATCAAGGCAATTTTGTATCTAAAGCATTTTGTCTTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54 G A ---			CATTGGTTGGTAGGAAAGATAGTAGTGTGCAAAATAAAATGGTAAACACGACAG[G/A]AAATGGAA TTATAGCTTCTTTTCATATAGGGAATGAAATTTATTTACTGAGGGTGATAGGCAGAGTAGTA
EST16183 2b				GCAGGTAAGTGTGGTTCACAACGTTATGTTCTTTCATAAAGAAAGAAATATCTAGTTG[A/G]GTAG AGGAAGGCACTGTCTTCTGCCCCCTCTTCGTTTCATATTTTATGTCACTGTCTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 G A ---			AATCTTAGGCTCTTGGCTTTCAAAATCA[G/A]TACAGACAGATAAGAGCTTTAAGTATTTTCGCATTT CCCCAGAGGAAAGTACGATCATATAAACCCACATGGGTACATGCTCACGCACATGGTGTC
EST16229 2c	52 T C ---			TGTGAACCTCGAATTCGCTTGTCCAAAGTCTGAGTCACAGTTTCATTTGGGAG[T/C]CCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGATACCTCACTAGCTGATTCAGACAGGCAGAGGCTGCA
EST16229 2b	45 T C ---			TGTGAACCTCGAATTCGCTTGTCCAAAGTCTGAGTCACAGTTTCATTTGGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGATACCTCACTAGCTGATTCAGACAGGCAGAGGCTGCA
WI-16816 124 A G TGGGGTTA		GGAGCCATTGT	GCCTAGATTTT	CAGACTTTCTCAGACCTCATTGGCTGGAAGTGGTGCACATGCACATCCTTGAACATCATTTGGCAA AGGGAATGGGTATCAAAATGCTTAAGGCCAAGCAGGAGCCATTGTTGGGTTA[A/G]ACTGTCC TGAACAAAATCTAGGCTC
EST16269 5b	49 G A ---			GCCACTCTCTGTGGCTGTCTCTGTCCAGCTGTCCAGTGTCCAGTGCACAG[G/A]TGGTCTAGCCTCATGG CAGAAAGCATTTTAGCCAACTCCTGGTGTCTCCACTCTCTCTTCCGCCCGTGGGCTCACCACC TCTTCTCTCTCAATC
WI-16824b	83 G A ---			GTCAACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTTGG[G/A]CTTACACCTTTAGCACGGATAGTTTCTGTGCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGTG	CAGCTTCTGAC	GTCAACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTGTTCTTATGAAGAAGTC AGAAAGCTGATAAACGTGGGCTTACACCTTTAGCACGGATAGTTTCTGGTCCCAAGTGGGTGTGGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ---			TTGCTTTTATTATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTATTATTACAAA AATGGCTTCCAAACCATTAATAATGAAC[T/C]GGATAAGAGCATAAACGGAAACAGTAACATCA
WI-16857	47 G A A	CAAATAAGCA GCTAATGGCA	TGTGAATTGGG AAGACCACT	TATAATCCATCTCTCAACACACACAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTTCCCAA TTCAAGAGACCTGTGCTTCAAAATGTTTCTCTGATAATGTGGAGAAATCTGCTCTTTATGTA



WI-16879	79	C	T	GATACAGGC ATAATTC	CAAGCTTTCT AGAACTAGAGT OC	AGACAGGTCAAACTCCTAGGGATAAGATATAAATCCAGCACAGCATTATTTCCAGATACAG GCCATATTTCCCA[C/T]ATAGGACTCTAGTTCTAGAAAGCCTTGGGGAGAAACAGGCCACCCAG
WI-16882	99	A	G	GAATGCGA CGTCTGAC	GACACATGTCA GGTAAATCGC AATGTTCTGAA	ACATGAATGGCAACCTCTTAGGTGGGAGAGACAATTCTCCCTTTACCCAAAGGTTACTCTGAC AAGGCTATGAATGAAATGCCACGTCTCTGAC[A/G]GCGATTACCTGACATGTGTCTCATCTCCCT
WI-16888	70	G	A	GCTAATTTGG GCAGGTT	TTGACCAAATT TAA	GTAGTAATGTTTCATCACTACCCGGGGAGAGACAAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC[G/A]TTAAATTTGGTCAATTCAGAACATTCCAAAT
WI-16905	75	C	T	ACTGGCCTGT GTGTCTCA	GTCTACTCT TCTAGGCGAGTG GG	TTGTGTTGTTGTTATTTGCCCTCCCAACATCAGAACATAAGTTCCATGAAAACAGGAACTTGGCCTGTG TTGTTCA[C/T]CCCACTGCCTAGAGAGTATAGACA
WI-16910	74	G	A	AAGAGTAAAG ATGGCGTAG	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTTCAGTATGTGCTTAAGGAGGTTATATTGCTATGACITTTTCATCTCAGAAAGATAAGATGGCG CTAGAA[G/A]GTATCTGTTATAGAAACGATACITTCATTTTGGGCTGAACCAAGTGAAGGT
WI-16918	93	C	T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAAATAAACTACCACCATTTCTCTGCTACCCAGAGGACATAAAATCTAGGAATTTGAC TTTACTGCAGCCATTAAACACCAGCAC[C/T]GATGCCACTTCTGTATCAGGAACCTAACGTGACAACC ATGAAAGGTCTCTGAAAG
WI-16947b	127	A	C	GGAAAGCAGA CCTGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCCTGGAGCACAGGATT TGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGAGACACCTGGGG[C/C]CCA CGGGCAATCAGATGAGATG
WI-16947a	58	C	G	CATGAAATA GGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCCTGGAG[C/G]ACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAGAGACCTGGGGACCA CGGGCAATCAGATGAGATG
WI-16966	43	T	C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTTGTTTACTTTAAATGCACACTACATAACAACCTAATA[T/C]CTTAACCTGGTCCAACCTATTT AGTATAACTAATATGAGTTTTTATCTGATACTTGCAATGGCAATGCAATTA
WI-16995	55	T	C	GAGCAGTAGA GACTGAGGTA	CATGTTGATTT CCAGCCGT	TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAATAGTATTT[C]ACGGCTGG AAATCAACATGCCTCTCTCTGTGAAAGTTGTCAGCATGGAGCTGAGAGGCTGAGTCAATCT
WI-16992b	60	T	G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGTGCGCCCTCATCTGAGA[T/G]GTG TAGGACTGTAAGGGAATGTGTTTGGGGTTAGGAA
WI-16992a	46	G	A	AAGACCCAG AAGTACACTG	CACATTCCTT ACAGTCTTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAGTACACTGT[C/G]AJCCCTCATCTGAGATGTG TAGGACTGTAAGGGAATGTTTGGGGTTAGGAA



WI-17010	23	T C	T T C A A G C C A T G	A A T A T A C G G T	A T G T T T C A A C A G G A A A G C C A T G T C I A T G A C A T T C A A A C A C C G T A T T A T T A G A A G C T C A T T T A A T
EST17127 9b	74	C T	C A C T C G G C A C	G G A G G G C A G G	T G T T A A T G C A G A C A A A A T C A A G G C T A A C T A A A A G C A G A T C C A A T G A C C C A G T G A T C A A C C T A G A
			A A T T C T C T T A T	G G A C T A T G G C T	G G T C C C A C
WI-17040	94	T C A	C A T C T C A A G C C	T A T T C A G T G A T	A T T C C G T C T C A A A C A G C A T C C C A G G C C G G C A T C T C C C C A C G A T T T T A T A T A C A C T C G G C A C A G A
			G C C A A G G G A T	G	C A G A G T C T C T T G G G A G C C A T G G G C C A C C C C T G C C C T C C C A G G C T T C C T A A G T A A C A A C T
WI-17044	47	G T G	T A A C G T A T A G	G G G G A T C C C C T	C A C G C G T T C A T T A A A T T G G T A C A A A G C A T G A A C A C A C T C A G G A C A G A T T G G C A C A A T A C A T G C A G T T C
			T G G A C T T G T C A	T G T T T A A G A	G A G A A A G A A A A G C A A G T G
WI-17021	62	T A A C T C	G C C T A T A A C T	T G T A G A G T T A G	G C A T G T T G G A G C A G A T C T C C A T G T A A G C C A A A A G T G G A C T T G T C A G C C T A T A A C T A C T C T A A G
			C C A G A A A G G A	T G G C A G C T G C	C A G C T G C C A C T A A C T C T A C A G G C A C A G T A A C T A C A C T T T A T A C A G G A C A C A T G C C A A A G T G C C T G G
WI-17065	90	T C C T T	A A G C A T A A A	A A T G A A A T C C T	G A G G T G C C A A T A A A A T C A A
			T G T A C A G C C A	G A G A T G T T G A A	
WI-17066	32	A C T	A C A T C A C T G T T	A A T G T T C T G G A	T T C A T A A G G T T G T A C A G C C A A C A C A T C A C T G T T T A C I A T T C C A G A A C A T T T C A A C A T C T C A A A A A G A
				A	A A C T C T G C A C C C A T T A G C A G T C A T T C C C T G T A G C T C C C T C A T A G G C A A T G G C A A C T G C T G A T C
WI-17074	86	T G ---		---	T G C T G A C T G T C A T G A C T T A G T A A G G C C A T C A C A G G T T G C C A G A A C A T C T A C T A A C T G T T C C A A G C A T
WI-17104b	108	T C ---		---	A A C C T C C T A C A C A G G C C T T T G C T A C A T A G G A G T A T A T T T G G C C A A G A C T C A C C A C T A G A A G T G A T T
				---	C A G A T G A A A C T C A T G C T G C T C A T C T G C A A G C T T C C T G A T G C T T T G C G A G C T T T C C C A T T C A T T C C A
WI-17114a	37	T C	T T C C A T C A A G	T T G T A T T A A A	A A T C A G A A G C A G T C A G T G G C C C G T G T T T C C A G A C G G C T T C I T C T C T T T G T T A A G A A A T T A
			G A C T T T G T T T	A A G A G A C	A G C G T C C A C A G A T G T T C C A T C A A G G A C T T T G T T T T T C I G T C T C T C A C T G C T A T T T A T A T A C
			G A T G A A A T T C	T T C T C A G A A T C	A A G C T A C C T C C C A A G G C C A G A T G C T A A G T G C T A A A A G A A G A C T G C A G C C A C A A T C A G A G T T A C A T
WI-17150	76	T G C T C T T	A G A T A G T C T T C	C T G G A A G A T A T	G G G A
			C A T T C T T T G T	G	C G T G G C T G G A C T A A G T G C T C T T T C C A T G T G G A C A C A T C C A C T G A A C A G A G A T G A A A T T C A G A T A G T C
WI-17163	43	A G T A A C G T T	A A A A T A A C A A	C A G A A T C T T G C	T T C C T C T T T T G C A T A T C T C C A G G A T T C G A A G G G C C C T C C T T T G T C T G C T C T A A T T T
				T T T T G C C T T	G A A A T C G A A T A C G T C C A T T T C T T T G T A A A A T A A C A A T A A C A A T A A C G T T A G I A A G G C A A A A G C A A G A T T C T G
					T A A C C A A C A T T G G A A A A G G G A C A C A G G G A G G G C A G A G G G A A A G G C C A G A T T T T C A A C G G T T T
					C C T C C A C A T C T G C A G A C A A A



WI-17178	127 T C	GGACTCCCTCA	CCCTCAATTTT	AGCAAAATGTCCTCCCTCCAAATTTTCATTAGCTATGATGGAGTTATCAGTTTCATTTTCAGAGCGAAATTAAGG
WI-17180b	81 C G	... ..	CAACTGCTTC	GGCGAGGGGGTTTAAATATCTGATGGTTTAAATTCAGTGAGGACTCCCTCATGAGGAGCTTC/JAGAA
WI-17180a	47 T C	CACAAAAATA TAGAGAATCC	---	GCAGTTGAAAAATTGAGGG
WI-17156	54 G C	TGTTCTCTAAA CTTTAGATATC	TGCGACGAGAC TTGGG	TCATGGACATCTCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACATTCCTCCAAAGTCTCGTCGCA
WI-17149b	79 T C	... ..	---	CAGGCTTCAACAATTACCAACATCTTGCCCATTTTGTTCATTATCCGCAACCCACACTGCACAGATGAG
WI-17149a	48 C G	CAAGTTTGA AGGAGGAACA	CCACGCACGTG CATGA	GGAGTC
WI-17197	67 G A	GCAGAAGTAG CTGGGGCTAC	GGTGAGGTGGT GCATACC	TGAGGTAGCAGGGCATTTTAAGAAATGTTCTCTAAACTTTTAGATATCTCCCATG/JTTCCACAGA
WI-17198	38 A C	TCCCGCTTGT CCTAGTTT	TCCATTTGTCC ACTGAGAAAT	ATCAAAATATATTTCTTGGTTGGAAATTTTAAATGTTCTTAACTATCTGCCTACCATCCACCTCAAT
EST18753	27 C T	CTACCCAGGCT GGTCTCAT	GGATCGCATGA GCTGA	TAATATCTTG
WI-17108b	74 C T	GCCATTGAGTC TCAAAGTAAA	AACACGATTT ATCATATGCTC	CAGGCAATTATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAAACATCTCATGCACGTGCGTGGAA
EST19067	41 A G	... ..	---	ACCCAAATTTGTCATGTTGATGATGAACACTACAAGGATGGGAAAGAACACATTTCTCTCACA
EST19067	40 A C	CGTGACCATTT AAGGGTATAG	AAAAATTGAA TGTAATTAATG	ATTTTGCTATGTTGCCTGGCTGGACTCCAGCAATCTCTGCTCAGCAAGAGTAGTGCGGGTAC/G
EST19125	28 A G	... ..	---	/A/JGGTATGCACCACTCACCTGCTTATCAGTTTCGTTTAAAGAATATTTGACTTTTAGATGCGCA
				TGATTTTCAGTACTTTTCTCCCTGCTGCTAGTTT/JTAATTTCTCAGTGGACAAATGGACAA
				ACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCC
				TTC
				TCGCTATGCTACCCAGGCTGGTCTCATCT/JTCAGGCTCATGGATCCTCCTGCTCTGCAGTGGCTGG
				GATAAGACACAACCTGCCACCGCTGCCCTAGGAGTAGTCTTAATGCCTGATGGTGGG
				TTATTTTAAACATAACCAGATGCACCTTGGTTTTCATTCTCTGGTTGCCATTGAGTCTCAAAGT
				AAACAC/JTGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCACTTACAGAGT
				ACACAAAATTTACCATCGTGACCATTTAAGGGTATAGTTCA/JGJGTGGCATTAAAGTACATTCAACT
				TTTTGAGCAACCCGCCATCACCATTTCATCATCCATCCGTT
				ACACAAAATTTACCATCGTGACCATTTAAGGGTATAGTTCA/JA/JAGTGGCATTAAAGTACATTCAACT
				TTTTGAGCAACCCGCCATCACCATTTCATCATCCATCCGTT
				CTGTTTCTCAGAGATGACACTGCCAACAJA/JTACAGATTTGCATACAATACAGTTATGTATTGGC
				TATTCACAAATTTACAGTAGTGTGTTTTTCTCTGAAAAA



EST20824 8	115 T	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCCGA	GTGTGGAAGCCGGAGTTTATTATTATTCAAATCAGTCTCTCTGAAAACTCAGGGATTGAGGTTTTTA AGGATAACTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTGTCTGATTGTTGJTCGGGTCCAAGATAAA ATCTTAGG
WI-17347	50 A	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGCTA	TTGGTTAATGATGCCAGATGGGGTCACATCCTCAGAACTTCTCAGCCTTACGJTAGCACAAGTGG ATGCTTGAAGAACTCAGCTTGGAACTCAGACAGCAATGGAGACGGGATGTGAGTGGGACCA
EST21904 b	128 GA	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTTT AGAAAGCAT	TGATTGGGTCTGGGAGCAGGTGGGCAGTTTCAGTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTTCATATGGCCATTTTAAATAAGTG(G/A)TA TGCTTTCTGAACACCTGCC
EST22111 3	82 T C T	GAAGATCTGT CTGGCATCTT	TGGAAAAACA GCCCCAC	CAAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGTCTAAGAGAAGAT CTGTCTGGCAITCTTTTTCGJGGGGCTGTTTTCCAAAGGCACA
EST22197 2	78 T C	AATTATTCTGC TATTCCTGCCA	ACCATGAAGG ATGCGGT	GTTTAATGATCAGTCAACCAAAATCCACAGGAGAACTCTTAAATGTTTACAAGCACCAATTAATCTGCT ATTCCTGCCATTCJACCCGATCCTTCATGGTAGAGTATCACAAGTAAAAAGTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92 T C ---	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG TAGCATCAATGGTTTTTACTCTATTCJTGCAAGCTGGGCAACTATCAGTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9b	54 A G ---	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG CAGTAGCATTCATGTTTACTCTATTCJTGCAAGCTGGGCAACTATCAGTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22311 9a	41 T C	GGATTAGATC ATCTTTTATT GAGTTATAA	TTGAATGCTAC TGTTTACAGTG G	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG CAGTAGCATTCATGTTTACTCTATTCJTGCAAGCTGGGCAACTATCAGTACTATCTAATTCAGAA CACTTTCATCATCCAG
EST22319	19 A C ---	---	---	TCGAGGAGCTCTGAGGAGCJACJACCAAGGGACGTGTGTCACAGGGCCACCCGTGCAGGCAAGTGTG GTCCAACTCCTTCCTCCCTTTACAAAACCTCCAGCCTCACCCACACAAACACTGGCTGACAGGCCCTCT TAAGCCTTTTTTAAGTGT
EST22433 c	103 A G AA	AAGACATGTT CACCAAGTGA	CAGCTTCAGCT TAACTGACAGA	GATGTTAATGACTTTCTTTGAGATATGATGGAAAAATATTCAGGTACACATGGAAAAAGACATGTT CACCAAGTGAACCAATCTAACCCAGAAAGCTTTTACCJAGJCTGTGAGTTAAGCTGAAGCTGAAATTT CTGGGAGCTTGACATGCTG
EST22657 9	71 A G	AAATGGATCC TTATCTGCACA	AGTTTCAGTTT GCATGAATTTT	TATCCATTTCAAGAAAAAAATGACTTAAAAAATACAATCTATCCAGAAATGGATCCCTTATCTG CACAJAGJCCATTGAAGAAAAAAATTCATGCAAACTGAAACTATGCTTT



EST22993 5b	71 T C	ATCCTTTTGT TCTACCCC	TTGCTGTAA TTTGACTGTAA TG	GCCTTTTATGTCTCTTTTAAACATCAAAATGTTTATAACACACTTGATCCCTTTTGTCTACCCCCA ATT/CJ/CATTACAGICAAAATTACAGGCAATATAATAGGCTAACAGAAATGCTTGCAATT
EST23021 0	108 T A	---	---	TTATTTCTCAGCTTACCAATTTGTGTACTTATATCTCTGTACAAGGTGTTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTAAATTTTATTAATCTTTGCCTTT/AJATGGTTTTGACAGTTTGTGTCTTTCT T
WI-17387	55 C G	CCTTGCAGAT TGAAGAAAA	GCTTTGCCTA AGATTAATAGT AACTACT	ACAGAAATTTTAACATGCAAGTTTCATTTACATTTACCTTTGCAGATTGAAGAAAAA[C/G]JAATATTAG TAGTTACTATTAAATCTTAGGCAAAAGCCATTTCCTTG
EST23669 1	101 A C	AATGTAAGCT CCAGAGGCAG	CCTTCCCCTOC TGTAAGC	TTTTTGGCTTGTCTGCAGAAATAGATGAAAAGAGAAAAATATACCCAGATACCTTTGCTCACTCTCCCA AGTGCACACTAGGCAATGTAAAGCTCCAGAGGCAG[A/C]GCTTACAGGAGGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG
EST23733 9	31 T G TT	GGCTGTTAGTT TTGTTTTGTTT	TGCACCTTTAAA TCCCATCAAT	AAAGGCTGTTAGTTTTGTTTTTCCCTT/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAGTCCAAGGCTAGAGAAAGATAGAGCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAATACCCACCTAAA
WI-17470	83 A G	GTCCCGTCCCG CCAG	CCAGTGACGAG GCGGA	CTGACACGTCCTGTGTGCGGGGTGTCATGTGGCGTGTGTGAGTGAGACTTTTTTACTGCGTCCG GTCCCGCCAGCCCTT/GJTGCGCTCGTCACTGGCCCTTGGTCACTTTTGTATTTCTGTCTGGTTGGAAA TACCATCAGCCTTCC
WI-17519	55 T C A	GTGTGCTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	TTTTTAACGAAATCTCACTACTGCAATGCAATGTTGTCTAGTAATGAATGCAIT/CJAGAGIATTG CCTGCAAAATAATAATTGAGATTCTATTTTAAAGAGCTTAGAACAGTACATGGTGCATAG
EST25356 3b	95 C G	---	---	TCCTTGATACAGGTAACCACTTTTGTAAACATTATTCAGAACTTCACTGTATCTTCAAGTTTTTAT CAGCATCTCTGTGGAGAAAGCAGTGTG[C/G]TATAATGTCAACATCAGGATTTCTTTTT
EST25356 3a	26 A C	---	---	TCCTTGATACAGGTAACCACTTTTGT[C/J]ACATTTATTCAGAACTTCACTGTATCTTCAAGTTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
WI-17581c	99 C T	---	---	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGAGAGATGGATCCAGCTTCATTCACACATT ACTACCAGTTATTGATAATGATAGAACCCAA[C/J]TAGGCGCAATTTACATTGACGCGTCATGC
WI-17581b	86 T C	ATTCAACATT ACTACCAGTT ATTGCGCT	CGTCAATGTAA ATTGCGCT	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCACACATT ACTACCAGTTATTGATAAT[C/J]GATAGAACCCAACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17596	86 A G C	ACTTCCCTGTG TAAACACTCC	CATTCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGGTAAATGGATAATAGCAGTCTCTCATCTCTGAAAGGTGGGAAGTAGGAGAGGCGCTACT TCCTTGTTGAACACTCCC[A/G]ATATTGTGCGATTCTAGCTATAAGAATGGGCCACTAAGTGGGTC



WI-17623	46 T C ---			---	TGTGGTTTTAAATTTCCCATATAATTAATGGTGGGCACATT[C/G]CATGTGCTTACTGGGTC ATTCATATATCTTTTGTGAAGCATCTGCTCCAAATCTTTTGCCTGACTTTGGAGTTTTTGGT
EST26419 1b	46 T C ---			---	ATTTTCATACAGATACAAAGGCAACTATGTGCAGCAACAATCTGAT[C/GGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTAAATGTCATGATGGCTGTTTCGAGGAGAAAGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26419 1a	35 C A AG	ATACAAAGGC AACTATGTGC		CAAGAAGTTTG GACTGCC	ATTTTCATACAGATACAAAGGCAACTATGTGCAG[C/A]ACAATCTGATGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTAAATGTCATGATGGCTGTTTCGAGGAGAAAGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26780 5	69 G C ---			---	TCAGCTTTAATTTAAGGGACATGTAATAAAAGATGCATTTGACAGGACAGCAGACTAGTTC AAGC AG[C/G]AGGTTAGACCAGTAACAACAACCAAGAAAGCAAGTGTCTCGTTTCCATCTTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39 A G ---			---	TACTTCAGTTTAAGGCAATTCACACAGAGACTGTCTC[A/G]GAGACGGGCACAGAACCCAGACAC GTAGAAACACCACCATGCATGACGGGGAAGCAGAG
EST27152 1	101 C T ---			---	CAAAGGATTTTATTTTGTCCCTAAAAAGTAAATCTAGAAAATAGCAACCCACTGCAAGAAGAGTT CTATACATAAACATTTCAATCAATCTCTCTCT[C/T]TCACATGGTGTACTCTTTTCATGTACACAT CATCGGAAACACAGACTGA
EST27504 0a	33 G A ATTT	GCACTTTGCAA CAATTTAATA		GCTGGTGTGAT GCTACTGTAAT G	TTTTTGCACTTTGCAACAATTTAATAATTTAT[C/G/A]CATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGTCTTTTCAGTATTCTGTACACATCTGTAAACAAGAACCCCATACATT GGTAAATTCATCT
EST27662 4	51 C T C	CACATTCTGTT CTCCAGTCTG		TTATGGAATG GCTTATGTAAC C	ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATCTGTCTCCAGTCTTG[C/T]AGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTCTTAGAGTAACACACACTCTTGTTTAGGAAIGTTC
EST27788 3	100 A G ---			---	ATTTTATTAGCGGTACAAATTCGAAGGTGGTAAGGGTGAAGGAAAGGCGAAGGCGAGGCAATACAT TATTGAGCTGAAAACAACATTTACATTTCAAGGAC[A/G]GCTTCCAGACAAGCCCATGTAGAACCAGCAT GCCTTGGGACTGTGTGGAT
EST27828 4	58 G A AGAACCCAC	GGAAGTCATC AGAACCCAC		GTGCAGAGAGG TACTCCAAGTA C	TCTTCTAAAACCTTCTCTGTTGGATCCCAGTGACGTGGAAGTCATCAGAACCCCA[C/G/A]GTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTTCTGCTCAGTCACAAATTTACTTGAA
WI-18369	58 G A ACAATC	AATAAATTC AATCTGTCAC		TCAAGAAGGCC TTATCCATT	TAAAAATTTGAGATACATTCCCCAATGTAAACAATAAATTTCAATCTGTACACAATC[G/A]AAATG GATAAGGCCCTCTTGACAAATTTCTGCCACCTCCGTTTAAACGATCAGAACTCAATCTTATCTC
EST28036 4	37 T C ---			---	TCCCGCTTCCAAAAGCTTTATTGGCAATATGCTCTAT[C/T]AAAAGAATGATCAATCTGTGCTCT AAGTCAATGGAATGAAGAGCTGTGCCAGGGACACACCACCGCTGCTGAAGGAGACTGCTGTTGTG TCCACCCTTATTCATAG



EST28483 7	31 T A	GGAGTAAAG GTGTTCTCT TAAA	TTTCTCGCATT TATTTTATAC CA	CATTTGGAGTAAAGGTGTTCTCTTTAAA[A/JATGGTATAAAAAATAAATGCGAGAAAAACATTAAAC GGAGAAATGTACAGACAACAGACAGACAGATGTTGTTCTGACTGTGACACATTGGTGAAA
WI-17724	50 T C	TGGGCTCTCC TGTC	TGGGTTGGCAG TGTC	AGAATTGGTCTAGTAATCGTTCCAGGATTTCCGGTGATGGGCCCTCCCTGTC[C/JGGACACTGCCAACCC CACAGCTGGAGGGGCACTTAAGGCACGTCATTTTGATTAGA
WI-17730b	68 T C	---	---	TGAGCCTGGGGAGAAAGACACAGAGAGTGAAGTGCTATTAGTTACATCATACCAAGGTGACATACTG TTC/JCACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA
WI-17730a	39 A C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGGAGAAAGACACAGAGAGTGAAGTGCTATT[J/C]GTTACATCATACCAAGGTGACATA CTGTTACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA
EST29041 5b	53 G A	GGAACAAACA CATTAAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTCATGAGGAACAAACACATTAAAGCATCTTGTCACT[G/A]GCTAACTCCT CAAAATCAACAATACCCCTTTATTTTAGCCATGAAAAAC
EST29128 4	58 A G	---	---	CTTTTAGAAGGACACACAGTCTTGTGGACTTAGGGCTACCCCTATTCCAGCAGGTGCC[A/G]TTATTT TCACCTGGTTACGTCGTGAAGGACCGTTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTCTGCTGGGACACT
EST29912 3	103 C T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATCTCTCTG T	ATTTATTAGGTATCTGCTGTTGGGGTGGGGTGGGAGATTGTTTGGAGACTGCAACACAGACACAAA AGCAAGAAGAAACAATTTCTGCCAGCTTACAGGCT[C/JACAGAAGAATGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	---	---	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATATTAAATCTTAAAGTTAACTCACCATGAAA TTTAAACCTTCTGTACTGGCTTCACTGATGAGGCAGTAAACTACATAGGGATAAA[G/C]AGCTCAGTA TCTGGAATCATGCTTCTCTG
EST30223 2	99 A G	---	---	AAATAAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATTTCTTGGAGTTACAAGCAA TCCAATTACACTCTAAGTTATTTTAATATCC[A/G]GGATTTAATTTCTCTCTAGTTCAATCTTGGGA GG
WI-16260b	86 G A	---	---	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAGAAAAAGACCCAGA GTTTCACAATATAGGTAGC[G/A]ATAACAGGTCCTCACTTTCCCTTCGGTGAGAACTTCGTGGGAC
WI-16260a	59 G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAACTCTG GGT	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAGAAAAAGACCCAGA AGAGTTTCAACAATATAGGTAGCGATAACCAAGGCTCACTTTCCCTTCGGTGAGAACTTCGTGGGAC
WI-17835	30 G A	ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATATTGTGCTTCTTCTG[A/G]GCTGTTTCTATACCCCAATATCATAGAAT GTTGTTGCTTCTATAATGTTGAGCTTCAATTTCTTTGCTTAAATCAATCAATGAATTACCTGAATT TTCTCCTCTGTTTCAAAA



EST31951 4	87	C T	GGGTTGTCAG CCAACA	CCACCAAAAT CACTCC	ACAGCCATTTATTATGTTTACTTGGTAATATCAGAGACTGAACATTTTCACTCTTTTAGCAATGACA TCGGGTGTCAGCCAAACA[C/T]GGAGGTGATTTTGGTGGGAATTCCTATACAAATTATTCT
EST31968 8b	95	T G	---	---	CGAATTTGCTCTCTTATTTTGTGATTCCTAGTAATCCTAAAGATTTGGGGGGCGGGTTACTATAAGT GCATTTTATAATGGGATTTTCTGCTT/GJAACCTGCCACTGATTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCCC
EST31968 8a	75	T C T	GCGGTTTACTA TAAGTGCATTT	TGTAAGAATCA GTGGGCAGTT	CGAATTTGCTCTCTTATTTTGTGATTCCTAGTAATCCTAAAGATTTGGGGGGCGGGTTACTATAAGT GCATTTT/GJATAATGGGATTTTCTGCTTAACCTGCCACTGATTTCTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCCC
EST32063 2	103	C T	---	---	TCCATGGATGAACAGACGCTACCATGCCACATCCCCACTTCCCTCCGACCAGATGCTGTTGGCCAGAGC TGGCTTCCCCTTCCAGACCTAGCTGGCTTTGTAGT[C/T]GTTTCAGGCCCATTTGAAATAGCAAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65	A G	---	---	AAGCTTTCAGGATTCAAAGGCATTTGGGTGTTGTCCTAAAGTTTCTGGTCACTGCAGCCCC[AG T]CTGTATTAGGGAGCACCCCAAGCCAGTAACAATATGGTCTTGAG
WI-17800	29	C G	GGGAGCACAA GAGAACTCA	TTTCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACT[C/G]AAGACTGGGATTAATTGTAGGAATATTTTCACAG TTTCCACAAGTCAGAAGAGCTAATCCCAACCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGAAATACCC
WI-17857	34	T G C	CCTAAAGTCTG GGATGACTTTC	TGGCTTAGGT TCTACTTGATG T	AAACTGTCAATTCCTAAAGTCTGGGATGACTTTCCT[G/ATTTCTACATCAAGTAGAACCTAAGCCAAAT TCAGAATCAGAATCCTTTTGTCCATCAAAATCCAGCTAACTCCAAAGCTGAATTAATGTTCAATCT
WI-17860	121	T A	TTTCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	GTATCTGATGTAGTTAACCATGGCTGTGATGATTAATTGCTATAAGGAAGGGAAACAAAATCTTTA TAGTGTCCAAAGATAAATTAAATCTTGGTTTAAATCTTTGCCAGCAAAAGCAAAATAT[A]CCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17866	43	A T	TTTATAGCCT ACTTCTCAA	CCGTTGTCAC AATCACACAA A	CAGCAACCTTTTTTTTATAGCCTACTTCTCAAAATTTGTT[A/T]TTTGTGTTAGTGACAACG GGGGAATCTACAATGCTCACATCACAGTAACTACCA
EST33301 4c	80	G A	---	---	GAAAAAAAAGTCAAAATGTTCCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCATGATC AATCGCCACGAGA[G/A]ACTGGATGCCAAAAGAGTATGG
EST33301 4b	63	G A	---	---	GAAAAAAAAGTCAAAATGTTCCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCAT[G/A] ATCAATCGCCACGAGAGACTGGATGCCAAAAGAGTATGG
EST33460 1	44	G A CA	AGCGTGGTTTT CAATACTAAA	CTGTATTTATT GTTAAATATTT GCATTGTT	CTATCCAAAGATATTTATTGCAGGTGGTTTTCAATACTAAACA[G/A]GTGTAACAATGCAAAATATT TAACAATAAATACAGTGATTAATAAGCCATGGCATATCCAGTTGATGTAATACTTTTGCAA



WI-17904	50	A G A C A C	AAAGCATGAC AATAAAATGA	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAATGAACAC[A/G]TACGGGAATTAC TATTAAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACAAACACAAACAAATGA
EST34149 5			TGCCAAATAC TCAAGTGTGA	AACACTAGCG AGAACAACTA ATAAAATC	GTTTTCTTTGAGTGACACAAGCTTGTTCAATTTTGAGAAATGTGTGCCAAATACTCAAGTGTGAA T[A/G]GATTTTATTAGTTGTTCTCGCTAGTAGTTTGGTATTCTATGAAAAAAGCAGCTAGTTCAGC TTACAAATCACACAAGT
EST34343 8	95	C A ---		---	TGGGAAAACATAAGTTAACTCAAGAATATATCCAGTCTTTATGTTACTAAACATTTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCT[C/A]TACAAAGATTAAAGAACTTACCATCAAAACACTTC CAGTGCATCAA
WI-17982	98	C T C C T A A A A G C	GGACCATATG ATATATACT	CAGAAATTATG TGATAATACT CCTTCC	GGTACACAATTTTAAATGGAAGGAACACACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATACTCTTAAAGC[C/T]GGAAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAAGTTTTCATCA
WI-17993	118	A C ---		---	CTCAGTAACTCCGGTGTATAATCTGCCATTTATTGATTTATGATAAAACACCTCTCATTGTGA AAAACAGCTAAGGGTGACATCTCCAGACCCCAACACTGCCCCGTAAATGT[A/C]CTGCTGAGAGTCC ACATTTTGGAAATCCAAT
WI-17996	84	A G A G G G A A C A G	GTAGAGCGA AGGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCAGTGTGATGGTGAAGCAGCATGAAAACACATCTCCCAGGCCTCGCAGT AGAGCGGAAGGGAACAG[A/G]GCTGCCCATGTGCCCTGCTCTAAAGACGCCACCCCTCAGGTTGATGT CACCTGTGGGAGACCGGGT
WI-17136	33	C G ---		---	ATTCTTTATAAAACACCATGTGCCCTAAATGT[C/G]ATTCAACATATATGCACACCTTCGATGAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCCT
WI-18041	24	A C ---		---	GCCACTGAAAAAGGTGCTCTTCC[A/C]GTTTCTAACTCCCTGGACTCCCTCATTTGGAACCTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATACTTAATCA
EST35164 8a	57	A G C C C C	CACAGCCCTGC C C C C	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTCAAGCACAGCCCTGCCCC[C/A/G]TCTTGA GATTCAGAAATCCAGAGGGTGCTCAGTCCCTGGTTAGGTGCTTCTGTGACATTTCTCTTTG
WI-18052b	67	A G ---		---	AGCGAATGAAATGCTACATAGGCTCCCTGAGTCTTTTATGACGAATCTTGGTTACACATCTTAG[ A/G]ACAGCAGAGCTGCCCTGAGGGAGGGTGTGTTTAAATGCTGATGCATGCTCAGCACAGTGTCTGGC ATGGCCCATCCATGCTTT
WI-18052a	50	T C A T C	CCTGAGTCTTT TCATGTACGA	CTCAGGCAGCT CTGCTGT	AGCGAATGAAATGCTACATAGGCTCCCTGAGTCTTTTATGACGAATCTTCTGTTACACATCTT AGAACAGCAGAGCTGCCCTGAGGGAGGGTGTGTTTAAATGCTGATGCATGCTCAGCACAGTGTCTGGC ATGGCCCATCCATGCTTT
WI-18054	46	G A G A G T A A A A A	GGGAGTGGG G A G T A A A A A	CGTCAACCTGC TTCCA	CTGTTGTGCTGAGAACAGAAAGGGGTCAAGGGAGTGGGGAGTAAA[A/G]TGGAAAGCAGGGTGACG CATGCAGGAGTCCAGACAAAAGACGGGTGATTTGCTCAGGTTGGTAGCAACAGAGGTAATG



WI-18064	54 G A A G A	GTAGCTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAAACCCCTGTGGGTAGCTGCTAAGCTGTATTTTCAGA[G/A]GAATGTCAC AATCATACCACTGGGGAGAAAGAGTAAGCACAGTGCITATTAGGTGCCAAACTGGGGTACCTGGGAG GCAGAAA
EST35347 2	97 T C A A	GCATAAAATT TTCCAGTTGGT	CCCTCGGCACC TGCT	TTTAGCACCATCTTAGTGGAGCAGGATCTTGATCATGGGGTGAATTTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAGT[C/J]AGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28 A C G T G T A T	AACCCACTAC TTACTCAGAGT	AAACTAATA AGAACTGGA GGTTTT	AAACCCACTACTTACTCAGAGTGTGTAT[A/C]ATATTAAACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGATATTTCTGTACTCAGAGCATTTTAGGTGCAAGGATATAA
WI-18080c	80 C T ---	---	---	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTTTTGTAAATTAATAATCTACTATGCCGTG TTTGACTTTTAT[C/T]CTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080b	65 G A ---	---	---	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCT[C/T]CTTGTAAATTAATAATCTACTATGCC[G/ A]TGTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080a	41 T C A G T C T C	GCAATATCA ATATCAAACT AGTCTCTC	CAATTTACATA AGAGATAAAA GTCAACA	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCT[C/T]CTTGTAAATTAATAATCTACTATGC CGTGTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT GTGGCATCCTATAAAGCAGCCATGTGTGAAACAAATGATATGCACAGAAAGCATACTTCT[G/A] TGGCTTTGTACACGGTTTCTTTCAAGAGGAAGATGACTCAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGTGTTGAA
WI-18086	63 G A ---	---	---	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAAGCCCTTAGTGTAACCTTTGGTATTCCC TTC[C/T]TTTGGTATGAAAGACAGACAGCCCTCTGCTGGAGGACTCATTAACAATGTAAGAAAGGGGTGAG TCAGT
WI-18115b	71 C T ---	---	---	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAAGCCCTTAGTGTAACCTTTGGTATTCCC TT[C/T]CTTTGGTATGAAAGACAGACACCTCTGCTGGAGGACTCATTAACAATGTAAGAAAGGGGTGAG TCAGT
WI-18115a	70 C T T T	TTAGGTACCT TTGGTATTCCC T T	AGAGGTCTGTC TTTCATACCAA A	TTTTGAGAAAGCACTCTGTAAAGCAAGGATGCATTCAAAAATGGCTTTGAGGATTAATCTTCTCTTTA GGTAAATTTGC[A/G]TAAGAACATAAAAGCATTTTAAAGTCCACTGCCGCTTAGAACT
WI-18136	78 A G ---	---	---	GGCAAAATATTTTACATCACACCTGGAATCTGCCCAAGTCTTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTTATCCAAGCAGCCATCTTTCCGGAAGCTC[A/G]TGGAGCACAAGCAGA ACTCGTGGGTAGAGTGA
WI-18169	115 A G G A G C T C	CCATCTTCCG G G A G C T C	GAGTTCTGCTT GTGCTCCA	TGAAAGAAGTCGACACAGCGGACACT[G/A]TCATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGACAAAATCAAGATGAGCTGGAGACATTAATCCTGGCGA
WI-18190b	26 G A ---	---	---	



WI-18190	62 G A	---	---	TGAAAGAAGTCGACACAGCGGACACTGTCATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGACATTAATCCTGGCGA
WI-18181	100 A C	CAGATC	CGTTTACCAT TTGTTAAGCTT TTG	GACAGTGAACACATTGAAACACACAAATACAAACAACTAGGAACAAGAAATGTGTAAATCCAA TGTGTGAAAAATATATACAAACACTCCCTTCAGATC[A/C]CAAAAAGCTTAACAAATGGTAAACGTA TGTGTTCTTGAAC
WI-18215	78 G A	CTGCCCTC	AGCAGAGTTC CCTCCCTCTCT CCCC	ATTTCATCAAGCATTTCTGAGTACAAACTAGGGGACAGGTATTTACAAAAACAAATAGAGCAGA GTTCTGCCCT[G/A]GTGTGGGGGGAGAGAGGGAGGATTGAGCATTTGGTGGAGTATGTTAATT CCCTCAAGTTAATTCCTC
WI-18232	60 T A A	TGGTGTGATT GTGATACACTT	AAATAAAGGT TTTCAGGGGT C	CATTTCCGAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAGT[A/GAA CCCCTGAAACCTTTATTTTGAATTTGAAGTTTTGCTCAGAAACTGGGCAGAACTTTTCACATTCTG AC
WI-17892	76 T C A C A	GGAAACTTG AGTTTGAGATC	CACAGAAGTG AATAGACTAGT GAGACA	TTTAAAAATGCTTAGATTTTCCTCAGTATTTTATCAATAGTGTGTAAGCTGGAACCTTGAGTTTGAG ATCACATAT[C/T]GTCTCAGTAGTCTATTACCTCTGTGGCATTTTCGGCAGAAGTGGC
WI-18242	30 G A	AATCGTAACA	GCTAACACTTC TACTGTAAACAG CTTTC	AATATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTGAAGTGTGACAAAAAT TGGATGCCACAACTTATCTCACCATTCTTCAAGCAAGTGAAGGTCAGAAATGTTCTTGCCTATATC TGCAAAAGATCGAACAAG
WI-18266c	119 C T	---	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124 T C	---	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97 C T	TTTGTGCA	TTTCATGCATCA TTTGTGCA	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73 A G A	GGAGAAAAGG GAGCAGAAGA	GGAGAAAAGG GAGCAGAAGA	CTGAGCCTCTGGATATGTGGTTAGTGTCTATCATTAATTTGGAAAGCTGCAGCTATTGTTATTC AAAT[A/G]TATCTCTGCTCCCTTTCTCCTTTCTGGGATTCTCATTTCTGCATGTGTTATA
WI-18330b	66 A G	---	---	AAACATCTACAGCTGTCTTAGGCCATCTGTGAAGAAATCAGGGATAAGAGCTGAGGAACAAGAGGG[ A/G]TATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAAATAAGAACATAATTTTTTGTGAT TCACA



WI-18330a	49	G A A A G A	TCCTGTAAGA AATCAGGGAT	AGTCTGACTC ACTGCCTACA	AAACATCTACAGCTGTCTTAGGCCATCCTGTGAAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAATAAAGAACATAATTTTTTTTGTGAT TCACA
EST37564 5	85	T C I A G A	AAATTCAAGC CATCTACAAA	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGGCTGGAATTCGCTGTTAGAATACTGCATGTTATTTAAGCTAAAAATTC AAGCCATCTACAAAAGATTC/JCTCTATTGAGGCCCTCCATAGGCTGCAACACATCAAAAGGCATTAC TGTAAGTGGAGAGGACTGAG
WI-18327	104	G A T T	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAGGGATTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGGCAGTTTCCCAAAGCAGTACCTC CCAAACAATGGTGAACACAGCTTTGTTAGGCTAGTT[G/A]GCTGAGGCCATTGTATGGGGAGGCAGA GT
EST37624 6b	102	G A ---		---	GTGGCAAGAGCAGCTAAACACACACTCAITTTGCATGAATCCAAATACGAACAGTGCACGCTGATGG CCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACG[G/A]TTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
EST37624 6a	58	C T ---		---	GTGGCAAGAGCAGCTAAACACACACTCAITTTGCATGAATCCAAATACGAACAGTGCACGCTGATGA TGGCCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACGTTTACATCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
WI-18357	89	C G G C A T C A A	CCAGCCCTTA GCATCAA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAGTCTACCGTGCTGAGTGGCCATGAAGCCAGCCCATGGAGAGACATTTTCAGA TAATCCAGCCCTTAGCATCA[G/G]TCATCTCAGTCTTTGAGTCTTCCAGCCAGGTCCTCAAGCTT GTGGACCAGAGACAAGCC
WI-18012g	117	A G ---		---	TTTTATCTGGTCAAGTCTCTTAATGGCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTTGGAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCG/GA/GGTGTTTCTCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113	G A ---		---	TTTTATCTGGTCAAGTCTCTTAATGGCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTTGGAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCG/GA/GGTGTTTCTCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	C T C C C T	GCCACTTTTGC CCCTT	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGTCAAGTCTCTTAATGGCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTTGGAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCG/GA/GGTGTTTCTCTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46	T C ---		---	TTTTATCTGGTCAAGTCTCTTAATGGCTGAAGGTCATCTCCTTTCAACTTTCCAGACTTTGGA AGATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCG/GA/GGTGTTTCTCTGATACA GCTGACGTTTCGAGGG
EST38390 4	75	A G C T C T G C A T T G	GCAAAAAGGA CTGATTAATAA	GCTAAAGTCAG CTGATTAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGTAATCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCATTG[G/A]TTAAGTTTATTATCACTGACTTTAGCATTTGGGAGATTATCTGGAT



EST38512 7	91 T G	TGACGATGCC AATACTTCG	CACTGCACTCT GGGAAGC	TAATAAAAACCTGACCCAAATTGGTAAACCTGTGTCTGGACTGAGAGAGAAACAATGAAAAATCTGTAAAT ACCTGATGACGATGCCAATACTTCGT/GJGCTTCCAGAGTGCAGTGAATAACTGTTATAGCC
EST38519 0	24 C T T	CCTGCACTCC TAAAAGATCT	TCTGTTAGGAC TTGGGGGA	CCTGCACTCCCTAAAGATCTTTTC/TJTCCTCCCAAGTCTAACAGAAATGGTATATCTCTCTGGAAAA AGATGAACGTATCAATGAGATTGCTGCTCTGCTTCAGCTTTGATTTTTTTGCTTGGAGAACCTTG TCTCCCTGCTGATTT
EST38575 1	66 T C A A	GAACATCCCA TGTTTCTGTTT	AGGGAAGGTA GTATAACACAT AAGAGA	AGTGGTCAAAATGTAACAACTAATGGGGACACCAAGCCTCAGGAAGAACAATCCCATGTTTCTGTTTAA T/CJCTCTTATGTTATACCTACCTTCCCTTCTCTTCTTATACACATAGATTTTCCTTAATTGCAGC CCA
EST38616 9	101 C G C T T C	CCTGCTCCGCC CTTC	GAGGAATGGAT GGTGGC	CCATCTAGGCAGGCTACCTGAGCTCTGTGCTCCAGAGTGGTGGCTCACGCCCGGGGCCCGCTGG AGTCTCGCGGGCCCCGCCCTGCTCCGCCCTTC/CJGJGCAACCATCCATTCCTCCAGGGG
EST38652 8	59 T C C A T T T C A A	TCTGAACCTGGG CATTTCAA	TTGCAAAAATG AAGGAAAAA	TATAGTAGGTACTTTCCCTGCTGCAGCAGGAATATTATTCAGTCTGAAGTGGGCATTTCAA/T/CJGCGTG GTATTTTTTCTTTCATTTTGTGCAAGTAAAAAATCAT
EST38654 5	42 T C G T T T T A C A	AATGGTCATTT TAATATATCA	CAGTGATGGTC CTTAATCTTCT ATC	CTCAAGCTGAGAAATGGTCATTTTAAATATATCAGTTTTACATA/T/CJAGATAGAAGATTAAAGACCAT CACTGAGGTACATAGCTCAGAGGCAGAGTTAAGATTTGGACCCAGGCAGGTTGGTTCCAGCATATA GGATCCTCACTCACCTGGGACAGCCTGAGAGGGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTTCCCC/JGJAGGCCAGCGGGATGTGTGCCCTCCTCCTCCCAACTCATCTTTCAGGAACACGAGG ATTCTTGCTTTCTGGAAA
EST38759 2	86 A G G G T A T G G	TGCTCCCTGA GGTGATGG	TCACCATCGTG GACTTAAGG	TGACCTTGATTTCTCACTAGAGGGGAGAAATCACTACCTACCTTTTGGATGCCCTCCCACTCTACTTGT CTCCCTGAGGTGATATGG/JGJCTTAAGTCCACGATGGTGACCTAACTCAGTTTAAAAATTTCTTGCC TAGCAGCACC
EST38775 1	40 T A C	AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATTCAAA	GACTCTCAACCAAGAGAAAAATCAATAGGAGAGGATTGGCT/JAJTTGAATTCAGAGCAAAAGCCCT CTTACTGAGAGGTGAGCCCCAGCCCCCTCCAAATGCCCTTTTCATGAGTTAGGATCTCCTAAGTGGTAC AAACAAACCAACATGGTGG
EST38815 4	91 C A C A	TGTTATGAGA ACCCATTACA	GCTGACTGGCA CATGCTTT	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTTCACTTATGTGTTCATTCAACAAG TGTTTATGAGAACCCATTACACA/CJAJAAGCATGTGCCAGTCAGCAGATTCTGTAATAA
EST38858 4	98 C T T G A C	CACGAGTAAA AAGAACTCA	GGAGCGAGTCC AAGGAGAA	TCCTTACTGTGCTTACAACCTTCTCCCAAGTTTGGGGTGTTCATATGTTATGTTATGTTATTATTA TTCAACACGAGTAAAAAGAACTCATGAC/CJ/TJTTCTCCTTGGACTCGCTCCTCTCCCCCAATCTCGAT ACCGACTGCACTGTTG
EST38865 2	72 T C T G T G C G A T G C	GCTGTAGAATT TGAC	GGAGGACGG AGGACACAG	CCTTAATGGATTTACAGCTCATCTGAGTCTCTGCTGTGTTCTCTGAGGAGCTGTAGAAATTTGTGTCG ATGC/T/CJCTGTGCTCTCCGTCCTCCCCAAATGAGCACATATGCAGGGCAGGCAAGAGCATGCTGGGA TTTGTCTTAGTTGTTAA



EST38878 9	47 T	AAACATCATT ACTAGCCTAG C ATCCCTAA	CCTCAATAAA TCTCATGTCT CA	CCAATGAGAACCAAGTAATTAAACATCATTACTAGCCTAGATCCTAAAT/CJTGAGGACATGAGATT ATTGAAGGGAAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAAACATTTCCC TTATCAATGTCTATCTCACACATCTTTATTTTATTTTATTTTACCTTTCTCAAAATATCGGATTGTTC TCATGAGAATAATGGCTGAGGGAGCTGGCAGCGCAGTCTCTCA[G/C]GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G	...	...	TTATCAATGTCTATCTCACACATCTTTATTTTATTTTATTTTATTTTACCTTTCTCAAAATATCGGATTGT TGCTCATGAGAATAATGGCTGAGGGAGCTGGCAGCGCAGTCTTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T	TGTCATCTCAC ACATTTCTTTAT TTTT	CGATATTTGAG AAAGTGAAAA CAA	
EST38909 5	47 A	GCACAGCATG GCTAAACG	GGTATTTGTG ATTCCTCATCTT T	GCACTAACTAACTTTTCTTTGTGGATTGCACAGCATGGCTAAACG[A/G]TAAAGATGGGAATCAA CAAATACCATTGAAGATATGGAGCAAGAGAACTCTCACATACTGCTGGAGGGAATATAAAT
EST38911 9	85 A	GTTGAGGGAA ACTTATAACCT CAC	TGTTGTTTGT GAAACAAGCG	AACTGAATGGCAGTGAACACACTACACATCAAACTTAGGGAATGTGGTTAGTGTGACGTTGAG GGAACTTATAACCTCAC[A/G]GCTTTGTTTACAAAAACACAGCAGACAAACAGAGATTTTCCAACTC CAGCAATGACAGGCTAGGG
EST38955 5	30 G	TGAATCCCTT GGTGG	CACTGCAATCT CACCCC	TAAACATCCCATTTGAATCCCTTTGGTGG[G/C]GGGGGGGGTGGATTGCAGTGTCTCAAGATAAA TATCACAATAATATCAAAACTTCAAAATGCTATGCACTTACACACTGACATGAGCCACAAACAT CCTTTCACAGGGACTGTAC
EST39002 0	42 G	GGACCCCTTCGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCCTGGGAGATCCCGGACCCCTTCGGTGACC[G/A]CAGGCTCCCTGCCAGGGCTTGG CCCTGACCCGGGCTCCCGAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39004 8	79 T	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG CGG	CACGTGGCCCTAAGTTTCCGGTCTTCTCAGTCTGGATGGCTGTGGAAAAAGCTTGGTGGTAAG GCCTAAGGAATTT/GJAGGGGCAGGGGGCGATGCCGCCAGCCGAGATGGTCTCTGTAAGCCTGTGGGTC AAAGACCTAACCTTCTGGA
WI-16398	90 T	TCCCTATTATT CCATGATATTT TCA	GAATGGTTGT GAAAAATATA TTGATAT	AAAGATAATGTCTATCACAACGCAACATATAGAAACATAAAAGAAAAATAAGTATCCACCCCTAAAAAT CCCTATTATTCATGATATTTTCA[T/C]AGCAACTAGTATATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16403	69 T	CCTTGCTCTC AATTTTAAAC TACT	TAAGGGCTAAT TCCCTATATAA AAAG	GGTGTCTTTCATGATTTTCTCATTTCTCATTCCTATCAGGTTTCTGGTCCCTTTGTCTCTCAATTTTAACTT T/C]CTTTTATATAGGAATTAGCCCTTAACTGTGGTACATGCTGCCAAAAATTTCTCTCCAGTT
WI-16406	24 C	GCTTAAATGGC TACAGAAAGA AGG	CCAGAACCAG ATGTGTTTAAAA AA	GCCTTAATGGCTACAGAAAGAGG[C/T]GGTTTATTTTCTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATTATGCATTTAGAGCAATAGGTGCCCTGAA



EST39236 0b	57 C G	TCATCTGAGA ATAAACCTTCCT GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTCATGATTGTTTCATCTGAGAAATAAACCTTCCTGTCTAAATTTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAATATATTACCTGGCAAATGAATGAGGTGTCTC TTT
EST39294 4	63 G T	CCTGAAACAG GGAIGCC	GCACAATTAA ACATAGTACCG AGAA	CAACAGACCTTTGGTTTGGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATTGC[G/T] TTCTCGGTACTATGTTTAAATTGTGCTGAGCCAGCAACCTCGAGTTACCGGGCTTTTACCCCAAGGCC AGCTCTGCTGTGTCAT
EST39366 2	72 T C	---	---	AGAAACATCTGTCTGATCAGAGGAAGATGTATGTAGAAAAATCAGAAATCTGACTGAATTCCTAAA ATCTATT[C/J]ACACTGAGAGGAAAATGGAAGAAAATGTTTGCATAAAGCTTTTCCCTGACTCTCA GAGGGTTTCA
EST39371 9	86 A G	CATTGGATTA GCGTGAGAGG TT	TGATTTGAGAC ATTTACATTT TT	AAAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTATGTGTGTAATTTCCAGTTGAGCATTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAAATGTCTCAAATCAAATGCTTCTCTCTAAAGATTA GACATTGCCCAACCTGC
WI-17177	23 A G	---	---	ACAAAGTACATATCCAAACCAACC[A/G]TCCATCCCCACCTGTGCCCTATTCTTCCCTTGTTCTTT AGAGCCTTTTCAGCTATTTCTGTGAAGCAAACCTGCACGAAGGCTCCCCGTACTCCTCCCTGGAA G
EST39428 8	31 C T	GCTOCCACA ATTTTGATT	GGTCCCTTATG AAGCCACC	AGGTTCTGGTTGCTCCCCACAATTTGATT[C/T]GGTGGCTTCATAAGGGACCCAGGATTCTGCATT TTCTGGTGGGCTAGGTAATTTCTGTGCCCTTTGGTCCACAGAGCAATTAAGAAAGATCAGGTCT GGCTGTTC
EST39430 2	45 A C	GGCAGAGGAA TAACTGATGTT	CAGGGTGCGGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTT[C/A/C]CAATACCCGACCCCTGA CCAGTACCTTTTCCCTCAGGCCAGGCTCCGGTGAGGATGTCCTGGG
EST39446 7b	117 C T	CTACTGACAT AGGGACTTCA GAGTAA	TCCTGGAAAAAC TGACATAAACCC	AAAGCCCTGTAAACTGAAGCTAGACAACGTCACACTTTGGAAGAAAAATAACAGGAACCTATTATAT ACGTAATCACCTTTCATACCTGCCTACTGACATAGGGACTTCAGAGTAAAT[C/T]GGTTTATGTCACT TTCCAGGATTGTTCTCCC
EST39465 2	80 A G	AATGCAGGAG GGTGGC	CAATCTCGGCC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAAAATAACATAAACGAACTGAACAGAAA TGCAGGAGGGTGG[C/A/G]AGAGGGCCGAGATTGGGTGTTTCAGGGCAGAGAGGTGGAAGACCAG
EST39501 0	81 A G	AAAGATTCTCT GTAGACATCT AACATTAG	CAC TTGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTTCAGACATTTTGACCAGCCTAAAGATTCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAITGCAAGTGAAGTTCAAGTCAAAACCAATTC
WI-18387b	84 A C	---	---	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACATTTGTGGTCA CATGCTTTAGCCATAC[C/A/C]CATGGTAAACATTGACTATGGAGTCTTGTGAAAGTGAATGTGCGGATG GCTATGTAGACATAAGA



WI-18387a	57 A G	CCTTACTTTGG	GCTAAAGCATG	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATAC/A/GJTTTGTG
EST40601	78 A G	GCCTGGAACCT	AGGGCGTC	GTCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGCTTTGTGAAAGTGTATGTGCGGATG
		AGTGTATCAC	ATCTTCAGGAT	GCTATGTAGACATAAAGA
EST41935	32 A G	AGGT	CACTGTGA	TCCAGGATGTTTATCCAAAGCTGTGGACGGTGAACATTAAAGACGAAAGAGTGACTCGCGTGGA
		CATTCTGGCT	AAAACGTGATT	ACCTGAAACAC/A/GJAGCGCTTCTTCCAAAGGGCTGTGGCATCAGGCCACTCAAGG
EST43091	28 C T	TTATTTTGGGA	GTAAACATG	TCCATTCAAGTGTATCACATCTTCAGGATAGGT/A/GJATAACAGTGTGAAGGGTGTGCTCATTTTCTTC
WI-18420c	108 T C	TTCCATTAAAC	AAATTCTCAGC	AGCTGTGAGTAGAGGAGTCTTCCCGAGAGTAGCAGTTGTTGA
		AGGAAGTTTC	ATTGCTATAAG	ATGTCATTCTGGCTTTATTTTGGACA/CJTGTAGCATGTTTTTAAACAAATCAGTTTTTTCATAGGCAA
WI-18420a	38 C T	GAATAAGGGA	CCAAGATTTGC	CCTTTGAAACATCAAAAGAAATACAATATATTTTACAAAATTTCTCATCACIGTAAATCA
		AAATGGGAAG	TTTAATTTTCA	AGAGAGACAACAAGAAAGAAATAGGGAAGAAATGGGAAGAAACAGAGTGAATTAAGCAAAATCTT
		AA	TC	TTGAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA
WI-18425b	101 T C	---	---	TTTCATAGGTACTTCATGGGA
		CACCTGTCT	AGACAGATTTC	AGAGAGACAACAAGAAAGAAATAGGGAAGAAATGGGAAGAA/CJTAGAGTGAATTAAGCAAAATCTT
WI-18425	81 A C	AGACAGATTTC	TGTGTGCA	GGATTTCAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA
		CTTTTGGCTCT	CTCCCTGACT	TTTCATAGGTACTTCATGGGA
WI-18449	129 C T	AAGTGGGACT	GTATCCAGA	AGCTGATCAGCTGCTGTTACTGTTTATGTGTGGCCAGGGAAGCCAAAAGATCAGACACCCCTGTC
		---	---	CTAGACAGATTTC/A/CJTGACACAACAACAGGAGGTGGGGTCAACGGGGGAGAGCCAAAGAC
WI-18457	120 T C	---	---	TAGGGC
		CCACAATGGC	TTTAGGCTTTG	AAATTGAGGTCCGGGTGGAACATAAAAAAGGAAAGGAAGAGAAAGTAATCAAGGGAGGCCAAAGTG
WI-18462	39 A G	AGAGGTGA	AGATGGTTTCT	GGAAGCTGTATTGCTGATCTAACGTGCTGTTCCAGTCTCTTTTGGCTCTAAGTGGGACTA/CJ/TTC
		GGTGGGGTGC	GCACGATGGGA	TGGATACAGTCAGGGGAG
WI-18476	60 C T	GAGG	GTGACC	ATCGTTCATTGAAGCTGTAAATTTCTCAGTCAACTGTGCCCCCAAGACATTTATTTTATCTT
		---	---	AAATGTCCAATATCTGCTGATGCTGTGTTTGTGCACATGGGGGCCACAGT/CJ/AAATAGGCTAAA
		---	---	AGGAGTCCCACTGCT
		CCACAATGGC	TTTAGGCTTTG	GGTGCTATAGCTGCTGTACACCACATGGCAGAGTGA/A/GJTAGAAACCATCTCAAGCCTAAAA
		AGAGGTGA	AGATGGTTTCT	TATTTACCATACATCCCTCACAGCAAAAGTTTGCTAATCTCGGGTTTAGGACTCCATTGAG
		GGTGGGGTGC	GCACGATGGGA	TGAGGAGGTGTGACAAGCTCCAGCAGGGGTGGGGCCGGGCTGAGGGTGGGGTGGGAGG[CJ]TGGT
		GAGG	GTGACC	CACCTCCCATCGTGGCCCTGGCCGCTCCCTCCACTCACCCACACCTGGCCAGTCCACGTTGAGGT



WI-18491	109	G A	AACAAATGGT AGGTGGTATT	CGTGTGCATTT TCCTGTAATCC	CTAATGAGATGAATACATGGAAGGCGTTAGCACAGTGCCTAAACACAGTAAGTAACCAACAAAT GGTAGGTGGTATTAACTACTATTATTAAATCCAGAAATGAC[G/A]GGATTACAAGAAATGCACA GGT
EST50757 b	79	C T	GAGCTCGAGG CTGCTTCT	ACCCTTCACCC GCCC	AGCCCCCTCCACTCTGCTTCACAAAGTCGGCTCCGAGAGCTCGAGGCTGCTCTCTTTTATAT GTGCAGGGCC[C/T]GGCGGGTGAAGGTCAGAGA
WI-17675	103	T C	GGACATTTGG ATGGTGACTT	GGGGAACCAAC CAGG	GATCTTGGAAAGCACTAGAACTAAACATCTTCACCAGGTGCTGAAGAAAAGTGTCTCGTTTTAAT TGCCAAAGCAGGGATGTGGACATTTGGATGGTGACTT[C/C]CCTGGGTGGTTCCCCATAGATTCAACCAT TGCTCTAATGGTGCTA
WI-16543	67	G T	AGATAAACTA CATTTGGGTTT	GATTCATCATT ACAGGGGACTT	GATCCATTACCTAGGGTAAATTTCTCTGAATGTCAAAACAGAGATAAACTACATTTGGGTTTTGG[ G/T]AAGTCCCTGTATGATGAATCAAGATCTCTAAGTCTGCTTGCCACCCATTTAATACGTATT TTTGTTAAGGCTGAAGTT
WI-17687	107	C G	GCCAAAAAGG TTGGGGAA	TTACTTTTGT CCGACCAACA	ATCTGAGATGGAAGAGTTTCATCCCAAAACCATCTCCCTGACCCAGTCCCATGGAATAATTGTC TTCCACAAAACCGGTCCTGGTGCCAAAAAGGTTGGGAA[C/G]TGCTGGTCGGTACAAAAAGTAATT G
WI-17690b	79	A G	---	---	ACAAATGTGAAAGAAGATATGTTGCTTTACTCACAGTGAGGCAATTTTCTAGCTGTGTTGATTT GGCTTCCCTAT[AG]GATTCAGGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG
WI-17690a	63	G A	AGGCATTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAAGAAGATATGTTGCTTTACTCACAGTGAGGCAATTTTCTAGCTGTGTTGATTT ACAACATGTGAAAGAAGATATGTTGCTTTACTCACAGTGAGGCAATTTTCTAGCTGTGTTGATTT[G/A] TTTGGCTTCCCTATAGATTCAGGACCCATAACTCTTGTTCTCACTCATCTGCTATGCTGCTG
EST51717 b	128	C T	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAAATCTCAGTGTCTAACTCATCTCCAGATTATTTCTGAAGTGGAACCCACCCCTCCGACCCAA TGGCAACATCACCCACTACCTGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGTT[C/T]GAG CTGGATTATTGCCTCAAA
EST51717 a	39	C T	---	---	GATCCAAATCTCAGTGTCTAACTCATCTCCAGATTATTTCTGAAGTGGAACCCACCCCTCCGACCC CAATGGCAACATCACCCACTACCTGTTTCTGGGAGAGGCGGGAAGACAGTGAGCTGTTGCGAG CTGGATTATTGCCTCAAA
EST53012	97	C T	TGGTCACTTTG GGGOC	GGCTCTGCCCA GGC	TTTCCAGGTTGACAGGTTTTATCCACCCCTTCCATCCCATGGCCACCCAGGAGGAGGAGACAG GTGTGCTGGAGTCTGTCATTTGGGGCC[C/T]GGCGTGGGAGAGCCCACTGGGTTTACATCTCTGT GGCAGGTTGGACAC
EST53349	96	A G	TGTTGAAAGC AGTCACAATG GTAC	CATCTGGATAT CTTGTCACATT TT	AAACTGCAATAACAAAAACAGAAAGTCCAAGAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCACAATGTAC[AG]AAATGTGACAAGATATCCAGATGTTTAA
EST53389	74	A G	GGAGACCTGC AGAACTTAAA CA	GGCCTTCTAA CAATAAATGCT C	TTTCGAAATGCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTGCGAAGACT TAAACAC[AG]GAGCATTTATTGTTAGAAAGGGAAGTCTTACACTCAATAGGTTTTAACAATGAAC ACATTAAGGGAGATGGCC







[illegible]



TIGR- A003P30	117	C G ---			ACAAAGTTCAAAAGGAGAACTTCCTTTGTTTAAATGCAGCTGTGCTCAGAAGCCTGTGATTTCTCTAGGA AACCATCTGGGTTTAGCCCATTAGAAAAATGCAGTTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TIGR- A004S34	156	C T A			GCCTTGTCTTTTATGTTTAGGTTGGGGGAAAGGAGGGGCTGACAACCCGACAGACATCTGGACACCAGC AAGGGTCACAGGGGAGGTTGCAGAACTTCTTTGCTCTGGCTAACAGTCTGTCATGTGACAAATAGCCA AACCTCCTCATCTCTATAAA[C/T]CTTAACAAAAACAGTTAGCTGTTTACAAAAACAGTTAGCTGTT TACATG
TIGR- A004T44b	97	A C ---			AACAACAGTGTAACTCTTTAACAGGGGATGTTAAAGGTAAGAGTCAGGAAGATAAACCAAAATGAT TGAGTATGATAAAGAAATTTTGCATGGCGATT[C/A]AAATAGAAAACTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004T44a	69	G A TGA			AACAACAGTGTAACTCTTTAACAGGGGATGTTAAAGGTAAGAGTCAGGAAGATAAACCAAAATGAT TGA[G/A]TATGATAAAGAAATTTTGCATGGCGATTAAATAGAAAACTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAGAAACAATATGACTTAGCAAGAAACAATATAG
TIGR- A004V08	60	T C GGCATTCTT			CCTACAATCCTATAATATGCAAGGGTTGGGAAGGATGCAGGAAAAACAGGCATTCCTTA[C/G]GCC TTTTGTGGGAAGGATCAATTTGGTGCATGCACCTTAGGGGACAATTTGGGCAGTAGCTGTCAAAATTC AGTAGCTGTCAAAATTTCAAA
TIGR- A004V26	125	A G ---			TCTAGCTATAAGACCAGATTTTAAATATCTAGATATAGAATTATCCAGAAATAATCTATTGAATTGA CTGATTACAAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTATCTTCACATGA[A/G]AAGGT TTCAGTTTATAAATGCTTAAATCTGTATCTATTGCTTAAATACGTATCTATTGG
TIGR- A004V28 a	29	A G CGATCTC			CCAGGCTATAATGTTGTGGTGCGATCT[C/A]GCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAA TTCTCCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCACCCGCCACCCCTAACCTAAATTTTGG TATTTTITAGTAGAGACATTGTATTTTITAGTAGAGACAGG
TIGR- A004X20	25	T C GA			TAAGTTTTCCTTCTCTCTGTAGGA[C/G]GTCTCCATGTTACAGTCAACTATAAACACATGGCTCATGT TCACTCTGGCTTCGCTTCAGAGGAGTTTGATATTTTGGAAAGTGGTACCTTTGTTCTGTGCTTTTCA GACCAACCGCTCTCTTCAATTTCTCAAGGCTTCTTCCAAAGGAGTTAAATCATCATCATGTCCAATC ATCATCATGTCCCT
TIGR- A004X30	26	T C CCAC			TTTTGAATCTTAGAGTAGAACCCAC[C/G]ACTCTAGTAATACTTGTAAATAAAATAGTTTT AAACACTTCCATAAAGAATTAGGGTGCCACGCTCCTTGATTTCCCCCTAGGGATAAAGATATCCAT GTAGGGATAAAGATATCCATGTAC
TIGR- A004Z04	102	T G ATGCAAAACT			CACGGTATATGCCCTTATATATAGGTATATATACAGATCGTACACAATATATTTAACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAAACT[C/G]TTGCTTTTCATGAAATTTCTAATTATAAGG ACTGTTGCTTTCTTCATATTCATTTGGACATTATACAAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCTTTAGTGATTTAAGACTG



TIGR- A004Z19	85 C T	GAGAACAACT GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGAGACAAAGTTATTGGAGGAGCTTGACACCCCTCTTCCCTAGCTTGAGAGAACAACTGC AGCATTTTTTCTTTTCTTCCGATGACCATCTTTGGCTGGGGCCAGGCCCTGGGTGC TCCCATATCGCTGCTTTAGTGAGACTGAGGATCTGGTATAGGAAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGAGGT AGGAGACT	CAGGGCTGCCG GTDC	GTCTTAGCAGAGGAGATAACTTTGAGGGACAGCCCCAAGGGCCAGGTAGCCTTCAGGGCGGGCA GGGTGGGGAGGTAGGAGACTCTGGACCGCAGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGTCTTC
TIGR- A005D17 c	81 T C	---	---	TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCTCTGTCTAGATCTCTTGGCTCTCTGTGAGGATTCCTTCTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAACAC
TIGR- A005D17 b	79 G C	GGGGAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCTCTGTCTAGATCTCTTGGCTCTCTGTGAGGATTCCTTCTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAACAC
TIGR- A005D44	97 G T	TTAACATTATT GAACCTTAAAA CTGTACAC	TTGTCTATTAT TTAAGCCCAAC AAAA	CATCAGTAACATATACACAAATTGGTCATCACTGAACCTTGGCTCCAATATATTTCTATACAATACCTT AACATTATTGAACCTTAAACCTGTACACTGTCTTGGCTTAAATATAGACAATGATTTTGG TCTATTACTTAGTGATAGACAAAGTATTACTTTGTAGACAAAGTATTACTTTGTTC
TIGR- A005E31b	27 G A	---	---	GGAGTTCAAATTTATAACCGGCTCTGTGCTACAGCTGTACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCCACCTGCCCTGCCATGTGGATAGTACTCTTTGGCTGCTGGCCCTACAAAGGCCACCTTCTAT TTCATACCAATACCTCTATTTCATACCAATAAG
TIGR- A005E39	182 G C	---	---	CTCAGTGTAACAACTTTGTTAGGGAAAAAATAAATCCAATGGATATATGGGAAGAGAGTG CCAGGCTGGATGGTGTGCTGAGACAGAATGACCCCTTGGGCTCTTATTTTGTCTTTTCAACAGGACC CCACAGATAATTTGCGGTATGTCATGAGGACTGGGGATGCTCTTCTATTGTCGCTCTCTATTTT
TIGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAAGGTACTGCACCTTACAGAGAGCTCAATTTCCCTGATTAGGA AGGCGATGCTAATGGGTATTGCATAGGTAGTAAATGTTGTAATTAAGAGAATCCCAACAG CTTGGTATAAGGCAGAAAAATAAATGGTATAAGGCAGAAAAATAAATAG
TIGR- A005E46	76 A G	CACCTGACTCG GTGCTTTAC	COCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTATTAGCTACCGTTTGTAAAGCACCTACTGCGTATCAGGCACCTGACTCGG TGCTTTACAGTACATTACCTCACAGCCAGGGTTGGCAATGGTCATTTTGACAAATGGTCATTTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAACTGTAGGTGTCTCCCAACAGAGCAGATACTTTGAACCG ACTCAATTCCTGTGTAAAGAGCACCTTGTCTGTCTCAGGACCTCCCCAAAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTTCCTTTGATATTGTAAAAATCCCCCAAGAGCCGCATATGAATCTGCC



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X57830	106	G C	AGTGAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTCACCTATCTGGAAAAAATAATGAGATTGGA AAAAATTAGACAAGTCTAGTGAACCAACGATCATATCTG/CJATGCCTCATTTTATCTGTCAAT GAAAAGCGGGTTCAATGCTACAAAATGTGTCTTGGAAAATGTTCTGACAGCAATTCAGCTGTGAG CTTTC
X74070b	72	T G	CTTTTAAAGAA ATTTTGTTTA	GGGCTTAAAAA TATTAGAGATC	AACCTGAAGAAGTTACTGGGAGCTGCTATTTTATATGACTGCTTTTAAAGAAATTTTGTATTG GATCT/GJGATAAAATCTAGATCTCTAATAATTTTAAAGCCAAAGCCCTTGGACACTGCAGCTCTTT CAGTTTGTCTTATACACAAATTCATCTTTCGAGCTAATTAAGCCGAAGAAGCCCTGGGAATCAAGTTT GAA
Z48804	44	C T	---	---	ACTGCGAAGTGTAGCGGCCCCCAACCTTGTCTCTCATCACCAAG/CJTAGAGCTTCTTCCCGAAGGG CCTTAGGATAGGAGAAAGGTTTCATGCACACACGTGTGAGAAATGGAAGAGCCCTCCAGACCACT CTACAGCTGCTCTAGCCTTAGTGGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGAAGG TCCA
D28513b	133	A G	---	---	ATGACCAAAGCCACCACATTTAGAACITTTGGCTGCCCTTGGAAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCAGAGGGTACAGCACTTTGGACATGGCTCACAAGCAGTTTGTATTGACTGCATGAATGCJAV GJTGCGTGAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAAACAGTTCTGTCTTC AGCTGTACATA
D29833b	85	A G	---	---	CCACTCCATCCTGATGCCCCCAAGTTATCCACAGCCTCCTTCCCGACCAAGACCCCTATCCACCTGGACC TCCATTTTCCCTGTAAJAGJTTCTCCAACCTGATCCTACCTCCCTACTCTGACCCCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAACAAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D29833a	21	A G	---	---	CCACTCCATCCTGATGCCCAJAGJTTATCCACAGCCTCCTTCCCGACCAAGACCCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATCTCCAACCTGATCCTACCTCCCTACTCTGACCCCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAACCAACAAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D31762	82	G A	---	---	CTCCTGCCCTCCTCCTCCTGCTGATGCTCCGTCCTCAACAGCCGAACCTGCTTGTGAATGGGGG GAGGGGCGTTTCGJAGJTTCTCCTTCTTGGCTCCTCTTATCTTCCACAAACCATCTCAATAAA GCCAAAATCTTCTCTTCTCCCCCTCAGGCCACCTCCTGCTCCTACTCCTGCTGCTGCTGGCTTTT CTGGA
D37931	64	T C	---	---	ATTATCGGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTGTCJ CCCAGGCTCTGTCTCCTCAGCTCATTTCTCTACTCTTCTCTATATACTCATTTCTATTAATACATT GCACCAAAGAGATATGGAGACATAAACCTGTAAATGAATGAGGCTGGGCTTTTCTGTAAATAGCTTCC TTT



D63807	101	C T	---	---	---	CAGGCAGGAC TTCAGTGCAGTATCCCTGCCCTTCAGTCTCTTTAGAAATCACATCTGTGTCAATCC ATTGTTAGAGGGAGTGATTTTCTGTTCAC[C/T]GAAGAGGACTTTTGTTCACAAATGGATCAC AATGCAGAGGAGTCTGTCTCCCGCTCGGCTCTCGGTGCGGAGGGTGACCTGTCCACAGATGAC TGGGAACATGCGGTGACCTC[T/C]ACAGCTACCTCTCTATGGACTGGTTATTGCCAAACAGCCACA CTGTGGGACTCTTCTTAACCTAAATTTTAAATTTAATTACTAATTTAGTTTTTATAATTTATTTTGAT TTACAGTGTGTTGTGATTGTTGCTCTGAGAGTCCCGCTGCCCTCCACCTTCCCTCACAGTGTG TCTGGTG
D90145	21	T C	---	---	---	ATTATCACTCTCAAAAATTTGGTGTGTGTTAAGTACTTTCTTATTAATGAGCCCC[T/C]GAGGA CCAGACATGTTATTATCAAGCCCCCTTATATACCACTAAT
EST14035 1a	59	T C	---	---	---	GCATTTTAAATTCACATTTGAATCAATTTACTATTTATGATGTTACATAACAATTCAGTATCATTT ATG[C/T]GTAGATTCAGATGTAGGTCGTCATCTAGCACTTATCT
EST16868 5	71	C T	---	---	---	ACAGACTATCGCCAACCTTATAATGCTTAACTTTATGATCAATAGTAATAAATTACA[C/T]GAGATA TTCACACTTTATTATAAATAGGGTTTGTGAAGATGATTTTCCCAACTGTAGGTTAACAT
EST16904 7	57	C T	---	---	---	TTTTTAAGTACCAGAGGCACCTGCTGGAACAGGATGAAAACTGATACACC[AVG]GTTACTACTACTC TTCACCTCTCAAACTGATTCOCCTAAAGACTTCTACTTAGCAAA
EST21863 9	49	A G	---	---	---	GGCTGAAGTAGAATCAAAAGTTAAGAACAATTTATGCACCTTATTCACAAAACATTTACTGAGCATA CTAGGTCTGGG[A/G]GTGACAGTGAGCAAAAAACACAA
EST21885 6	80	G A	---	---	---	ATTTTAGTGCAAATGACAAAGCCCA[A/G]AGAACAGAGGATCAAAATAGATTGAAATGTATTACC TTCTCATAAGTATACGAAGTTTAAACAAAGTATGGGAGT
EST22623 8a	26	A G	---	---	---	AAAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTTAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTATTTACAG[A/G]AAATGTGGAAAAGATGGCTTTTAAACCC
EST22644 2	98	A G	---	---	---	CCTCATTTATTTAAAAAGACGGACATAAAA[A/T]ATACAAACAAAAACCCCAAGTCACATTTTCAG GAGGTAAAACTAAAAAGTCTGATATGAAAATATGGTGG
EST23587 1	31	T A	---	---	---	AAAGATCTGGCATTATTCACATCATTTCTAAATATTTTGTAAATACITTTTCCATGAGTATTTTTTCA TGTCGAAGCATTTTAACTATCATTTTAGCGTAAATACC[T/C]GAATAACCCATAGTTACAGAAATTGG GTCTGTGTAACCTCAATT
EST24246 7	106	T C	---	---	---	TAGTTTAAATTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT[A/G]CATTTAAAAATGTATCAAT GCACCTCTTCAGTAGTACCACATGAAAATATATAACCTCGTTC
EST24308 3	45	A G	---	---	---	CTTGAACCTCTGGTCTCAAGTGTACGTCCTCGCTCAACTCCCAAAATGATGCGATTACAGGCATAAG CAGCC[G/A]TGCCCTGACCCACATTTCTTTATCCGATCTGTGATGGACATTCAGGTGTTC
EST24435 6	73	G A	---	---	---	TATGTTGCAATTATCAAAATGGTT[A/T]CJAGTTTTCAATTAACCTGTAATTTGATTTCTATGTATAAA ACAGCTTTGAAGTTGTAATGTAGTTTCCAAATCGTTAGTTAATGCTACATT
EST25089 6	25	T C	---	---	---	



EST25476 9	33 G A ---	---	AATGATCTTTATTTCAGACCTGCTCCTAAAG[G/A]CTTTCTCCTCCTCTAAAAAACCAACAACA AGAGTGCTCTTGTGCCTTCCACTGGACTGIGCGGCTGGGACTGGACCCTGCTGCTGA
EST26183 2	70 T A ---	---	AGATAATGCATTAGAGCCTGCCCTCATTTGTATCTTGATTAACTTTGTAAGAATTGATCTCTAAATAAG AT[T/A]ACATTTCTGGGTACTGGGAGTTAGAACAAC
EST27231 1a	28 T C ---	---	AGAAAATAAGGTGCTACCAGAACTCATG[T/C]GATAGCGCTTTCTTTTAGGCACATATTATAGCAATT CAGATGAAAGTTCTGTAAATCACACACACACTGTGCCCTAACAACAACAACACGGTGACTCTGA
EST27816 5a	26 T C ---	---	CAACTCAAGGTACAAGACAATTGCATTT[C]TAACATTTGTTATAAATAAAAGGAACATCAGATCAAT CATTAAAGGGCTCCAGAGTGAACAGCATCTTCATAACTTCATGTT
EST28588 0	78 A T ---	---	GTTTAATTGGCGTATGGTCCACAGGCTGTACAGAAAGCATGATGGCTCTCGGGAGGCTCAGGAA ACTTACAATCA[AT]GGTAGAAGGCCAAAAGAGAAAGCAGGCATCTCTCCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGGAT
EST30226 5	25 A C ---	---	TACTCACACCGACATACATATCTCA[AT]GTAGAATTAGCTATACTGCATATACTTAOCTTCAATTGTAGT AGGGAATATAAACTACTGAACAAGACAGACTTGTCTAACTTAAACAAGACAGACTCATTTCCCTTTGA G
EST30935 9a	59 C G ---	---	AGCTATGGTAGAGCAAATTCAGTGGTGGTAAATCAAGAACTCTAAAGTTCAAGTAGAGA[C/GIAGGT GTTTTGAATGTCAAGGAAATCACTGAGGTAGATTTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGTGAGG
EST32515 7	25 G A ---	---	CCGAATATAAGGAAAAAATGGTGGC[G/A]TGCCCTCTAAAACCTGTTGAATAGAATAATGGCCAAAT ATTACAGTTTCTCAGTTTCTATGAATACTGGCAGCTGTTTATTTCATGTTTATATGTGAGTTTCTATGC ATAAAAATCCCAGTAAGA
EST33274 4	27 T C ---	---	TGCTTTGTTCCCTCCAAATCCTA AAAA[T/C]GTGTGCTTCCAAGAAATTCGIGGAAAGGACTTTGAA TACGAGTTTGACCAATTCAGATATCTTGAATACAGGTTTCAGATAACTATGGAGATGATACCATT GGACTAGGTA
EST33352 7b	75 C G ---	---	TACACATTATCAAGAGACCACCTGACATGCATCTCCTCCGCAGAAATACATTCGTCCTCTCTTAGAGA AGTTTAA[C/G]GCACATAGTATTATTTTACTAAGAGAAATATCTTTGGTGCTATAICTAGGGG
EST33424 1	126 A C ---	---	ATTTTCCCACAGCAGAAGTATATTTATTGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACCAGTACAGAATGTTCAAAAAGATTACA AAATCTCAGTCATTACACACTGAGCAAC[A/C]JAAA CAAAGGTGTTGAATCCTCTT
EST33488 7	90 A G ---	---	CCTTTGGGGGAGTTTAAAGCCAGAATGTGACAAAAGTCACTTACAGGAAGACTGGAATGTAGCCATAG TTGAACTCTAACATCGTCTATAG[A/G]ACCAATTTCCCGTCTCCAGTTAGGTTCTAGGCATACTAAGCT GCTC
EST33508 1b	45 C T ---	---	AAAAACATGCTATTTGAACAAAACTTTTTATAAAGAAATAAGTTGA[C/T]TGA AAAAGCAGTTTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCCAATAA



EST33508 1a	36 A G ---	---	---	AAAAACATGCTATTTGAACAAACTTTTTTATAAAGA[A/G]TAAGTTGACTGAAAAGCAGTTTTTAAAT AACATCAACTCACAATGACTTTTAGAAGCCAAATAA
EST33863 4	77 C T ---	---	---	ACAACATAGGACTGGTTATCTTGTTTTGAAAAATTAATGTTGCCACTTCCTATTGTTTTAAAAATGA TCATTTAAC[C/T]CTTTGAAC[TACAGCCTGAATCCCC
EST34739 3	97 T A ---	---	---	GAAGTATCCTTCCCAGTGGCAGGAACCTGAAGACTCCAGATCAACCAGGTGGACCTTTTCGTTGAIGA GCTGATAGCTTCTAGGCTGTGGGAACCT[C/T]A/GGTGCCCTTACAACCTCCAACCTACTGCAGAAATTTCT TGTTGGCCTCATAAACA
EST34792 6b	104 A G ---	---	---	ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCAGATCACGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GTATTCAGGAATTCCTAGTCCTATTACA AAGATTTGTTGCTGTG
EST34835 9b	93 T G ---	---	---	GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTCGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGCTTTCTGGT[G/G]GGCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST34835 9a	82 G A ---	---	---	GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTCGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGCTTTCTGGTGGCCTTAAAGAAACAGACAAATTTGTGCTAAAGAT
EST35230 0	93 G T ---	---	---	CACAAAGGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAGAGGTTCTC[G/T]GCCCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---	---	---	TCITTTCAAATTTTTGATGAGGCATTTAATG[C/T]ATAAATTTCTGCTTAGGAATGTATCTGCT ATATCTCAGAAGTTGGGCATGTTGTTCCATTTTACTTAGTTGAGAACTTTTTCATTTTCATCT
EST35708 9	32 C T ---	---	---	CTGCCCCAAATTAACCTTTAGGCAATGGAAA[C/T]AGACTTACTGTATGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGCAGCGTGTGCTTCCCTCTCTGAGGTTGGCACCTTTCCCTGTTGTG ATGTGCAAGTGTGGCT
EST35747 9	51 C G ---	---	---	ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAAGGCTCCA[C/G]ATGTTAAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCTTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---	---	---	TGGTCCATTATATTAACACTGAGGGAACAAACGGTGTGCTGACATGGCAGACATTTATTTCAATGGAGA AGTTCCTCCCATGAACCAAGA[C/A]CTTGCTCCTCATGATAAAGTGGAGACAATTAAGAAAGCCAGGT ATATAATTAAGGCCTGTGA
EST36301 4	93 C T ---	---	---	CACCTGTTCAITGGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGCACGCTACAGC AGTCAGGAGGCGAGCCATGGCCCTG[C/T]GCTGATGGAGCTTGTAAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACAACAAA
EST36519 0a	33 G T ---	---	---	GCCATCAGCCCAACAAAGACATGACTACCAACGC[G/T]GGCCCCCTTGACCCATACTGGCCTCAGCAC CTAAGACTGGACAACCTTTGTACCTAATGACCGCCCCCACCTGGCATATACTGGCTGGCCTCTTCTCTGT CACAGGGGCTCTAGTCGT



EST36620 6	50 G A ---	---	GAC TTATTAGATAAGGGTTTCGGCTACCCTCAAAGCTCAGGACTGG[G]AGCTAGGGTTTAAAGG AAGGCTTATTAAATATGGGAAATAAAATACAAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89 C G ---	---	CCTGTGATGTGCATGGTGCCTGAGCAGTCGTACTTACTATGCTCAGACAGCTCAGCTACGTATGTCAGGA AAGGAAGTCTGGGATTCTTA[C]GJAGGGGACATATCACACATATCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTCA
EST36729 9	62 C T ---	---	GAGACAGAAGCCCATCAGTTAAATGAGGTAGGCCCTCTCCTCCTAATATACTGATTGACAATG[C]TJA TATTAGCCAGGTAATGCACTTTAGCTACCCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAG
EST36823 6	103 A T ---	---	ACTGCTGGCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGTCTATTCAAGCAACAATTJA/TJCTTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 C G ---	---	ATGATCGCTTATGTAATTTGAGGGCGACATGGGTAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTAAACAGCTGATCAGAGGCTAAATTACAAC TGACATTTTGTATGCAGTTT[C]GJGTTA GGGAATTAAGACAATGCAG
EST37054 3	88 T C ---	---	GGTCTCACTCTCTTGCCCGAGGACGGTTTGAAACTCCTGAGCTCAAGTGACCCCTCCACACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T]CJGTGAGCCACCACACCTGGTCTTGGTTTAAAGTAACCACTGAA C
EST37269 3b	105 T G ---	---	AATAGTCTATGGCTACGGGCCCCGGGATGTTAAAAATGGGATTTTAAATTAAGATTGTGAACATG CAAAACCAGCAAAATTTCTCAGCTTATATTTGAAAGT[C]GJAGGAGAAAAAATGGGGTCC
EST37284 2	93 G T ---	---	AAAAGACCTTTCTCAAGCAGTAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCCAGGAA GCTCTCTGGATAATGTCACCTCTAGGAA[G/T]AGTAAACAGGTTTAAACCCCTGAGATAGCAACCCCT CTTGGCTTGCTTGAGGAATA
EST37315 2a	90 A G ---	---	AGATGGGCTCTTGCTAGCTTGCTGGGCTGAACATAAGATATCCTCCTGCTCAGCCTCCAGGTAGT TGGAAC TATAGTAGGAGTATCTJAVGJCCCTGCCCTGCTAGAAC TCAAGTTTGTATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 C T ---	---	CCTGCCATGATAATGTTAAACATATCAAGATCCTCCTCAAAC T[C]TJAAGGGTGAAAAAGCATACC ATTCATTTTAGTTGAAATATTCCTTCACATAGCCAACACATTTTTTCAAGGCACTCTAGCTACTACA GGA
EST37376 8b	101 G C ---	---	GTGACATCATGTCTCTTCAATGCCCTTTCATTAATAGTAGTJAGCGCTGGGGGCTGAAGTCAGACT CTCTGGGTTCAAATCACAGTGTGTCTCTGCA[G/C]GCTGTCTCAGGCAAGTTGCTGACTTCTCTG TGCCAGG
EST37376 8a	41 T C ---	---	GTGACATCATGTCTCTTCAATGCCCTTTCATTAATAGTAGTJAGCGCTGGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCACAGTGTGTCTCTGAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG



[illegible]



EST51340	51 G A ---	---	---	GATCAAACTGTATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTTCAAACCTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134 T C ---	---	---	CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTGCAACCCCATCAT CCTCAGGCCCTCTCTACAAGCAGCAGGAAACATAGAACTCAGAGCCAGATCCTTTATCCAACCTCTCGA T/CJTTCCTTGGTCTCCAGTGAAGGGGAAAGCCCATGATCTTCAAGCAGGGAAGCCCCAGTGAGT AGCTG
K01506	63 T C ---	---	---	CTGAACCTCCAGCTGCCCTACAACTCCATCTCAGCTTTCTTCTCAGCTTCATGTGAAAACCTA[C/T]/C/C CAGTGGCTGACTGAATTGCTGACCCCTTCAAGCTCTGTCTTATCCATTACCTCAAAGCAGTCATTCCT TAGTAAAGTTTCCAACAATAAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTTC ATTGAGCCCTTTATCCT
L18877	69 T C ---	---	---	TGAGTCTGAGCACGAGTTGCAGCCAGGGCCAGTGGGAGGAGTCTGGGCCAGTGCACCTTCCAAAGGOC C/T/CJATCCATTAGTTTCCACTGCCCTCGTGTGACATGAGGCCCATTTCTCACTCTTTGAAGAGAGCAG TCAGTATTGTAGTAGTGAGTTCTGTCTTATTGGATGACTTTGAGATTATCTTTGTTTCTGTTGGA ATTGTTCAAATGTT
L31848	36 T C ---	---	---	GCTATTTACATATCCCAAGCCCTTTAGGGCTACAGT/C/CJCTCTTGTCTGACCCCTGTAGGGTGCCA TTTGAGATTACAGCCTAGAAGAAGAAAGGCTTTGGCCCTGGTGTGGCTAGGCCCTGTATCGT AGCGCTTTGAGAGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGTTCGAGACAAACCTGGGCAAT GT
L38517	137 G C ---	---	---	GGTCCAGAAAGCCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGACCTGAGCTGGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTGAGACTTGACTGGGCAACACCCAGCGTCCCCAC CC/G/CJCGTCTGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123 T G ---	---	---	ACTTGAGAAAGCAGAGCTGCCACCTTTGAGGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGGACAGGGCAACAAATAACAGTAGTCTTTCTTTGTATTTGTATATTTGJCGCCTGA AGATCATCCCGCAAGGCAGGCTGGAGGTGCCGTGGCCCTGTGTGCTGGGATTTAGTCTGTGCTGG GAG
L41268d	173 G A ---	---	---	CAAAGTTGTCTCCTGCCATGAGCACCAACAGTCAGGCCCTTGAAGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAAACTGGTTGCCAGCTCCAATGTACACGACAGCTGGAATCTGAAGCGGTGAGTCTGCAT CTTAGGGCATCGCTCTTCCCTCACACCACAAATCTGAAC[G/A]TGCCTCTCCCTTGCCTTACAAATGTCT AAGGT



L48728b	111 T C ---	---	AAGTGAACAGAAAGCAAGATGGATTGTGTTCCCTATAAAAGCACATAGTATGTTTACTGGTATCGT AAGAAGCTGGAAGAAGAGCTCAAGTTTGGTTTACTTTTTCAGAA[T/C]GAAGAACTTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAAACTCATCCTGTACCTTGGAGATCCA GTC
M18079	52 G A ---	---	GCGCACAGTCCAAAATACAAAATTGGACAGAAGATCTATATTGACCAGAACT[G/A]TTTATTTTCAAC CCATCAAGTATAAGGTTACTGATTGATTGGTCCCTTTTATAACAATTGGTATATTTCCATTTCATGCCAA AGCAAAAGAAAGTAAAGCTAA
M19169	113 T C ---	---	TAGGGATCTGTGCCAGGCCATTGCGACCCAGCCACCACTCCACCCCTGTAGTGCTOCCACCCC TGGACTGGTGGCCCCCACCCTGCGGGAGGCCCTCCCATGTGCC[TG/C]GCCAAGAGACAGACAGAG AAGGCTGCAGGAGTCCTTTGTTGCTCAGCAGGGCGCTCCGCCCTCCCTCCTTCTCTCGCTTCTAATA GC
M21539	114 T G ---	---	TCACCTCGTCCACAGCTCCACCTGCATCTTCTCATCAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCTTAGCCTGTGATCTGCCCATGATGATCCCGACAGCAAA[T/G]GTTTCTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAAAGGAAGTCTCAGCTGACCGGCCCTTTCAGAGCT TCTCTTGGGTG
M26041c	173 A G ---	---	CCTAGCATTATTTTCTGGCCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTAATTCCTGACTTC CTGATTTTCTTCTTCTCA[TG/C]GTTTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157 A G ---	---	CCTAGCATTATTTCTGGCCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTAATTCCTGACTTC CTGATTTTCTTCTTCTCA[TG/C]GTTTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45 C G ---	---	CCTAGCATTATTTCTGGCCCCCATTTATCATATCCCTTTTCTCCTCCAAATGTTTCTCCTCTCACCT TCTTCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTAATTCCTGACT TTCCTGATTTTCTTCTTCTCAAGTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57 G C ---	---	TAAGGCAGCTGTGAGGGAGGCCAGTCCAGCAATTCACAACCCCTTGAC[G/C]ATGCT TGCCAAGCTGTTTAAAGCCCAAGAACACCCCTTCTTTGTTCCAAATTAACCTTTAGAAGAAACCCCA CAATAAAGCAATTCAATC
M81695	34 G A ---	---	ACTTACTTACCCTCACTGTGAGGCTGACGGGA[G/A]GAACCACTGCACCACCCAGAGAGGCTGGG ATGGCCTGCTTCTGCTTTGGGAGAAAACGCTGCTGCTGGGAGGGGCTTGTCTGTGCAAGGTTCT CAACTGGAACCCCTTAGGACAGGGTCCCTGCTGTGTTCCCAAAAGGACTTGACTTGCAATTTCTACC T



U06641d	166	C T ---			CTCCTCCTTTATTTGAGCATGGAGGGTTAAATGGAGGATCTCCTTTTCCTGTGACAAAACATCTTTC ACAACTTACCTTGTTAAGACAATTTTAAAAAAGATCTTTTCAAACTTACCTTGTAAAGACAAAAT TATTTCCAGGCTATTTAATACGTACTTTAGTC/TTGGAATATTCTATGTCAATGATTTTTAAGCTA TGAAATACAATGGGGGA
U09607	39	T C ---			GAGGCCTTATGAGGTCCTCTACTTCAGGAACACCCCA/TGACATTGCATTTGGGGGGGCTCCCG TGCCCTGTAGAAATAGCCTGTGGCCTTTGCAATTTGTAAGGTTCAAGACAGATGGCATATGTGTGAG TGGGGCTCTCTGAGTCTCTGGCCCAAGGAAGCAAGCAAAATTAAGACTCTGCGCATCTTCCCAAC CCCTTA
U09608	82	T C ---			GAGCAGAAGGCAAGAGCGGCAAGATGAGTTTGAGCGTTGTATTCCAAAGGCTCATCTGGAGCCTC GGGAAAGTCTGGTCC/TGACATCTGCCCGCCCTTCCAGCCCTTCCCAGCCCTCCTCTTGTTCCTTC ATTCATTCAACAAAATTTGGC
U10694	20	C G ---			GTGACATGAGGCCCATTTCT/GGCTCTGTGTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCATCTCTGGGTCCTGTCTATTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATGTTCAAATGTTCTTTAATGGTCAGTTAATGAACCTTCAACCATCGAAGTTAA TGAATGACAGTA
U13877b	162	T C ---			AAAAAGACTCTGGTTCAAATCCAGGTTCCATTTTGCTATCTTTGTGACCTTGCACAAGTTGTTTAAAC CTCTTTGTTCAGAAATTTCTCCATGGAGTAACAATACTAGGTTGGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGAACACAGCCCAAGAGAT/TCTTACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTACCTTCAGCA
U15555	187	T C ---			TTCTGTCCACTTTCACCTGGTTTTAATAGCCAGCCAGTCATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTGGAAGAAATTAATAGCAATGCTGAACATCAGGAATTTAGATATCCGTACAGAGAGT TCCAGTAAATTTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG/TG/TGGTCTCATAC CTCATATGCAGGATTTCATCA
U17077	122	T C ---			TCCAATTATGGTCCCCAAAGCAGCTTCCAACGTTTGCCATCTGGATGACAAAACGGAAGATCCACT AAACGTCCACGGGATTAAACAGAACGTCCTTGACAGACTGAGCGATGACACCACACAT/TCTTGTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTTCTTTTCTGGGAAACAACTGTCTCTTGG AATTA
U18543	58	T C ---			GCACATGCAGAATAGACTCAGCCTATGTCTGATTCAGCTGGGTAGTCTAGAACTTT/CJAGAAG CTCCATCTTTAATGTTTTATTGTGTTATGTCCCTCCCGCTTCCACCTAAATTTAGAGCTTTAAA AGATGCACTGCCCAATAGGACACACGATGGTGTAGCTGAAGTTTGTAGCAATTAGGCACTTCC AAGGCTTTAGTAGAGAGAGCC



U25975b	164 C A ---	---	---	TCACTGCTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCCTTTAGTATATGAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAAGAAGCAATGACTATTCTCTG AAGACAACCAAGAGAAAATTGCAAAAAGA[C/A]AAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25975a	143 C G ---	---	---	TCACTGCTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCCTTTAGTATATGAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAAGAAGCAATGACTATTCTCTG AAGACAAC[C/G]AAGAGAAAATTGCAAAAAGACAAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25997	61 A G ---	---	---	CAGGGAGAGGTTATTCAACACCTCACAACTAGTATCATTTTAGGGTGTGACACACCA[A/G]TT TTGAGTGTACTGTGCCTGGTTGATTTTAAAGTAGTTCCTATTTCTATCCCTTAAAGAAAATT GCATGAACTAGGCTTCTGTAATCAATATCCCAACATTCTGCAATGGCAGCATTCACCAACAAAA TCC
U28413	29 C T ---	---	---	ATTCTGACAGCTAAATTAGCCCTAAATG[C/T]GGGTAATATTTTCTCATGTTTAAATGAGGTT AATATTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTAGTCAAAATGTGTTCCCTTGATCC CAGATGTTGTGGCCTGGGAAAGCCCTCATTGCTACAGTACAAGTAACACAAGTCGTTGTACCTCAGTT G
U30884c	89 A G ---	---	---	TAGGGGTAGCATTTAAGATTGAGGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCTGT CTTCTATCCCAAGTTAGCCA[A/G]TTGTTCTTGATGAATCTATATGAGTCATAGAACAACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACACAGTTGAACACAAGT GCTGTCA
U30884a	34 A G ---	---	---	TAGGGGTAGCATTTAAGATTGAGGAGTCATTAGC[A/G]GTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATCCCAAGTTAGCCAATTTGTTCTTGATGAATCTATATGAGTCATAGAACAACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACACAGTTGAACACAAGT GCTGTCA
U31216b	78 A G ---	---	---	GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCAATGAGAGGCCCTGCAACCAACA GCCGTATCA[A/G]CCCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCCCTTTACAACGTAGAGGAGGAGGATGCCAGCCGATTGCGCTTTAGCCCGCC TGTTAGCCCTTCCAT
U31216a	70 G A ---	---	---	GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCAATGAGAGGCCCTGCAACCAACA GCC[G/AT]CATCAAAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCCCTTTACAACGTAGAGGAGGAGGATGCCAGCCGATTGCGCTTTAGCCCGCC TGTTAGCCCTTCCAT



U31416c	76 GA ---			AGTTGCCAGTCCCATGTACACAGAGCTGGAATCTGAAGGGGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G/A]CCACAAATCTGGTGCCTCTCTCTTGTCTTACAAATGCTAGGTCCTCCCACTGCCTGCT GGAAGAAACACACACTCCTTTGCTTAGCCACAGTCTCCATTTCACTTGACCCCTGCCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 CT ---			AGTTGOCAGCTCCCATGTACACAGAGCTGGAATCTGAAGGGGTGAGTCTTCATCTTAGGGCATCGCTC [C/T]TCTCAGCCACAAATCTGGTGCCTCTCTCTTGTCTTACAAATGCTAGGTCCTCCCACTGCCTGCTG GAAAGAAACACACTCCTTTGCTTAGCCACAGTCTCCATTTCACTTGACCCCTGCCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 CT ---			ACGGGTACACAGAGAAACCTGAGTCTAGCCATGAGGGGCTTATGCTCCCACTCACATTGTTCTCTCC AGCCGAGG[C/T]TCCCCAGCCTCAGGTGCTGGAGCTGTACATGACTGCCTGCCTGCCAGG GCTGCAAGCAAGGCTTCTCTATCTGGGGACGCTGCTCGAGAGAGCCGAGAGGCCGAGAAC ATGCCAGGTGTCC
U37690	54 AG ---			GACCAGCTGAACCCACCCACCGCTGTGCTGACCATGGGCCCTGAGCGTCTCT[AG]CCCCGAATTC ACGAGCTGAGGCATCCGGAGCTGGCGTAATGCCTGGCCGAGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGTCTTT
V00540	39 TC ---			TGAAACCGTTTCAACATGGAATGATCTGTATTGACTAAT[C]ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCCTATAACCCAGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAGGAACATCATGTTTACCTGTGACAGGCACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 AT ---			TCAGAAGGTGACTGCCCTTGTATGATGGATGGGAAGATGAATGACTGTTTTTACTGGGTGTAA AACCACCTGAGCCTCTCTGAGACCATGTGTTTTAA[A/T]ATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTCCAGTAGCTAAGACCCTAGAAATTTGGATTCTCTGTTTTTTCATGTCTCTCCTT GTAAACCTGAGATCATCAG
X52011b	148 CT ---			AGGAAGATCCACCGACCCCTCCTGGCCTAATCCTTTAGATTAGGTACATTACATTAACTTTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAAAGTTGCGAAAATTTGCG AAATCTGTTGTGCA[C/T]GCTCAATGAAACGCCCTTTCCGGCTTTGGGCTTTTATTTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT
X52011a	118 A/C ---			AGGAAGATCCACCGACCCCTCCTGGCCTAATCCTTTAGATTAGGTACATTACATTAACTTTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAA[A/C]GTTGCGAAAAT GCGAAATCTGTTGTGACGCTCAATGAAACGCCCTTTCCGGCTTTGGGCTTTTATTTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT



X54741	24 A G ---	---	CAGGCCACCTGCTTCTCTCCACAG/GJTGACAGCTTCCCTGAGTCACCCCTCTGTCCAGCCAGCTCCT GCACAAATGGAATCCCCAGGGCCTCAGGACTGGGCTTCCAGGCTTGTCAAATAGCAAGGCCAG GGCAGACTGGAGACGATCTTGTGGCAGGGCCTGGCCTTGTCCAGCCCAACCTGGCCCCCTCTCC
X54869	99 A G ---	---	AAGCATTTCGTTTACAGTGCATCAGATACATTTTATATTTCTTAAATAGAAATATTATGATTGCAT AAATCTGAAATGAATTTATTTGCTCTG/JATACAAAAATCTAAATCAATTTATTGAAATAG GATGCACACAATTACTAAAGTACAGACATCCTAGCATTTGTGCGGGCTCATTTTGTCAACATGGTA
X66924	147 G A ---	---	GCCGTGCTCCTGACACCTCCAGAACGCGAGGTGCTGGGCCCCGTTCTGCCTGGGACCCCGGGAACCTCTC CTGCCGGAAGCCGACGGGATGGCCCCAACTTCGCCCTGCCACTTGACTTCACCAATCCCT TCCTGGAGACTG/JAAACCTGGTGTCTCAGGAGCGAAGGACTGTGAACCTTGCGCCTGAAGAGCCAGA
X78932	62 T G ---	---	GAAATGTGAAGAATGTGACAAAGCCTTTAAGCGTTGTACACTTGATTGTATATAAGATAA/TGJT CATACTGGAGAAAACCTCCAGAAAGTGTGACAAATGTGACAAAACATTTAATTAATCTCATACCTTA TTGCACAGGAAAGCATTATATCTTGAGAAAAATTGTATAAAGAAATGGAAGATCAATTAATATCTGCT CATATCTTAACATCAGCGAGTT
X80026	25 T C ---	---	CTAACCCATAACCTCAACCCACATCT/CJTATCTCTCCACCCACATCCACCCACATCCACCTCCATCC CCAAACCATCTCATCCCCAACTACAGCCCCAAACCCAGCCAGCCAGACTAATCCACAGCATCCCCAA CTCATCTCATCCCCAACTGCAGCCCCAAACCCACCCAGGGCCATCCCCAAACCCATCCCCAAGCC AAACTCAACACCATCC
X80197b	99 G C ---	---	ACCCCAACTCAAGTCCAGGCCCGCCAGGCATCTTCTGCCCCTGCCCTTGTGGCCCATCCAGTCCAGG CGCTGGAGCAAGTGTCTAGCTACTTCTCCTG/CJACATTTGAAAGACCCCTCCCACTCCTGGCCTCA CATTTCTCTGTGTATCCCCACATCTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG
X80197a	28 A G ---	---	ACCCCAACTCAAGTCCAGGCCCGCCAGGC/JGTCTTTCTGCCCCTGCCCTTGTGGCCCATCCAGTCC AGGCGCTGGAGCAAGTGTCTAGCTACTTCTCCTGCACTTTGAAAGACCCCTCCCACTCCTGGCCTCA CATTTCTGTGTATCCCCACATCTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCTAGAAAG
X85106	150 G A ---	---	GGCACCCAGAGTGACCAAGTCCAGCAGGGAGGGCGGCCCTCGCCGTGCCGTGTTTCTTTT CAGCCCCGGAGAGGCTCTGACCTGGGGGCTTCTCAAGCCTCACTGGCCACGCTCCCCGGCCGCTCT CTTTCTCCCAAGC/G/JAAACCAATGGGCCCTTCACCTCGCGTGGCCGTGGAGGCCGGGGGCTT CTTTCAGAGC
X87160	128 T G ---	---	ACCACAGCCATGGTCTAAGGACATGGATCGGGTGGCCCCAGACGTGTGCACAGGGGACCCCTCTGCC CACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCGCAAGATGGGGCTT/GJGGC ATGCGCAGGAGGAGCCATCGGGTACTACGACGAACAACACTCACAACTGTCCAGGCTGAGATAAATCCC GGGA



[illegible]



1282	130 C T ---	---	GTGCGATCACCACACTACAGTCTAATTTACAGATGTTTTCATTACCCCTAAAAGAAATCTTGATCCCATTA GCAATTAATCCTCATTCCTGCOCTACCCCAAGCCCTACTCTTTATCGCTATAGATTTGCCIC/TA TGACATATCATACACATGGAGCCATACATATGTGTGCCCTTCATGATGGCTTCTTTCACCTGAGAATA ATGTTTCAAGGT
6810	68 C T ---	---	AGTATCACACATACCTTAATATATTAGATATACACAATAATAAATACACTCCCTACCTTGAAAACTTT A/C/TAAGAAGCATTTTAAATTTTACACACAAAGCTCAACGAACCTACAATAAGTCTAGTCTG TTTACGTGCCAAGGGATAAGGCTGAACAATAAATTAACCCCTTAAAAATGTCTATGAACAAGTACAA TTTTCTTTTGTAGTTCTGCAGAGCAATGACCACTAAGAAATATTTTAAAGGC
6817	118 A C ---	---	CCAGTACATTGGGTGAACGATGAGCTAGCTGTCTAGTATTTGCTTTTGTAAATCCAGTTAAGACCA TCAGCATATACACATCATCACTAACTCAACAATGTAGTCGAGGGTAAC/A/CJTGTTGGATACCCCTG TGTCTCTACTGGCTCCAAAGGCATTGAGGGATCATCAAGATGTTGGACACCTTGTGTTCAAATC TTGTTTCAGGTGGGCTGTGCAGATCGGCTTTTGGTTGGTTGCTTAG
6819b	212 C ---	---	CCATTTTATTTTCTCTAAATTTTAAATAGAAAGACTTTAATGGAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTGTGCATATACAAAATTTTCTGCTATTTTGTCTTAGCAAA CAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
6819a	166 G T ---	---	CCATTTTATTTTCTCTAAATTTTAAATAGAAAGACTTTAATGGAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGAGGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTGTGCATATACAAAATTTTCTGCTATTTTGTCTTAGC AAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
681xx	39 A G ---	---	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATTG/TTTACTATGGCACCATTTGGGACA CAGATTATATATGTCAGACACACCAGAAATGTCTTAAAGATATGCAGCAAGCACAAATCTGTCATGGT TTAACAAAAGAAATGAACGTCTAGG
6972b	149 G T ---	---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCTTGACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAAACTATTGATTATTGC CACAAATTCAGA/G/TCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCTGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT
6972a	122 A G ---	---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCTTGACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAAAG/TA/GTCTATTGATTA TTGCCACAAATTCAGAGCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCTGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT



7598k	210 A C ---			AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCCTTTTA ATATTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTTCCT CAATGCAG[AC]
7598j	208 A T ---			AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCCTTTTA ATATTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTTCCT CAATGC[AT]GA
7598i	192 G T ---			AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCCTTTTA ATATTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCG[GT]TATTTT CCTCAATGCAGA
7598h	144 C T ---			AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCCTTTTA ATATTGATCC[CT]ATTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598g	142 C T ---			AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCCTTTTA ATATTGAT[CT]JCCATTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598f	120 A G ---			AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAAATATTCTTG[AG]GGATGCCCTT TTAATATTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598e	83 C T ---			AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAA[CT]CAGATTTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCCTT TTAATATTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598d	77 C T ---			AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGC[CT]GCTAACCGATTTTACCTTGGAGAAATGAAAATATTCTTGAGGATGCCCTT TTAATATTGATCCCATTTATGTGAGAGATTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA



7598c	56 A G ---	---	---	AAAGGTAAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCA[A/G]AGGAAC TCAATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATGCCCATTTATGTGAGAGATTTTCTCGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	---	AAAGGTAAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACA[C/G]CCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATGCCCATTTATGTGAGAGATTTTCTCGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	---	AAAGGTAAATCAAAGTCCCTCTATAAATT[A/G]TGATTTACAAAAGACACCCAAAGCCAAAGGAAC TCAATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAAAATTATTTCTTGAGGATGCCCTT TTAATATTTGATGCCCATTTATGTGAGAGATTTTCTCGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	---	GTGTTGATCTCACTGGGTGCTGCAGCGGAGCTGTCTCTATTTCAGACATCTTGCCAGCTCTCCTGTGA ATACCTTTAATGAATGGGTAGTCTCTATCTTCTCAAGGTCCTCCCAATA[A/T]CCTTGAGGTTCCCT
7998b	94 A C ---	---	---	GTGTTGATCTCACTGGGTGCTGCAGCGGAGCTGTCTCTATTTCAGACATCTTGCCAGCTCTCCTGTGA ATACCTTTAATGAATGGGTAGTCTCT[A/C]CTTCTCAAGGTCCTCCCAATAAACCTTGAGGTTCCCT
7998a	75 A T ---	---	---	GTGTTGATCTCACTGGGTGCTGCAGCGGAGCTGTCTCTATTTCAGACATCTTGCCAGCTCTCCTGTGA ATACCTTT[A/T]ATGAATGGGTAGTCTCTATCTTCTCAAGGTCCTCCCAATAAACCTTGAGGTTCCCT
8071	119 A G ---	---	---	AAATACAGAAATTTTATTAGAAACTGTTTAAAGTAGAAAAAACCTGTCAAGAAAGACCAGGTGG AAAATGGGTTCCCAATAAAATGGAATTTTAGGGCAACAAAAGCTTAAAGGCC[A/G]CAAAAGAGA AATAGCACCACCTGTCAATTTGAACAATGGCTAGTACTTGCAATTTTGGCATTGTTAATCACTGAATC TGGGTTTTCCTCTGAATCCACACAGAGCATGCACTACACAACATTTTATCAT
8467b	93 C T ---	---	---	AAGGCTTTCCTTAACATCAGTCTACGGAGAACTGGGAAATCCTGGATATTTGGCTTATCACTT TGACGCAAAATCCACTTTGCTGTAA[C/T]GGTCATCCGAACTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATAGTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAGGAAAAATTACTG
8467a	70 A G ---	---	---	AAGGCTTTCCTTAACATCAGTCTACGGAGAACTGGGAAATCCTGGATATTTGGCTTATCACTT TG[A/G]CGCAAAATCCACTTTGCTGTAACTGTAACGGTCAATCCGAACTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATAGTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAGGAAAAATTACTG
8498	84 C T ---	---	---	AGGGTTCAGGGTTTGGTTTAAATCAGGCTGCACACCTTTCAATCAATCTGACATCTCTCTATGTCA AACTGGCTTCAGCTAG[C/T]AATCTTCAATTAATCGAAAAAGAAAAAATGCTTTAAGGAAAAAA AATCCAGTTTTAAGAACAAATTAACATTAGCTTTTAAATAAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCCTTCTCCTCAATACAGAACCAAGGAATGTAATTTTCTCAACTCAG



WI-18562	29	G A ---			CTAAGGAAAAATTTAATGATGGAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAAGTAG CTTCTCTATTACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATTTTACATT TAGCATTAAATCAGAAACGA
WI-18618	51	A C ---			ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTGAGCGGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTCGATGCAAAAGTATAATTGTAAACCACAGTGCTCGCACAGTTC AC
WI-18683	22	C T ---			TAAGCTGTTTCAGGACTGGACT[C/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAAATAAATTTCTCTCCCAAGCCTGCCTGCAGT
WI-18520	75	G A ---			GACTTTGGTGATTTAATGCTTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAAATACTACCTACTGCTGCAACAAACACGGGCATCCACTCTGTCTTCAA TGCTCTTCGGTGAGAC
WI-18563	94	A G ---			AAATAAGTTTTATTGGCACACAGCCAAAGCCACTGGATGACACATTTGCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACCTAATGTGAC[A/G]GACATGGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69	T A ---			GTCTATTTCAATTTAGCTAGACCATTTCTGTTTAAATGGCTACATTTGTTTTCATTGTGAGAC [T/A]GTGCCATAATTTAATCAGTGCCATATTGAAAGACATTTGGATCGTTTCCCAG
WI-18723f	94	G A ---			AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTTGACTGTCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAACCAA[G/A]TATATAGCTTATTTGGTGAATCTTCATCCT
WI-18723e	71	T C ---			AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTTGACTGTCTGTAGATTTTGAAG TGGT[C/A]ACAGGTACATAGGTAACCAAAGTATAGCTTATTTGGTGAATCTTCATCCT
WI-18723c	96	A G ---			AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTTGACTGTCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAACCAAAGT[A/G]TATAGCTTATTTGGTGAATCTTCATCCT
WI-18619	44	G A ---			TTTATTACAATATTAGGTGGCACAAATAACTAACAGCTTCTGA[G/A]ACAGGAGGTAACATTCTCA TAGACTTTGCAACTCAGCCAGAACTCGAAATA
WI-18715	76	G A ---			TTATTCACAAAAAGTGATATTGCAGAGGTCTGGGGCTGTACATGGCAGGGGCTTGGTGAGCTTTG TACATGGG[G/A]CTGGGAGACAAAGGAGCCTCCAGGTGGAAGGGTATTTTTTAATAAAAAATAA TGGAGCTACAACCAACCCCC
WI-18535	107	G A ---			GTAATAAAGTTTTATTGGCACAGCCACGCTCGTTCAATCATATGCCATTGACATCTGCTGTTGCCCT ACACAGCAGGTGGGACCTGCTCTTCACGGGAGAGTA[G/A]TTGTTTAAAGCAGTGGTCCCAAC CTTCTGTGTCCTCCCGTG
D17525	107	C T ---			AGAGTGGTGCAGAACACAGGCCGAATCCAGGCTCTATCACTTACTAGTTTTCAGTTCTGGCAGGTGAC TTCATCTCTTCGAACTTCAGTTCTTCATAGATGGAAG[C/T]GCTATACCTTACCTACCTCGTAAAA GTCTGATGAGGAAAAAGATTAACTAATAGATGCATAGCACTTAACAGAGTGATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAGGTGATGTGTCTACCAAGGCAGACGAAG



DWU-133c	313	A G ---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGTCATGACTTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTGACAGAAATTTTGTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTGTTAAATGAATATGTCAGTTTTTGAATTTAATAGTAACCTC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236	T C ---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGTCATGACTTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTGACAGAAATTTTGTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTGTTAAATGAATATGTCAGTTTTTGAATTTAATAGTAACCTC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199	C T ---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGTCATGACTTTTTTATGTGTTACCATCCT TTAATAGATCTCATACACCAGAATTCAGATCATGAATGACTGACAGAAATTTTGTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTGTTAAATGAATATGTCAGTTTTTGAATTTAATAGTAACCTC TCCCAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102	C T ---	---	ATGAGATCCTTTAAATCCTTCCATGAAACGTTTGTGTGGTGGCACCTCCTACGTCAACATGAAGTG TGTTTCCTTCAGTGCATCTGGGAAGATTCTACQ[C/T]GACCACAGTTCCTCAGCTTCCATTTCGCC CCTCATTTATCCCTCAACCCCGCAGGTTTATACAGCTCAGCTTTTGTCTTTCTGAGGAG AAACAAATAAGACCATAAAGGGAAAGGATTTCATGTGGAATATAAAGAT
DWU-387	169	G T ---	---	GTGTATAAATGCAACTGTTGATTTCCTCAACATGGCTCACAAATTTCTATCCCAATCTTTCTGAA GATGAAGAGTTTAGTTTTAAACTGCACCTGCCCAACAGTTCACCTCATATATAAAGCATTATTTTA CTCTTTTGAGGTGAATATAATTTATATTACAATG[G/T]AAAAGCTTCTTTAATACTAAGTATTTTCA GGTCTTCACCAAGTATCAAAGTAATAACACAAATGAAGTGCATTATTCAA
DWU-447b	172	--- ---	---	ATTTTAGTGTCTTTGCGTTAAAAATCATTGCAAAAGTATTCTGAACGTGCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAAATTAATTAGTTTGAATAGCAGCACAAGCTTAGCTAATCAA CCATTATTTTCAATTTGTTGTTCTAAGAGGATTGANAATCAGTTAGTTTAAATGTCTTCTGTAG GCCCTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-447	85	A G ---	---	ATTTTAGTGTCTTTGCGTTAAAAATCATTGCAAAAGTATTCTGAACGTGCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAA[G/AT]CACTGTAAATTAATTAGTTTGAATAGCAGCACAAGCTTAGCTAAT CAACCAATATTTTCAATTTGTTGTTCTAAGAGGATTGANAATCAGTTAGTTTAAATGTCTTCTG TAGGCCCTTCTTCTTACAATGAAGAGATGATTCTTCTAGTTTATGGTTA
DWU-476	63	C G ---	---	GTAAATTCAGTTTTTTCCAGTTCCTCTTTTGTGCTGCTCTCAATAGCGTTTAAAGTGAG[C/G]AT AAATCACTGTCCATCAGGTGAGGTGTGCTCCATACCCAGCGGTCTTCAATGAGTAGTGGCTATGCA GGAGCTTCTGGGAGATTTTTT



DWU-505	67 A T ---	---	---	TCATACTAGGGCAGTATCTCCTCTAGCTAGTGCCCATACAGAAAATTTCTATCACCATACAAAATTTA  A/TJTGCAAGTATTTATGTTTTAAAGCACAGGTGTACCGAAAAGTGTGAAGTCTGAATTTATGGGTT CTATGCATGCATTTTGCCTAACCTAGAGAAAGAGTTTGATAAAATTTTACCAGCTTTGAAGATGGAT TAACTTTGTACITTGAGCTTTAACTTTTAA
DWU-512	131 A G ---	---	---	AAAATCCAGGCAITTCGAATCTGTTTTTCATGATTTATAGAGGGTTTACACAAAAGTGCCACTTATTAA AGAGCTTCCACAGTGAAGATGGAGAAAGGTGAAGTCTGTTTGAATATCCAGATGTTTGGTC A/G  TGCGTATGGCAGTGAGCAGGTATGTTTCTTTGCTTGCACTGAAAATTAATTTGCTATCAAGAGC AACTATGAACGGTTTTTATTCAGATGCTCCAGAGTGAAGATGCCGAG
DWU-525	97 A C ---	---	---	AACGTCATATAGATAAATATCCAGGATGTGTGGCTCAITTTTTCAGCTTGTCTATCTACTGTTTGT ATATACAGTTTTTGTAAACATATGATTGA A/C AAGAAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAATAACATATTTCTTGTCTTTCACAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAATCTCTAAATTTCTAGTCTCTGATTGC
DWU-59	94 C T ---	---	---	CATTTCTTTGTAAAGGTAAATGGACTCACAAAGGGGAAGAACATGCTGAGATGGAAGTCTACCGG CCCTTTCTTTGTGAACGTACATGGC C/T GAGCCGTGTTCAAGTCCCAGGTGGCAGACTCGTTTTTG GTAGTTTGTTTTAACTTCCAAGTGTGTTTACTTCTGATGACCGGTGATTTTCCCTCCTAGCAGACATG CCACACCGGGTAAGAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68 C ---	---	---	CTTGATCATGGGTGGAAATTTTGTGATCTGGGCTTCAGGATGCATAAAATTTTCCAGTTGGTAAG CAGCAGGTGCCGAGGCTGGATCAGAAAAAAGGCA
WI-19856b	63 C T ---	---	---	CACACTGGCATCTAGGCCCTTCGCCTGCATTGCAGAGGAGAGCCAGGTCCCTCTGGAGAA C/T G  CTGCGTTCCCGAGCCCCACACCGGCTTTGCACCACACAGGCTGTTAGGCGAGGAGGTGGTGAAGACGT AGCTGTAGACCCAAAGCAACCAAGCCCTGGGACCTCGGGAGAGGAGCCTTTTAGAACATGGAA AAGTGTGGTCATCCCATCAATTAGACAAGACACATCCTACATAATAAAAAAGT
WI-18014	40 A G ---	---	---	TCCATTTACATTTGGTGGCATTTTGTGAATAGCTACAGAA A/G GAATGAAAGTGCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTTCTCAAGGGCAAGTGGCTTCT A
WI-18036b	97 T A ---	---	---	TTCCAATGTAAGAGTCAAGTACCAAGTTAACTTCTAGAAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTTAACTCTTTCATAA T/A CTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27 T C ---	---	---	TTCCAATGTAAGAGTCAAGTACCAAGTT C JAAACTTCTAGAAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTTAACTCTTTCATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72 C T ---	---	---	TGTAAGGTGACTTCTATAAGCTTCCCTAAAGTGTCAAACTTTCATTTTACTGAGATTTATTCAGGCCAAT GTGTC T J GTGGGTCTGAGATTGATTATCAGCTGGGTAAAGTTAACTGTCTCTGTTTCA



WI-18063	105	G A ---	---	AGGCTTTAACTGATAACAAATTTGCCCTTTAATCACATACAAAAAAGCTGACACTTTTCATTCCTTCCTTC CCATGTTTTCTGATTTGATGTAACCTTAAATTTTGATCTCTTTAACAATATACTGAGCTGCA
WI-18078	86	A T ---	---	AGTTGAAAGATCAGAGAGGTTATGTTGGTAGTAGCTGAACATCAGATTCAAAACCTGGTCCAGTGTG TTGTTTTTTCAGCATCAGATGTCCTCACTAGCCAAGTTGATCTCTGCAGTATCTACATGTGGT
WI-18091	90	T C ---	---	CCAAAGCTCACTCAGTATTTAATCATCTGCTAATTCATCCTTTTAAATCCATCAGACACTGTGGT TTTCATCTCTAGAAGTTTGACTTTGCGGCCCTTTTATACCTTCCATATCTCAACTTGTAAAGC
WI-18119	38	T C ---	---	GCAATCTGTAAACAGTTTGGTAGTGGTATTACAGAGGAT/CJTTGTAAAATGGATTGGAGTACTTAC CACTATTTTCATCTGCTCTGAAATAGTTCACTAACCAACTACTGACAACAGTTTAAATTTGGTCTT
WI-18142	66	T G ---	---	TTCAAGATAATTACAAATGGAAAGGGGACCAATAATTCACCTTTTAAATCGAAAAATAATCTATATAC T/GJCCCAATAAACTCACAGTAAAAAAGCTTCAAAAAAGCCTTAAGACACCAAAAAAGAGGAAAA
WI-18178	68	T C ---	---	GCATAGGGTTGAGGGGTGTACAAGAGGAGGAACCAAGATTCACTGCTCCATGCCTGGAGGTAGTCTGGGG GT/CJCGGCGGGATGGACACACAGACAGACATAGATCTGGCATCTGATAGCAGGGCATACAG
WI-18244	35	G T ---	---	TCAATCTGAAACTTGTGTAGCCAGCATGGGTG/JGGGGAGGTGATTATGGCTGGGGAAGATG GGCACTCACCGACAGCAGCATCTAGCACCACAGTGACAGGGACGTTGAGGTGGCAGAGGGCTTT
WI-18245	115	G A ---	---	ACAGATGTCAGTTGTTGAATTGGCCCATTAAGATATGGGCTTTTCTGTTAAAAAGTCAATCCAAA AGGCTTGGCAAGAGTTTGTATACAACGGAGGACAGAGAAACATGA/GA/CTGGGGAGTAGGCTCT GACAGAAGGTGGGCTGTC
WI-18261	26	G A ---	---	GATTTGAAGGGATTGCTTTTATTAACTG/GA/JTGAAGGCGTGATAGAGGAACTGTTTAAAGATAAACAA CTTATAAATACTCCCAATTGTAGAAGTGAAGATTG
WI-18268	88	C T ---	---	TAGGAGGGAAAGGAGGTGGCTGCTGGCCCTCAAGACATGAGAAACGGGTGGTGGCTTCCAAAGC TTCTTACTTCCCCCATAGATC/TJCTGACAAATGTCTGCAGAAAGCCTCCAAACCTGGAAC
WI-18299f	107	C A ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCAATTAACCTGGTTTGCCAAATTTTT ATCTATTTGGGTCTGAGAATTCACAAATTTGA/GAATTCCTTTTGCCAAATTAATGACATATTCG CAG
WI-18299e	101	A G ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCAATTAACCTGGTTTGCCAAATTTTT ATCTATTTG/GA/GTCTGAGAATTCACAAATTTGAAGAATTCCTTTTGCCAAATTAATGACATATTCG CAG
WI-18299d	77	G A ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCAATTAACCTGGTTTGCCAAATTTTT T/GJATCTATTTGGGTCTGAGAATTCACAAATTTGAAGAATTCCTTTTGCCAAATTAATGACATATTCG CAG
WI-18299c	67	T G ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCAATTAACCTGGTTTGCCAAATTTTT T/GJATCTATTTGGGTCTGAGAATTCACAAATTTGAAGAATTCCTTTTGCCAAATTAATGACATATTCG CAG



WI-18299b	52 G A ---	---	TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCAATTAACTTG[G/A]TTTGCCAAATTTTATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAATCTTTTGCCAAATATTGACATATTCTGCAG
WI-18299a	48 C T ---	---	TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCAATTAACTTG[G/A]TTTGCCAAATTTTATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAATCTTTTGCCAAATATTGACATATTCTGCAG
WI-18307	76 G A ---	---	TCAACTTGTAACCAAGTTAGCAGCAAGAGGATAGTCTCCTTAGAGACTTTTCAGTGGACTTAAACTCAGTTCCGCTG[G/A]TGCTATGTAAAGCATCCACGATGGTTTATTGTAATCTGCAATCTGCTTGGTCAC
WI-18324	72 C T ---	---	TTTGGTATGAATCTTTCTCTGACATTTACCAATCATCACTTAACTCCGGGGGGTGGGTACTGATTATC[C/T]TAGATCCAAATAAAGCATGCAGAAAGTG
WI-18350	48 T C ---	---	ATGAAAGTCACCTCAATCATAGGGTCAAGAGAGAAAGAAATGTTTTCAGA[T/C]TAAATCTATGAAAAAGTGTATCTGCTTGCATTTAAGAAACAACAAGTCA
WI-18395	77 G C ---	---	TCTTGACATGATCTGTGAATAACGTGATTGTGGTTGAATTTCTCTGGAAAAATTTGAAGATAAAATTGATTATTCAG[G/C]GTGTCATTGGTTTATACATATCTCTCTCTTCTTAATGCAAGCTATG
WI-18398	62 G T ---	---	TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAAAGAAAAAACAACACTCAAGGGT[G/T]GATAACATTGCCAGTAAACCATATTTCAAAACAAGCAGCAGAAATTTGGAGGATAATTTGTT
			CTCGTTGGTATTCTCTCATCC[C/A]TTCCTTTTTCGCTCTTTCTAAATTAAGAAAAAGCAATGGAATT
WI-18396	21 C A ---	---	TAAAGATCATCTAAGAAATAAGAACTTACATATGTAACTTTAACTTATCAACTTGACAAAGTCAATGAAAA
WI-18409a	20 C A ---	---	AAGATGGGAAAGAGGAAATC[C/A]TTTTTCTTACTAGAGATTTTTTCCCTTTAATCCTTTTCAATTCAAAGGATCATCAAGGAGCAGGTGCAGAGCTCTGGGCCCCAGAGCCCCCAAGTGCTA
WI-18442	62 C T ---	---	AAAAAGGAAAGAAAGGATGGAGTAAGAGAGAGAGACAGAGAGGAAACAAAAATAGTTTCTGG[C/T]TTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAGGGGAAACACAAGAGAAAAAAGGTTTATAGGTGGGAGAGAGGA
WI-18452	38 G A ---	---	TTGATGTTAATACTGTCATTCTGGAGATCGGCTAAAAT[G/A]AAGCATAGTTATTATTAGCTTTGGTATATTCTGCGACAGATTTAAACAAGTAAGACATATATCAACCTCATATTTTCCAACCA
WI-18489	102 A C ---	---	ATATAAGCTGGAGACTGTGGAGGGTGAGAGGCAGTGGGACTAGCTGTTGAAAGAGAGAAATGTAGCAGTAGTAAAGATGAAGACTGCAAGGATTCAAAAC[A/C]GGTTATGGCAATAGAGGTGAAAAAGAAAGGCCATATAAA
EST5b	93 A ---	---	CTGGTGGGAGGAAACAAATTTGTGGTATATTATACAAATGAAAAACTCTTCAGAAATAAGAAAGGAAACAACCACTGAATCACACAACATGGACAAATCTCAAAATCATTTATGCTGATGGAAAGAAACCACTTCA



EST5	93 A ---	---	CTGGTGGGAGGAAACAAATTGGGTATATTCATACAAATGGAAAACTCTTCAGAAATAAGAAGGAA CAAAACCACTGAATCACACAACTGGACAAATCTCAAATCATTATGCTGATGGAAAGAAACCAATTCA TAAGAATACACAGTACAT
EST6	48 C ---	---	TTAGCTACTTTTCAGAAATTGAAGGAGAAAAATGCATTATGTGGACTGAACCCGACTTTTCTAAAGCTCT GAACAAGCTTTTCTTTCTTTTGAACAAGACAAAGCAAGCCACATTTTGCAATTAGACAGAT
EST8	158 A ---	---	GGACAGGACCTCTATCCCGCTGGTGCAGCAGCGGCTGATGGACTAGGCCGCCAGGGATACTGGGCC CTCTCTCAGGGGGCTCTCCAGGACCCAGAGCTGTTCCTGCTTTGAGTTCCCTAGAGCTGTGCGGCCA GATAGCTGTTCTGAGTTGCAAGCAGGATGGAGATTTGGACACTGTGTGCTTTGGTGGGGT
WI- 18740c	104 GT ---	---	TCCTCAATTGTTGGGGATGATGAGAAGAAATGATTTGGGAAAAATTAAGTAACAACGACCTAGAAAAAGT GAGAACAACTCTCAATTTACCATCATGTATCCAGTAGTG[G/TAATAATTCATTTTATGATGGCTTCTATTTT TGGCCA
WI- 18740b	96 CG ---	---	TCCTCAATTGTTGGGGATGATGAGAAGAAATGATTTGGGAAAAATTAAGTAACAACGACCTAGAAAAAGT GAGAACAACTCTCAATTTACCATCATGTATC[G/G]AGTAGTGGATAATTCATTTTATGATGGCTTCTATTTT TGGCCA
WI- 18985a	105 CT ---	---	CCAAAGTCTCTGTTGGCTCATAAAGAGTTTGGGATGGGAGAGAAATCCAGACCATCTTGGGGCA GCCAGGCCCTGGCTTCAATTTACAGAGGTAGACAA[C/T]TGATTCCAAACAAACCCCTTCCCC TTTTAAATGATTTCTGTTCTAATGCCATAGATCAAGGCCTCAGAAACCATTTGTGTGTTTCTCTT TGAAGCAATGACAAGCACATTTACTTTACGGGTGTTTTGTTTTTCTTAT
WI-18746	114 GA ---	---	GCCAGCAGCTGAAGTCTTTTCTCTCTCGGCTGGAAGAACATCAAGATACCTTTGCGTGGATCA AGCTTGCTACTTGACCGTTTTTATATTACTTTTGTAATATTCTT[G/A]TCCACATTCTACTTCAGCT TTGGATGTGGTTACCG
WI-19112j	212 GA ---	---	CCGTGTTACACACACACAATGGCAAGCATAGTCGCTGGTTACGGCCCGGGGAATATGCCAAGG GACCCCTTAATGGAAACACAGATCAGTAGTGTCTATCTCATGACAAACCACAAAGAACCCGACGACAA TCTTTGCGAGATTTCTCTAGTGGCTAGAAACATGGCTTTAAGAAACACGGTGATATCTTTGAG GGTGACAAGGC[G/A]TCTCTTCAACAGTTCATACCAACTGCTTTGCTCTAG
WI-19092	232 AC ---	---	TGGTGGCTGGCTAGTGTCTACAGAACATAATTTGCCTCTATAGAAGGCTATTCTTAGATCATGT CTCAATGGAAACACTCTTCTTTCTAGCCTTACCTGATCTGCTTATATAAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGCTGAAATTTTCATCTTGAATGCTTTGATTAAACTGAAATTTTC TTTTAAGCTAACAAAGATCAATAATTTT[C/A/C]ATGATTAGCCGTGTAAC
WI-19057i	175 GA ---	---	CCCATTTATTATAGGCCAGTGTCTCAAGAGTAGAGGCGCTACTGGTCTTTCAACTCCTTCA GTCTTCTGACGGGACTTTACCGTGACAGCGGAAGTGTATTGACGTCCAGGACCCGACGCACTG TCTTCATGCAGGAACCAAGTGCCAGATCCCCACAGCTC[G/A]TCTCTTCTTCTGTTTGGTTTGGCCACA



WI-20103	168 C T ---	---	TGGGACITCCAACTCAGAGGATGTGGGAATCCAGCTCAAATGATACAGGATAAACTGGGCT AGGATGGACAGGCTGTGGATATGGGAGTCATGGGTCAAAGTCTATCCAGATGGCTCCAGGTACAG TGGGCTTCCTGGGCTGGAAGCTGGTCTCTCCCA/C/TTTCATCTGCTCAAAGCTTCTTGAAGGAGC TGGTTTGACTTCAACTTGCTAGAGCCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111 G A ---	---	GCCTTACCCATTTGCACATATATACATATGCACACCTTTGCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAAATCTTGTAAAGGACAAGAAATGGA[G/A]TTGAATAAGTACCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTCACATACATCAGAGGCAAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116 A G ---	---	TGGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAAGAACGT TTTAGTCTTTTAAACTGAGTTTAAAAAAAATAACAATGCAATTTT[A/G]ACACTGTTTTGAAA ACTTAAAGTGCAGCAATA
WI-20613c	165 A G ---	---	GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAATGGCATGGGAGGAGGCAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAGTTGGA[A/G]AAAGGGAGTTTCCACGAGCCAGTGGTGAGC TGC
WI-20613b	156 A C ---	---	GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAATGGCATGGGAGGAGGCAGTTAGAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATA[A/C]AGTTGGA[A/G]AAAGGGAGTTTCCACGAGCCAGTGGTGAGC TGC
WI-19984	47 A G ---	---	CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAAAT[A/G]TATAACATTAGAAAA GCAAAATTTCTTTAACTTAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTCCACACTGGAATGAAGGCAGTTTCCAAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135 T C ---	---	GCCAGTTGGAATATGGCCTATACGAACCAAGAGTGTATACAAAATGGAAGTGGTCATCAGGCAATA ATTGTTTCTTGGAACTCTGCACCGACTGTCCATGCTCTGTGGGACTTACACATTCAAGTTTGACAG[ T/C]TGAAAAACCAACTGGAGCTGCTTTCCAAGAATGTTCTGTCTTCAATAGGAATCCATG TTATTCTTTCTTGGCTTAAGCTCTTATATCTTTCAAATGACCTAAGCTGA
WI-18846a	49 G A ---	---	GAGTGCCATACCTTCTCCAGGCTCTGCCCAAGAGCAGGAGGTGCCT[G/A]AAGCTGGGAGCGT GGGCTCAGCAGGGCTGGTCACCTCCCATCCCGTAAGACCTCCTTCCCTCCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123 G A ---	---	AGCAGTGGCCTTATTGCATCCCAACACAGCCTCTTGACCAGGCTGCCTCCCTTGTGGCAGCAACGGC ACAGCTAATTTCTACTCACAGTGCTTTTAAAGTGAATGGTCGAGAAAGAGGCACC[G/A]GGAAGCCG TCCTGGCGCTGGCAGTCGCTGGGACGGGATGTTCTGGCTGTTTGAATTTCTCAAAGGAGCGAGCAT GTCGTGGACACACAGACTATTTTAGATTTCTTTTGGCCTTTTGCAACC



WI-20146	31 T C ---				---	TGAGTCTCTGTAAATTCATTGAGCAGTTAGC/T/CJCATTTTGAGATAAAGTCAAAATGCCAAACACTAGCTCTGTATTAAATCCCATCATTACTGGTAAAGCCTCATTTGAAATGTGTAATTCATACAGGC
WI-18922	74 G A ---				---	TAGGAATTGGTTTCACGCCCTGAGGCAATTAGACACTTTGGAAGATGGCATAACCTGTCTCACCTGGACTTAAGC/GAJTCTGGCTCTAATTCACAGTCTCTTTCTCCTCACTGTATCCAGGTTCCCTCCACAGAGAGCCACCAAGTTCTC
WI-18763b	53 A G ---				---	TTCTGTGTTGTGGGTCAACCGTACAATGGTGTGGGA/GJTGACGATGATGTGAJ/GJATTTAGAAATGTACCATAATTTTGTAAATTTATTTATGTTTTCTAAACAAAATTTATCGTATAGGTTGATGAAACGTCA TGTGTTTTGCCAA
WI-18763a	38 A G ---				---	TTCTGTGTTGTGGGTCAACCGTACAATGGTGTGGGA/GJTGACGATGATGTGAATTTTAGAATGTACCATAATTTTGTAAATTTATTTATGTTTTCTAAACAAAATTTATCGTATAGGTTGATGAAACGTCA TGTGTTTTGCCAA
WI-18771b	75 G A ---				---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAGAAGATGTTGGG AACAGAA/GJ/AAATAAAGTGAAGTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18771a	57 A G ---				---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAGJ/GJAGATGTTGGGAACAGAGAAATAAAGTGAAGTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18820	70 T C ---				---	GGGAAAAATTGAGACGCAATACCAATCTTAGGATTTTGGCTTGGTGTGTTGTATGAAATTTCTGAGGCCT/CJTGATTTAAATCTTTCATTGATTTGATTTCCCTTTTAGGTATATTGCGCTAAGTGAAACTTGTCA
WI-18742b	51 C T ---				---	ACAAAGTCTGTAGCCCCCTCACCTTTCCCTGTTTTCACATTTTGCCAATGTAC/JATCGGGTTTGGTTTTCTTGATTTAATAACGGTTGTGGTTTCCCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA GTTTTACC
WI-18882	94 C T ---				---	GTGTGTCCAAAAATGGGGTCTGCTCCTGCTACCTTGACCCCTTCCCTTTCCCTGCTCTCTCTCATCA TCATTCCCAACAACATCCTCTGCCA/C/JACACAACAACGTAAGTTTCATTTGGGCAAAAATTGA GC
WI-19970b	167 G A ---				---	TATAAGCCCGAGTCACCAAGGAGCGGCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCTGCCACCGGGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCCGTTCCCTGCCAGTTCTCACTGCGGGGAGC AGCAAGGCCCTTCTCACTGGTTGGTCAAAG/GJ/ATGTCACCTTGGCCTGGTGCATCCACAGAGGA TGTGTCAAACCCAGAAATCTTTTAAACGACTGACCTTCTTAAAAACAGA
WI-19970a	126 T C ---				---	TATAAGCCCGAGTCACCAAGGAGCGGCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCTGCCACCGGGCCCCGGCAGTGCAGTCCAGCGGGGAGGAGGCTGCCCGTTCCCTGCCAGTTCTCACTGCGGGG ACCAGCAAAGGCCCTTCTCACTGGTTGGTCAAAGGTAGTCACCTTGGCCTGGTGCATCCACAGAGGAT GTTGTCAAACCCAGAAATCTTTTAAACGACTGACCTTCTTAAAAACAGA



WI-19067d	202 T G ---	---	TATTGCTGTGTCAGTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTCCCAAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGTCCTGGAGAAATGTTGTAGGGGTTATTTTTTTTAAATAGTGTTCATAAAGAAAT/ GJACATAGTATCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067c	153 G C ---	---	TATTGCTGTGTCAGTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTCCCAAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGTCCTG/CJAGAATGTTGTAGGGGTTATTTTTTTTAAATAGTGTTCATAAAGAA ATACATAGTATCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067b	151 T C ---	---	TATTGCTGTGTCAGTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGC ACATTCCTCTGCTCCCAAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGTCCT/CJGGAGAATGTTGTAGGGGTTATTTTTTTTAAATAGTGTTCATAAAGAA ATACATAGTATCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067a	57 C G ---	---	TATTGCTGTGTCAGTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCCTCC/CJGJTGCTG TGCACATTCCTCTGCTCCCAAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTT CTCTGGGCTCTAGGTCCTGGAGAATGTTGTAGGGGTTATTTTTTTTAAATAGTGTTCATAAAGAA ATACATAGTATCTTCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19106	247 T C ---	---	TAAATCCAGCCCTACCTGTTAGTTATTTTAGGAGACAGTCTCAAGCAGTCAAGGCTGCTGCTAATTC AATTTATGGGGTATAGTGGCCAAATAGCACATCTCCACGTTAAAGACAGTGGATCATGAAAGT GCTGTTTGTCTTTGAGAAAGAAATAATGTTTGGAGCAGAGTAAATAAGGCTCCTTCATGTGGC GTATTGGCCATAGCCTATAATTGGTTAGAACCTCCTATTTAAAT/CJ/JGG
WI-18944	147 A G ---	---	CAAGGCAAAATATCAGGAGCTTTTACACACCTACTAAAGGTTATTTATGTAGCTGAAACAAA AATGCCAGAGGATAATATTGATTCCTCACATCTTTACCTAGTATTTACCTAGCATTTCAAACCCC AATGGCTAGAAC/CJ/GJGTTTAAATTAATTTCACAATATAAAGTTCTACAGTTAATTATGTGCATA TTAAACAATGGCCTGGTTCAATTTCTTCTTCCCTTAATAAATTTAAGTTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATTGGATGTTTTCATAATACATAAA GTTCTCTGTAATTACAACATAATTAATGCTCTCTCAGAGTCAAGGAACTGGGTGGTTTGGT TTTTGTTGCTTTTAAATTTATGTCCTCATGTTGGGATGAGTTTAAATGCCACAAGACATAATTTA AAATAAATAAATTTGGGAAAGGTAA[G/A]ACAGTAGCCCCATCACAT
WI-18932d	177 C T ---	---	CACACCTCATGCTAGCCTACGAAACTGGAATAAGCCTTCGAAAGAAATGCTCTGAAGCTTGT TCTGATATCAGCACTGGATTGAGAACTTGTGCTGATTTGACCTTGTATTCAAGTTAACTGTTCCC CTTGGTATTTGTTTAAATCCCTGTACATATCTTTGAGTTCAAC/CJ/CTTTAGTACGTGTGGCTTGGTCA CTTCGTGGCTGAGGTAAGAACGTGCTTGTGGGAAGACAGTCTGTGGCTTG



WI-19042	193 A C ---	---	---	TTTGTCAAGTGTGCCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGAAGTTTGGAGATAGATG GATAAGGGAATATAGGCCACAGAGGTGAACCTTTGTGCTTCAAGGACATTTGGTGAAGTCCCAACAG ACACAAATTTACTGCGACAGAACTCAGCAATTTGTAATATGTAATAACTCTAACCA/CJGGCTG TGTTAGATTGTATTAACATATCTCTTTGGACTTCTGAAGAGACCACCTCAAT
WI-18984	208 A C ---	---	---	ATTGGCCCTGTACAGTTTGTCTATTATAAAATTCATTAACACACTACAGGTGTGAATGGTTAAAA TGAGGCCCTCCAGTTTCATTTTCAGTTATTTCTGAGTGTGACAGACTATTTCGCACGTGATTAAT GTAACCTATTATAATGAATCAGAAGCAGTAGACAGATGTTGGTGCAATACAAATATTGTGATGCATT TATCTT/JA/JATAAAATGCTAAATGTCAATTTATCACTGCGCATGTTTGACT
WI-18851	90 T A ---	---	---	GCTTCAATGGCGATTGATTCAGTGCCCAACATGTAAACAGGTTGGTAGTTGTTACTCATTTTGAAT ATACCTTTTCCCTATTGTATTCT/JA/JATAATATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76 T C ---	---	---	TCAACTGAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT/CJ/JGGGGTAGCCATTGTGCAGTCATGGCCCCGGGGAACCTTGCCAAACCTTCGTGTGAG GTGCTGTGT
WI-18821a	69 C T ---	---	---	TCAACTGCAAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A/C/JAGAGGCTGGGGTAGCCATTGTGCAGTCATGGCCCCGGGGAACCTTGCCAAACCTTCGTGTGAG GTGCTGTGT
WI-19021a	20 C G ---	---	---	ACTCCTCTGCTGTCCATC/GJ/ACTGTCTCTTTTGAACACAGGAAAGTCACAGAGTTTAAAGAGAA GCAAAATTAACATCCTGAATCGGGAACAAAGGTTTATCTAATAAAGTGTCTCTTCCATCACGTTG CTACCTTACCACACTTCCCTCTGATTTGCGTGAGGACGTGGCATCTCTACTACGTACGTGGCATAAC ACATCGTGTAGCCCATGTATGCTGGGGTAGAGCAAGTAGCCCTCCCTGTC
WI-18908	70 G C ---	---	---	TGGAAATCCCTTCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTA TGG/GC/JTTAGGGAACATTCATCCTTGAGTCAAAAAATCTCAATTCCTCCCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---	---	---	CACGGTCTCTGCATCGTTACCAGAGCGCCTTCTGGTCTAGCCACGCCCTGTATGACCGCGCAATA TCCCCAAAGCTTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGTGTCATTTTCTGGAGAGGGTG OCTCCCTTACGAACACA/JA/JAAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGAGCCA GTGCAGGCACTGGGGGTGGAAGTGTGTGACACAGTGAATGGGAGGTGG
WI-19037a	47 C A ---	---	---	CACGGTCTCTGCATCGTTACCAGAGCGCCTTCTGGTCTAGCCACG/CJ/ACTGTATGACCGCGCA ATATCCCCAAAGCTTTTGGGTCTCAAGTCATGCCGAATTTAGATGCTGTGTCATTTTCTGGAGAGGG GTCCCCCTCCCTTACGAACACA/JA/JAAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGAGCCA GTGCAGGCACTGGGGGTGGAAGTGTGTGACACAGTGAATGGGAGGTGG
WI-19064	66 T C ---	---	---	TTGAGGAGGTGGGGTGAAGTGTGCTTGGCAGGGATTTGTGACACTGCAATGCTGGGCTGTGTTCC/T/ CJGGGCTCTTCTGGACCTTGACCGTGGATACAGGCCATGTGCCATGTTTGGGTCTCTGGGAGGG TGGGTGAATAAAGGC



WI-18972a	112 A G ---	---	AGGCCTGTGGCTTATGTCACCCACAGAGGGGTCTGAGAAGTCTGGCTGGCTGGATGCCCTGCCC CCCTCCTGGAAGGCTCTGCAGAGTGAAGTGGCTGGGAGGAGCAGAGTGGCTTGTCTGGCCATGGAGCC TCATTGCAAGTGTCTTGAACACCTGAGGCTTCTGTGGCCACAGGCACTACGGCTTCTCTCC AGAIGCTTTGGCTGAGCACAGACAGTCAGCATGGAATGCTCTTGGCCA
WI-19016b	184 C A ---	---	GTTTGAAACCAACATGTGCTCTTTTCAGTCATTCACTGTTTAAATATGACATGGTAGAGAAGATAAG GTTATGGCAGGTAAATTTTGTAAATGTGATTTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGACTGTATACAGAGGTTCACTCTCAA[C/A]CTCAACACTATTGAC TTTTGGGCTGGATAGTTCTCTGTTGGGGGTTTGTCTGTGCACTGTAG
WI-19016a	161 C T ---	---	GTTTGAAACCAACATGTGCTCTTTTCAGTCATTCACTGTTTAAATATGACATGGTAGAGAAGATAAG GTTATGGCAGGTAAATTTTGTAAATGTGATTTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCG[C/T]GTATACAGAGGTTCACTCTCAACCTCAACACTATTGAC TTTTGGGCTGGATAGTTCTCTGTTGGGGGTTTGTCTGTGCACTGTAG
WI-20096	21 T C ---	---	GGTTTGGGGCAATTTATTTCT[C/G]ATAGAGACTGGCACAAGCTTTGGGCTAAGGACACCCGCCCCC ACCTCATCTAGAAACAATCTCTCTGCCAGACTTG
WI-19591b	156 C A ---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAATATAAGTAACCTCAAGCCATG AGTAAAGATTAAAGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTGCC CTTAGGGTGGGAGCTCTTCC[C/A]CTACCCTCCACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACTTCTTACACGG
WI-19591a	45 T A ---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAATATAAGTAACCTCAAGC CATGATATAAGATTAAAGCAGTTACTTTATTTGAACAAGGAAGTGGCATAAGCAACTCAGTGTG GCCCTTAGGGTGGGAGCTCTTCCCTACCCTACCCTCCCAAGGCATCATTTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTTATCTAGGGATTGCACTTCTTACACGG
WI-20310	125 G A ---	---	TCCTCAGCTCTGTCATCCTTGTCTTGGGGTCTGTGTTACGGCCCTCCAGGCATGGTTTCTTCAT TTAGGTAGGAACAAAGGCCAAAGAACATACAGCCAGCTCTCTAGAGGCTCCA[G/A]TCAGAA CTGGACCTTTAACTACAAGGAATCTTGGATGAATTTTTCAGGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTTCTCCCAATGTCTCCCGGGGG
WI-20860	224 G A ---	---	CTCTCCCTAAGGAGCCTTGGCCTTGCAGCCCCATTACGAGGGATGGAAGTCACAAGACAATGAGT GGAGCCTCATGCCCTCCCATGAGGAAGCCCTTAGTATTGCTGACATGCCCCCTTATCCTGCTCTCT CCCCAGTGTGTACACTTGGGCAAGCAGAGTGTGGGCAACCCAGCCTTGAGAGCTCTTGTAGACC GGAAGGAAGGGGGCTCATT[G/A]GGTGTATGGCTTCTGGCTCTCTGGCTT
WI-19359a	39 T C ---	---	GACGTGGACAAAGGAGGTTTAAATGAATACCTTGTGTTTGT[C/G]CATGTTCAAAAAAGAGTATTAAT ATTTTGTGACTGCATCTGTGAATGAAGACACTCAAAAAGCCATGTTTCCAACTTAGGTTAATAATAA GGCTATTTGTCCACCCACTCTCGGGCATTGCTGCAATATCTCTGGCCTCAAGTGGGAGGCCACGTG GGAACAAGGCCCTCAGAAAAACAAGGACATGCAGCCTCCCTGAGCCAGTTCTCT



WI-19766b	93 A ---	---		TGGCCTCAATGACTGGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTCTGTGGTGGGCAGGCAGG AGATGAACCATAGGAGCCAAAGTC(A/G)GACAAAGAGGACACACCAAGCCTGAAACCCCTC CGGACAACAGCAGAGTACCAGCTGAGGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTC ACCTCCTTCAACCCTCCTCTACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---	---		TGGCCTCAATGACTGGTACATTGGAGAAGCTG(A/T)GAGCAGCATCCTTTCTGTGGTGGGCAGGGC AGGAGATGAACCATAGGAGCCAAAGTCAGACAAACAGAAAGGACACCAAGCCTGAAACCCCTC CGGACAACAGCAGAGTACCAGCTGAGGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTC ACCTCCTTCAACCCTCCTCTACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---	---		CTCCTCTGTTGGCTTGCATTGTGCGATTGGAAAAACCATTTGGAAGAGGGACTTTCCTGCAA AACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGAGCCCTTGA(TG/C)GAAAGC TTAGAAAGGAAGTAAATTGCTTCTTTGAATATGGATTTAGGGCGGGCGTGGTGGGCTCAGGCCT TATTAATCCAGGCACGTTGGGAGGGCCAAACGCGGGTGGGATCACTGA
WI-20512c	59 T G ---	---		CTCCTCTGTTGGCTTGCATTGTGCGATTGGAAAAACCATTTGGAAGAGGGACTT(G/T)CCTG CAAAACCTTAAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGAGCCCTTGA(TG/C)GAAAGC TTAGAAAGGAAGTAAATTGCTTCTTTGAATATGGATTTAGGGCGGGCGTGGTGGGCTCAGGCCT TATTAATCCAGGCACGTTGGGAGGGCCAAACGCGGGTGGGATCACTGA
WI-19599	230 C G ---	---		GGGCTTAAATTCCTCTGTTGGGACTGGTCTCCAGTTTACAGAAAGGATCGCACCCCTTTTCC ATAACCCCTTCTACATTGGAAGAGGCACACCTTGTATACAGAAATGGCTCCGTGAAGTCTTTTAAACG GACAAAGGTAATACAGCTAACAAACGTCATGTTGGCTCACACGTAACCAACACCCCTCTTTTCA GAACAGAGAGCGTTAAAGTAAAGGGC(A/C/G)TTCCAAAGAGTAACACTGCTA
WI-20679	82 T C ---	---		TGTTGAAATAAAATTCCTATGGTCTTAATTGAACCTGTATGTTACTTCTTTTAGAATATCCTTTT TTCATTAAATAATT(C/T)CTAAACCACTCTATGTGTTCAACCTTCTGTTTAACTAAGATATGGGT TTTTGGAAGGCCACAAAGTCACAGCTCCATGAAGTGGCGAATTGGTCTTGTTTTGAAAGCTCTC CAGGGTGTTCCTCCAGAAA
WI-19909a	29 T C ---	---		CCAGAAATAAAGCCTGAATATTCCTTCT(C/T)CTTAAAAATATAATTTTCTTCTTGTCTTCCAA GTAAATCTTAAATGAACCTGTTCTAGTCTATTTTAACTAGGCAATTAACACTACCTAGGCGGG TTTTTCTTTTATACCTTGTCTGTACTGTGGAATCAACTAA
WI-20341	221 G C ---	---		TTGAGAGGCTGAGAGAGGCTGTTGAGACATTGTAATAAGTGTCTAGGGCATGAGACATTAGGAAG GCCACAATTATGAGTAATGAAATGTGAGGCTGATGAGAAGCTACTGCTCCCATTTGTTAGCAGGA GGCAGGAAAGTATCTGGGCTCTCTGGCAGCAAGCGTGTGGTAATATTTGGGTGACGTCATGC ATCCCCCATGCATTGGTTT(G/C)ATGTCTCCAGTGAGCTGTTGGGCAAGTCT



WI-20113	60	T C	---	TTCTGGTACATGGTAAAGTGCTCAGTATTACTGAGTGAATGAGCAAAAGACCTGAAATACTGTTCTGGAA AACAGTAAAAGCAAAATTACCCACACAATTAGGAGGAATATTATTTTCAGACATAGGATAATTTAAAACAT CACTCAAATACTGGAGCATGATTCAGCAATAAATCTATTCCATAAACCAAGGTAGATAAATGTGCACA GCTTTAAAATATAGTTAAGTACAGTTGATCCTCGTTATTTCATGGATTCCGTATT
WI-20895	107	G C	---	TGATGGCAAAAGTACAAAGGCTGTGAAAGAACAGAGTAAACAAGAGCAGCGCAGTGCAGCGTGTGGC CACTTCCCACAGGAGCAACACTTGACTTCATTAAAGGCAAAG/CJCTTTACTCTGTTACTTTTCCCTC CCACATAGTTTAAACCAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATAACTGGTACTATAGGCAACAGATGCA
WI-20721	72	T C	---	CCTGCAATCACAAAAGTGGAACTAGTTGATATTTTGAATCATACTTGATTTAACCCACCTTCAGAAA TTCTAT/CJAAAACACTAGCAACTTCCTTTTATCAGA
WI-19415c	161	A G	---	CTGGATTTTAATATTCTGGCCTAAATAACCAATGTAAATCAATAAAATTTGGTCAATATCTCCACCTC ATTCTGTAAACATGTTTTCAGAGATTCCCCTAAGTAAGGTATTGACGACTGAGACTAGTCCGGCAAA GTCATGAGACCCCTTAGCTGATCTCATTA/GJAAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAAGTGTGGACATACAAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103	C T	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGTTGGGTAGCAAGTACGATGGGCCATGCACCTCTG GCGGTGATGAAGAGACTGTTGGTCATGGCGGTGA/CJTGCTCTCTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAAGTCTGCTGCTGTAGAAGCTTCCTC
WI-19348b	98	G A	---	GCTGCTCACTGGTAGCCAGCCAGCTGCAGGATGTTGGGTAGCAAGTACGATGGGCCATGCACCTCTG GCGGTGATGAAGAGACTGTTGGTCATGGC/GJAGTGACGCTCTCTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAAGTCTGCTGCTGTAGAAGCTTCCTC
WI-19635	98	A T	---	ATTAGTTCGTGTTGGCCACATTCAAAGCCATCCACACAAGCTTCTTGTAGGCCATTGTAACACAATG TTAAAAGGTACAGTAAAAATACAGTATTATJATJATCTTATTGTGAGCACGGCTGTGAGGCTCAT GTTGAATGAAGCATCCTTAGGCAGCACGTGACTGCATGCAGATATGTGTCTGCTGAAAGAACTTTGCTTT T
WI-19641a	46	A G	---	TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAGJAGJATTATAGTCTCATGTTT TTAATTTATGAATAACGTCGTGATTCATTGATTTTGTATTTACAGAAGATGTCAGGCTATCTCATTC AGTTATTAAATAATGGATCAGAGTAGTAAGTCAAGAATAAGTGCATAATGTGGTTTAAATTTTAAA AATACTCAGAATGAGGTAGTATTTTAAATTTTAAATTCATCCACCCACTTG
WI-19642b	52	C A	---	ATATAGAGTACCATCCATGGTTTCAAGCATGGCCTGGACACATTATCCCCCT/CJAGGGTAAACCAG GACTATTGCATGAGCATTCITTAATACGTATTTTGATGGACACAAGTTTTCATGCTATTA
WI-19673b	180	C T	---	TCTGCCATGATCACATTGTGATGAAGAACATGATGGTCACTAGTAGGTAACCTTCTGTGTCATTGCTC TACTCTCAGTGAGGTGCTAGTGGATTTACCTACCCCTGCTTTTGCATCACCAGCTGTAATCTAATAGT GAAAAGGCAATGATGCTCAGTATCACTGTGAAAACATTTTTC/CJCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCACAAAAAACACAGCC



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WI-19673a	35	G A ---	---	---	TCGCCATGATCACATTGTGATGAAGAACAATGATG[A]TCACTAGTAGGTAACCTTTCTGTGTCAATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTTACCTACCCCTGCTTTGTCATCACCACCTGTAATCTAAT AGTGAAGGCAAAATGATGTCAGTATCACTGTGAACAATTTTCCCTTGGACAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGCTCAAAAAACACAGCCC
WI-19724	35	A G ---	---	---	TTTATTGGGAAACAAAGGATTGTAATTTGGGTAA[A]GCTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAGCAACACAGAGATTTGGTTTTCTCTT
WI-19307	196	T C ---	---	---	TCCTCTCCCCAACTAGATGGTATTGATCACTCTGCCACAATGGTACCCCTTCAGCAAGAACTG CAAGCCCTCTTGGATTGCTTCATGAGAAATGGTGGCTTGGATGGAGTGACATTCCTTGTCTGT GGTGAACCTGCAAGAAGAAACCAAGCAATGTATCCATAGAGGCCCTTAAAGAGACCCG[T/C]TGG AAATGGCCATGGTCTAATTTGGTGTGAATAAACTAACCTCTTTGGCTG
WI-19269	85	A T ---	---	---	CTTCCCTCATCCCTCTTCCACCACACCACTCCCGGAACAAGTGTCCAGGATTCCTGCCCACCTGGC CATTTTGGAGTGTGCC[A/T]TGGGTAGCAATGTGGAACCAACCAGGGCCTTTGTGGAGAAAAATGG AGGGGTTGAGGGAGTCCAGAGGGGCTTATTGAGGGCCTTGGCACCTTGTCTCATAGGCGAGCTOG ATCTCTCATCATCTGGACAGGTGAAGCGAATCTTCCCGGCGTAGGCA
WI-19946	122	C T ---	---	---	CAATGGACTGAATGAGTGGTGGTGGGGGACACACACACCTTCAATACACGTCAGGTGCG CTTCCAGTTTTAGAAAACAGAAATCTGCATCTCAGCCTGAGACGCACAGAGAGG[T/C]TCTTCCCTG ACCCAGACGCACTCAGGAGCCAGTCTGTTTCAAACTGCATTAACCTGCGCCAGAGAGTTAC CGTAGGCATCTTTAATAAATACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141	G A ---	---	---	CACAGCATGGTGTAAATAGCATCAGATTGAATGAAAAGTTTGTAAATGCAACCATAAATAATTATA ATAAATACATCAAGTAACCTTACAGCACACATTTTATGGGCCAAGGTTTGGATCTGTCTGGACCT CAATGTG[A]CTCTCGGAGAAGCAGCCAGCTTAGCAGCAGATACCTTACAGCTTGTCTACTCTCAA GTGATGGCCAACAGAGCTTCTGAACCTCTCTCTGGGAGGTAGCTGACAAG
WI-19076	40	G A ---	---	---	TTGGTTGGATACTTGTCTGGAACAAAAAAGCAGTTTTAATG[A]GTATCAAAATACCTTTAAAAA GTATCTAGCACAGAATTTTCTGTAACCTAGATTATGTTGTAACCTTTTCTAAATCTTGTAGGAG TGTGGTTGTTAAGAACTAGAGCTTATCTCTATCCAAATCTATCTGCGCTCCTGAAAAACTGCAGA AAGGCACCTTGAAGCTGTTCTTTAAGATATGGGATTCTTTTATCTT
WI-20218	26	T C ---	---	---	CCACACACTCTGTTTTTATAAGCTA[T/C]AGGACAGAGCAGAGATGGAACTGAAAAACAGGGTAG AAAATAACATAAATTTGGAGGGAACAGTGGGATGCAGAAAGAAATGACAACAGCCACATGTGCCCA GTCAAATACTTTTAGTCCCTGCAGCAGAAGATGCCAACCAAGTCTCTATCTACTGGCTGGGATCCTGCC ATGGATGCAGGAGAAAAA
WI-20295g	154	T G ---	---	---	CAACCTTTTGCAGAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTTAAATCTCCAGGCTTGAATGGGAGGGCTGGGCTCTAGCCCTTCTCTTTTCCA TCCAGTCTATTGCCAGAT[T/G]CCAGAGAAAGCGCGGGAAGCCAGCTCTCCAGCATAGCCACTGTGG GTCCGGCTTACCTCTCTGTCGACTCTCTCATGCTGGGACTTGTCTTTCCGGG



WI-20361a	192 G A ---	---	CTGGAGTGTGACCTAAGTGACATTTTTTTTAAATGCCAAATACAGTAATCTCCAAGCTTTTAAATGG CTTATGCAAGATGACAGAAATATGTGAATCTGATTGTCCAGAGTTACACTCTGCACCTCCAAAGCTA CAACAGTCCACAGCTGAGAGGTTTCCCTATACTTCTACTACTGTGACAAATTTAGC[G/A]ATCCTTG AAATGGGAAAATTCCTAACTACACGAGACAATGGGTCTACAGTAGGCCCG
WI-20572	75 A G ---	---	GAGCCAAACCCAAAACAAAATAAACAGAACTCTTTTGTAACTAAGTCATACCTACTTTCTTCT TCAGAAATTA/GTTCATAAAACATCATCTTTTACAACATGGAGAGCGAGGTAGGCCATAATTGTTCA AATTCATCTTTCTCAAAATTTAAATTTGTTTAAATCCCAAAGGTGCCTATTGAATCTTCAAAAATA AACTGCCTATCAGGTATCATACCTGCAATGCTTCTAATATCTCTTGATTAT
WI-20588	133 G A ---	---	CATGACAAAAGACAAAAGATCAAGGAGTAACATAAAATTAAGTTGAATAAATAGTATACAGCAATC TTCACTTTTTAAAGAAAATGTGAGATCCTTTGTTGGTTTTTATTTCCTTAAGTACAAAATGCTAAAC[ G/A]GGAGCCGAGCTCTCCGCATTGAGG
WI-20593	79 A G ---	---	TGACCTCATACTGGTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTCAGTCTGTTG CTGTACTTCAGI/GJTTTAAATCTGGGAATGAGCATGCAGCAATGCTCCACCAGATGAGGAAAGAAA AGCTGTTAAAGGAACTCAGGATGTTGTTAGGAAGGGGAGTGGATGCCAGGCTTCACCAGACTAT CCAGAGCCATTCCATGGGTATTGGTCTGCATACTGTGAGACACTGAGCT
WI-19765	57 T C ---	---	TTCTTTGCCAAGCCTGTTCTTCAAGTTATTCAGAACTGGGTGTATACCTTGTCTCAIT/CJATGTATCT TGTCCTGCTGCTTTTAGGTTAGCAAGGTGTATGAATACITTTTAAAGTTTGTGTTCTTTCTCTCGT GGTATCAGTGAATACTGATCTATCTCTGGCTAGGGTCAATTTACAAAATTGCCATGGAACCTGAGC AAAAGCCCACTGGGATAAAATCACTACCATCGACGCCACCAAGTAT
WI-19066i	239 A G ---	---	TGACAAGGGAGAGAGGGGAAATTTCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAATCTCTCCATATCCGGATGCTCAATTACAGT ACCATTCAGGCAAACTTTTCTTAAACGCCCTTCACIT/A/GJTTCTTTTA
WI-19066g	184 C T ---	---	TGACAAGGGAGAGAGGGGAAATTTCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAATCTCTCCATATTC[C/T]GGATGCTCAATTAC AGTACCATTCAGGCAAACTTTTCTTAAACGCCCTTCAGTAGTTCTTTTA
WI-19066f	148 T C ---	---	TGACAAGGGAGAGAGGGGAAATTTCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACTGG CATATGTTCTTGCGT/CJTTGGTCACCTGTAGCTGAATTAATCTCTCCATATTCGGATGCTCAATTAC AGTACCATTCAGGCAAACTTTTCTTAAACGCCCTTCAGTAGTTCTTTTA



WI-19066e	147	GC	---			TGACAAAGGGAGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTACGCTGATCGTCTTAGCCAGTCCAATCTACGAGGAACCTGG CATATGTTCTTGCG[G/C]TTGGTCACCCTGTAGCTGAATTACTTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAAGCCTTCACTAGTTCTTTTAA
WI-19066c	100	GA	---			TGACAAAGGGAGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTACGCTGATC[G/A]TCTTAGCCAGTCCAATCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCTGTAGCTGAATTACTTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAAGCCTTCACTAGTTCTTTTAA
WI-19066b	87	CT	---			TGACAAAGGGAGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAAC[C/T]CTCAGCTGATCGTCTTAGCCAGTCCAATCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCTGTAGCTGAATTACTTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAAGCCTTCACTAGTTCTTTTAA
WI-19066a	72	CT	---			TGACAAAGGGAGAGAGAGGAAATTTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCA[C/T]TAAACCCATGAACCTTACGCTGATGCTGCTTAGCCAGTCCAATCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCTGTAGCTGAATTACTTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAAGCCTTCACTAGTTCTTTTAA
WI-20660	105	GC	---			TTTACAGCGAGTTTTCCCGTCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAGAAGAAATGTG TGCTAAATAAATCTCCCTTTTGAATGTATTTG[G/C]TTAAAGGGAAGCATTAATATTA CAGACATATTTACAAGGTTCTGAACATGAGTATTCATTACTGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCCGCCCAAAATACTGTTTAAACAACACTATGTTTAAAGA
WI-18768	120	CT	---			CTGCTGCCAGCTTCTCTTTGGCCCTGCTCCAGATGGCGGTCTCTGGCAGCCTCCCTCAGTCTTCC TCCACCCGCTCTTCTTCCAGCCTGCTGATGCATGTCATGTCACCCCTTGGT[C/T]TCGCTCCATCGCC TTGAAAGCTCTGAA
WI-19087	37	AG	---			TTCCCCAGGGTTCTGTATTGCAGCTAAGCTCAAATGTA/GTATTTAACTTCTAGTTGCTCTTGTCTTG GTCTTCTTCCAATGATGCTTACTACAGAAAGCAATACAGACACAAATTAGAGAAGCCTTTTCCATAAA GTGTAATTTTAATGGCTGCAAAACCGCAACCTGTAACCTGCCCTTTTAAATGGCATGACAAGGTGTGC AGTGGCCCATCCAGCATGTGTCTATCTTGCATCTACCTGCTCC
WI-18790	49	AT	---			GAAAGCCAGAGATTAGCCCCGCAATCCCGCATCTGTCAACCAGGACAGAA/TTGCATGGACAAGGGA TGAGCTTTACAAAGATGATGCACCTTGGAGATCAGAAAAATTCATATTTAAGCAAAAGTGATACAAACA CAGTGATTTGGGAATGCCT
WI-18987	35	GA	---			AGGAGGCTGTTCCAGGAGTCTGCCAGCAGCCT[G/A]GTGGCCAAAGCCAGACACTCACCCACCTT CCCCAGTGGCCCCGTGGATCCTGGTCTAGGCTGGACACAGGATTCAGAAAGACACCCAGGCTGCACA GAAAGAGCCAGATGGACCTGAGTGTGGTTCACAGCCCCCTACACTCAAGGCTGAGAGGCCTCAGGAA AGTCA



WI-18919			26 C T ---				TGGATGAAACACAGGGATTCCGGA[C]/TGCCAGACCCTTTTATACTCACTTTTCTCTACAGTG TTGTTTTGTGTTGGTTTTTATTTTTTATACTTTGGCCATACCACAGAGCTAGATTGCCCAGGTCT GGCGTAATAA
WI- 18741c			64 G A ---				CTTTCTGGTCAAGGCTTTGGACATCTCTTCAGTCATCAGACAGAGTATCTCTGCTTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI- 18741b			38 G C ---				CTTTCTGGTCAAGGCTTTGGACATCTCTTCAGTCATCAGACAGAGTATCTCTGCTTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI- 18741a			23 T G ---				CTTTCTGGTCAAGGCTTTGGACAT/GJCTCTTCAGTCATCAGACAGAGTATCTCTGCTTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI- 19179a			170 G A ---				TCAGAAGCAGACATGGCATCTGTTCTGCTTGTGTTGGTTGTGTACCTTTTCACGAGACCTGAATT TTAGAATTGCCAGTGCCTGCCAGAGTGAGTGAGTGAATTCCTTTTCAGGTAAGATAGGCTATCTC AACACTGCTGAGTGATTATATAACATATCAACCA[G/AT]TAGCATTAACCCATTTTATTTCTGTCCTT AGTGTCTGAAGATGCTCACCAAGTTTCTGTGTACAGTAAGGCAGCATGCT
WI-19212			46 T A ---				CCAAGTTGCATCCATGTTTGATTTTCTGATGAGACTAGAGTGACAGT[A/J]GTTTCAGAACCCAAATGT CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGATTATGCAGATGGCCTATGAAAAATGCAGCTGC ATAATTAAACATTATCAAAGTCCTCTTACAAATTTATTTCCGACGATGTCAGCTAAGTAGACCCA ATGGGAGAGAAAATGCCTGCTTCTTCCCCTTTTCTGCACTGCCATAT
WI-19183			210 G C ---				CTGTTGAAGGCTTCTCAGGCCAACTCCAGCTTAAAGCCCTAGACAGGTAAGACACACATTGGATG GCAGCATGGGTTCTTCCCCATTTATGGCATGAAATATGTGGTTTAGAATAAGGAACAAGCATTATT CCITTGCCAACAGCCTCACTCTAAGAGGCTTTTGTGCTAGTCAAGCAACACTTGCCTGCTCTGCOO CTTGGAG[G/C]TGCAITTGACCTGCTCTCACTGGTAAGTGACTTGGTGGC
WI- 20014b			214 T C ---				TTGAAATCCCAGTCTCTGGCCCCCAGGCAGGGTCTGTCAACCATAGAAATGCTTCTCTACTGGGGTC GTTCTGGCTTTTGTTAGAACTTGGTCTGAGATGTTCTTCCCCGTCCATTACCATTCGATGTTCTTT TGTTCAAGACAAATGTTTCTTGTTATCTGAAACTGGAACCTGAACCAAGTTGCCTTCTCTAGTCACC AAGCATACT[T/C]TCTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041			198 T C ---				GTTCTCCCAGAGTGTCTTGACCCCCAGCCCTGTCTGCTGAAGGGGATACAGAAAGCTCCCCG TCTCTGCATCCCTTCCAGGGGGTGGCTTAGTTTGACATGCTGGTAGCAGGACTCCAGGGCGTG CACGGTAGCAGATGAGCCCCCAAGCTCATCACACCAGGGGCCATCCTCTCAATACAGCC[T/C]G CCCTTGCAGTCCCTATTTCAAAATAAAATTAGTGTGCTTGCCTGTCTGT
WI-19135			20 G A ---				CAGTTACCCCTGCTTGGCTC[G/A]AAAGTGTCAATCAATTTTGTAAATTTTAGTATTAACCTGTAAAAAGT GTCTGTAGGTACGTTTTATATTATATAAGGACAGACCACCAAAATCAACCTATCAAAGCTTCAAAAAC TTGGAAAGGGTGGATTAAGTACAAGCACATTTGGCTACAGTAAATGAACCTGATTTTATTAACT GCCTTIGCCCATATAAAATGCTGATATTACTTGGAAACCTAGCCAGCTTCAC



WI-19236	54	G A ---	---	TACACAGAGGGTGGCACTTGGACTCTGAGGGTTGGGTGTGGAAGGGGGAAAGG[G/A]GATGGAGAC CTGCTOCCAGCTCTTCTGTGAGCCGGTTTACATGGGAACAGGGTTAACATCTGTGTAGGGGAGGT CACCTTACCCCTTTTCATAGGGGAAGAGTGCACACTCCTGGCTATCTCAGGGGAATGGGGAAAG AATCTTTCAAGGGCAAGAACTCGTGGAGGATGCTGTTGTATGTAATACT
WI-19144	222	G C ---	---	GTGCCAGTCTCCAGAAAGCAAGGACTGCCCTTCATTACGCTTGTGACCTCCAGCCCTTTCTAAGG CTCAGCCCCACGGGACTCTGGTGGCTGCCAGCTTGTAGCTATCTATATTCATTTCATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACACAGGGAGGCTGTAGCCAGGAACCCCTCTCTTCCCTGGT CTGGCTCTGCTGGAGCGG[G/C]TGGGAACCAACACCTTCAGTCTGGTG
WI-19139b	110	C A ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGCTGTATTTACACGAGGGTAGAC GGCAGATGCTGACAGAGAGTGGTGGCAGACAACACTAG[C/A]ATTTTACCGGGTGTGGGCAC ATGGGTGTGCACCTGGACGTGTGCAGCATGTGGCGTCTCTGTGAAGCCACCGTCTCTCTTTGG GGGCGCGGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66	C T ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGCTGTATTTACACGAGGGTAGA[ C/T]GGCAGATGCCTGACAGAGAGTGGTGGCAGACAACACTAGCATTTTACCGGTGTGGGCAC ATGGGTGTGCACCTGGACGTGTGCAGCATGTGGCGTCTCTGTGAAGCCACCGTCTCTCTTTGG GGGCGCGGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-18910	112	T C ---	---	GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACCTAAACATGAAGGAAGGGTGCT CATCCCAGCAACCTGTCCCTTGTGGGTGATGATCACTGTGCTGCTTGT[C/G]GGCTCATGGCAGAGCATT CAGTGCACCGGTTTAGG
WI-19235	173	A G ---	---	TTCAGGAGGTGGAGTTCGTGTCAGCTCTCCTGCTGTGATGTGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTCTGTAGCTTCTCTTCACTGCCAGTATTGCTCTGTATTTATCAGCGATGCCCTCTGT CACTCATGCCCTTGCCTAATTGTTCACAATGGTGGAA[A/G]GCTTCATGTAATGATCAGGACCCACC TCCAGTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTTCGAGCACTA
WI-19222	179	C T ---	---	CGTTTCCCTAACTCACCAGTTTGTGGATGATTTGATTTCTGTGTTGATCCCATTTCTAA CTTGGAAATTGTAGCCCTATGTTTCTGTAGGTGAGTGTGGGTTTTTCCCCCACCAGGAAGT GGCAGCATCCCTCCTTCTCCCTAAAGGACTCTGCGGAAC[C/I]TTTACACCTCTTTCTCAGGGAC GGGGCAGGTGTGTGTGTACACTGACGTGTCCAGAAGCAGCATT
WI-19117	134	A G ---	---	AAATAATGCAACGCGAGGAGAGAAAGAAATGCACTAAGACAAGAACATTTCTCTCATAGAACATTG ATCTGTTTTACAGGAACAACCTTGCCTTGAATTTACACAGTGAGACTGTACATAATTGCATGAA A[A/G]TAGCTATTTTTCCTAAGACATTTTTCATTTCATGAATAATTTCAAGTTTTTCATACTGTACA CATTTCTTAAACACATGATACCAGCAGCAACTGAAATGAATGCCGAATTTG



WI-19134c	263	C T ---	---	CTCCTGTTGCGTACCTGACAGGGTGACACAGCCCTTTACACACTCTGCTCCTCTATCTTCTGGGTAGA TGCCCTGGTGTAGGGCTAGTACTGAATGGTCTTCCATCCCAAGCAAGGGGTGACGCCAGGGTCTAG GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGAGCCAGCTGCACATCTCCTTTTCAGAGCAC TTATCCACTTGTCTCCTCTACCTCTACCTCGGCACCTGGTGGGAAAGGG
WI-19134a	162	T C ---	---	CTCCTGTTGCGTACCTGACAGGGTGACACAGCCCTTTTACACACTCTGCTCCTCTATCTTCTGGGTAGA TGCCCTGGTGTAGGGCTAGTACTGAATGGTCTTCCATCCCAAGCAAGGGGTGACGCCAGGGTCTAG GCCCTTCAGAGCCAGGGCTAGAGGATTCGCACGGTGGCTAGAGCCAGCTGCACATCTCCTTTTCAGAG CACTTCATCCACTTGTCTCCTCTACCTCTACCTCGGCACCTGGTGGGAA
WI-19224	112	C T ---	---	GGTTTCACCAAGTCTTTCCCAAGGAACTCCGATGAAGTGTCCCAACAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACAACAGAGGAGATAATCTCTCAGGATGCCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTGTTTATATCCAGCAGGCCAGAGACTTCC AGGGAACACTCATCAAGGAGGTGAAAATGATGATGACTCCTCCAAGATGAAAA
WI-19201	179	T C ---	---	GCAGCTCTAAGGACCACTGGCCATTAGCTCTTGCTTTTGATGGCATCTCTTTCCACCTTGTCTCTC CTTTGCTCTCTGTGTAGTGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCCTCACACTGCC CTTCGCCCCCCACACTTTGCGTCGAGGTGCACCCGAAAGGACTTCCTGGGGATATAAATTCAAAAAA GTGTGATGTGCTGCTCAGAGGTGAGACTCCATGTCTGCCTTGGCCTCAA
WI-19034	45	T C ---	---	GAAATGGCTCCACTCAGAGCTACCCCGGTGATGAGGATAGGGGAATTCJACTCTCTATTACATTAAAG GCAACAGCAGTTAGTAAAGGTTTTACAGTGTCTGCTGTTTGAAGTGCAATATAAATTTTTTG CTAGCCCATGATCAATCGACTTCTATTGTTTGATATACACTTCAGCATTTAAGTTCTGTCGAATTGAC ATTGTACTTATAAACTTAGTCCCTAAGTCTCTTATGCTGTGCTATATA
WI-19102	25	C G ---	---	TGTTCTGAGTCACGCTGAGGAGTCJCTTCACTCAGGATTCATCGATGATGATCATGATGATTCATCA TGCGACGTATATTTCTTTGGAACAGAATGAAGCAGAGGAACTCTTAATACTTAAATCGTTCT TGATTAGTATCGTGAGTTTGAAGCTAGAACTCCTGTAGTTTTGAACCTCAAGGGAGAGGTAT AGTGGATGAGTGTGAGCATCGGGCTTGCAGTCCCATAGAACAGAAATGGG
WI-18548b	65	A G ---	---	AAAGGAGGAGAAATCTTTTTACATAAAATGCCTTGCATCATCTCCAGTCCCTCACTGGGGAAJA/ GJAAAAAGCATCTNTCAAGCTTTTGTCCAACTTTGGCTGC
WI-18548a	62	G A ---	---	AAAGGAGGAGAAATCTTTTTACATAAAATGCCTTGCATCATCTCCAGTCCCTCACTGGGGGJA/A AAAAAAGCATCTNTCAAGTCTTTGTCCAACTTTGGCTGC
WI-18700	97	T C ---	---	GGCAGCAGCTTTTTTAATTTGAACACTTTCTTCTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTTCJAAAGATCCCAAATTCGAAAGGCCACTGCTGGCTCA CTTCTCACA
WI-18501	121	C T ---	---	CAGAGGGAAAAAGTTTATTGAGTCAGCCACAGAGGAACAGAGAAACAGACACAAGGAGGTTCTGTGT GCATGGAGGAAATCAGGGCGCCGNACAGCTGAACCTGCGCAGGACAGAGGGGCGCTJGGACAGCA GCGCATGCCACAACATTCA



WI-18017	87	C A	---	ACAAAAGAAATGAAATAGGTTTGGAAAACCTTATCTGCATGTACAAAGTAATCCCGTAGATAA GGAGGCAACCCNGGAACA/C/AJACTGCTGGATAAATCGTTCAATTAATAATATATCTCTTGTCAT CAGAGCTGGTGGAAATCAT
WI-18148b	101	A G	---	TTATTGCGTTCCTTCGATAACCTCTCTTTGGACTATGAGATCATCACCAGATGTGAAAACGAAAGCA GTGATTTAGAAAACCNCTCGATTCTGAATATCC/C/AJGTGGCGGCATATGCAAGGAAGATGA
WI-18254	64	T C	---	TATACGGATCATGATTTGTGTGACCACCACTACCACAGTCAATTTGTAGAGCAGTTAAATCAC/C JGCCAAAATCCCTCTTGCTTCCCTTGAGTCAGTCCCTTCCCAACCCAGGNACTTGGCAACCTGTTT TCCGTTCTTAGACATTT
WI-18265b	117	C A	---	CAATGGGTGGACTGAGTGATAAAACGCATATTGAGAACAAAGACGGCCTTCTGGCCNCTCTGCGTCC AAGGCTGTAAAGGCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCT/C/AJGTTTTCAACCTTTTC CTTGGGTGGTTCTTCAG
WI-18295	40	C T	---	ACCACATTTGTTGAGAGCCCTATTGTGGAGAACAAACAG/C/JTTGGGAAGTAAAGGTTGATTACT TCCTCTCCAAGGATGATGTTTAATGAATCCCTTTNCCCTTAGCTTCAATTCATATAATGCCAAA
WI-18459b	64	T C	---	GGGCAAGAGACAGAGATTTAATTGAATAAAACCTCCAGGCTGTGACACGGGTGGGAGACACAA/J CJGAGTAATTAACAACATAATATTTANATGACAGTGCAATTAATTAACGCTCCTGGGTAAAGCCAGAG GGGAGGAGGGGCTTTCA
WI-22585	56	A G	---	TTTATTTAAATTTGCATCCTGAGATAATAAAATTTTATCTGACAAAGTGAACAAATG/A/GJGAGAAAGC AGCAGTGAAGTTTCGGAGAGGCGAGTATCCTTCATTTTGGCACAGCTGTATATAGATTGA
WI-21155	36	A G	---	GGGCTGTGGAGTAACAGAACTTGATGGAAAATTTGGC/JGJCTGTGTAGATGATTCTAAAGCTTTTC AGACAAATGGCAGA
STS-F02766b	88	G A	---	GCCTTTGCTCTTTGCTCCTCAGAGGCCCTCAGATGGATACGCAGCAACTTCTTTTGAACCTTTTAT TTTCTGGCAGGAAGAAGA/G/AJGGATCCAGCAGTGAGATCAGGCAGGTTCTGTGTGCACAGACAG GGAACAGGC
WI-19888a	98	C T	---	GGCAGGATTCACCCATAACAGAGAAATAACTCCTTATTGGAAAACAGGTTTATTTTGATATGATG AAAATATTTTGGAACTAGAAAGTAGCAGTG/A/C/JTTGGACAAAGTTGTAAAGATATTAATGGCACT GAACTGTTCAATTTAAATGGTAATTTTCATGTTATGTGATTTTACCTCAATTAAGAATGGAACATGT CTTATAATTGTAATTTACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-21485	82	C T	---	TGAGACCATCCTCCTCAACAAAGAAATCAGTCAGTTTCAGCACCTAATTTTCCACACTGAAGTCTACG CAATTTTCATGCAG/C/JTGTGCACACAGTACAGTGCACAAATCCAGAGGGCAACACATTTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125	T C	---	TCAGAAATGCTTTCCTGCTGCCCCAAACCAAAAGAAATTTAATGAATGCNCTTACAATTTGAGATGACTT GAAGTTAAAGAAAGGTACCTTCCCTTGGAGGTTGCATGACAGGATTAGTCTCTCTGTTT/CJCTGGT GCAAGTTTGAACCAAGTATGATGACCATTTGATCAGAGCATCTGTTTCCCTGTGAGATCCCACTAG



WI- 20561b	94	T C ---	---	CGTTGCTATTAAAGATGGCTGTTTAAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTATG TACTTCAGATGAAAAATCCTTACATGTC/GJGGAATCAATGTCCTTTTAAAAATTCAGATAAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20561a	25	A G ---	---	CGTTGCTATTAAAGATGGCTGTTT/GJTAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATT TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCCTTTTAAAAATTCAGATAAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20116e	69	T A ---	---	GCCTTCATTTCTGTCAACCCACCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT AT/AATAAATCTATATCATATATTTATACACACAAAAACACATCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGCGCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI- 20116c	59	T A ---	---	GCCTTCATTTCTGTCAACCCACCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATATAATCTATATCATATATTTATACACACAAAAACACATCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGCGCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI- 20116a	22	C G ---	---	GCCTTCATTTCTGTCAACCCAC/GJCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATATAATCTATATCATATATTTATACACACAAAAACACATCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGCGCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGGAGATAA
WI- 20466b	133	G A ---	---	AAAGATTTGCAGTCTGGGACACAGTTTGGAAAAACACTATTTATAAGTTGGCACATATTACAAACAG NTCCCAAATGGTGAACTGGTATTCTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAAACGC G/AJGTGAACATAATGTTAAAAAGTTAGAGCTTGTCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTTATTCTTTGCTCTTTTATCCCTTTTCAGGTTTCGATT
WI-21444	39	A G ---	---	CTGGGCGCAAGTAACCATTTTAAAGAAATACTCTCAAC/GJAGTCTTTTTTTTATGGGGTATTTCA GTTGTTAACAAAGTTAAATACTTATTGGAACTAATCTTTGTATTTTTCGAGGAAGAAGAAATCT ATAAGATTGACTTACTCATTTGTTGACTGGTTTTTGAAGCCTTACTGGGG
WI- 21034b	148	T C ---	---	AGAATGGACAATGATGCAGATGATTTGTGAGCAATTTTGTAGAGAAAGTGGTATTAGAAGGATACAG CATAAATTTAATTGTAAACATGCTTATCTAGCTAACCTAATCTGTTTCTGTAGAATTAAGTGTCTGG GAGATTGGATAGAT/GJGCTAACCTATCTCAATTTTAAAGTAATGTGAGCAA
WI- 22091c	205	G A ---	---	GGCGTGTATTGTGCAATGTCCCAACCACTCAAGCTATCATTTGAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCATGTAAACATACAAGCATATTACCTCCCCCTTAAGTGACTCATAATTC ATTACTTGCTGTAGCTTTTAAAGGTTTAAAAATGTGTAGCATTAAAGTGTATTACTTGAGGGCA ACA/GJAATTACGGCTTAACAACACACACTAAATCATGAGGCTCAGGGATTG



WI-21805a	45 A T ---				CAACTGCTCTGAGGCTTTCACTAGCTGATTTATAATCCTATATTAT/AAAAAAAAATCTATAGTCTG CAGTCTTTGACATACCTCTCAAGGTGGATATGTGGTGAATCGAGACTCCATCAATATGTGTGGTT TTGTTGCTTTTGTAGCTTAAGTCTGTTAGNAATCCAGAGGAATATGATTGAGGCCAGAGTTA CAATGGTTCATAAAATTCGAACAGTTGAAGCTGTTTTGTTAATTGCTG
WI-21778b	155 T C ---				AAAAATCCATAATTATTGAACCCAAAGTTACAGAGAAAGTTCGTAACTTTTTATTGAATTATTGAC TCTGCCGCGTGTCTGTCGCTTCAACTCCAGTCTGTCAATGCCCTGTGTAGTGGGTCCCGAG GTCTGGCTTCTGAGGTCCT/CJGGTAGAAGGAGGCGAGGTGGT
WI-20907	241 A C ---				TGAGTCAGTGGTCAGATGGGCGAGTTGGCTCAGCTGCAGTCCCTGACTCCGGAAACACTGTGCCTCT CAAATGATCTAGAGCTCATCCTTGGCGTACATGAGGGCGAGTTGTTCTAGTACCCATTAGCCG ATGGCTCTTCAAGCCAAATTCACACTGGGAAAAACACACCCTCAAGATGCCCTATCCATTTGAGTTC ATACAGGTTTTAGTAGCTAGAACTAAAAACATTTTTTAA/CJAATTATCTA
WI-21449b	222 C T ---				AACAGCAGCAGTCACTTCCAAATGCAAAAAAATTAATTTTAGAATAAAATTAATGTTTA TAATGCGGTGAGAAAGANTTGAAGGTACACAGAAATCAATACGACGACCTGGAGGGCTGGAG AAGCCAAAGCCCACTGGTCAGGGTCCAAAGCTGACAAGAGTCCCAACCTGAGAGGTCTCCACACACC AAATCATACCCCTCAGCTTCCCA/CJTGTGACAGAGCCAGTGTCTCTGGGTTAG
WI-21558a	157 G A ---				GCTTACAAAGAACCTGTGGACAGGCGAGNTGGTGGAAACCGACTCCAGCCTGGAAAAACCTGCCCTC CCATCCCTTAGCGCTTCTGGCTTCCGGCTGATTTCTCGACAGAGTCTTGCCAGGGCAAGG AGCTGTGTGGGGGCGAGTATG/AJAGCCAGGAGTCCCTTCCACAGATGAGGCTAGGGCTGCAA AAGGGCCCCGTGAAAGAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACC
WI-22187b	178 G A ---				TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCCGTGGCTAGCAGAGCTCATGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAAAACCAACCAACCAACCAACCAACCAACCA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG/G/AJAAATTTTCATGAAAAATTTCC CCTAAACCATAACAAAAAAGTGTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI-22187a	110 C A ---				TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCCGTGGCTAGCAGAGCTCATGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAAAACCAAA[C/A]CAAAACCAAAACCAAAATACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGAAATTTTCATGAAAAATTTCC CCTAAACCATAACAAAAAAGTGTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI-21609b	146 G A ---				TCATGAATATGCAGCCTCCATAATCTTCTCCCTTTGAACAAACGTGCAGTCCGTTTCAACAGCTGTAAA AACAAGCCCCAACCCAAAGACATCACAAAGAGGCAAGCAGTGGCAGTGAGAGGGAGCCTGTAAAG GATGTTTCAAAG[G/AJAGGGTCCCGGCTATGTGGCCACTGGATGAGGAGTGTAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG



WI- 21609a	42 C T ---			TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAAACAA/C/TJTGAGTCCGGTTCACAAAGCTGT AAAAACAAGCCCAACCCAAAGACATCACAAAGAGGCAAGAGTGGCAGTGAAGAGGAGCCTGT AAGGATGTTTCAAAGGAGGGTCCGGCTATGTGCCACTGGATGTAGGCAGTGAAGTCCAGGC TTTCGGTCTGGGAAGTGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104 T G ---			ACATTCGAGGCCAGTTTTTCCATATTGCTCCTCACTGCCTAAATCCCTGGTGCCTCCCTAGGGCTTCA GGGTAAGCCCTGACATCATGGTCTTTGTGATCTGT/GJACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGTCTAAGGCGAGGCTACACTTGACTGCA
WI- 21028b	139 A G ---			ATCGGAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTCACATGAAAGGGTCGTGATTGATTGAGCAATCTAGGGGATGTGACAGGGG TTTC[A/G]TGCACTGGTACAGAACACACAGGGAGTTTCACAAATTTTTTATACAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C ---			ATCGGAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGTCCCTTTAAGGGCTCA CAACACTAAAGATTTCACATGAAAGGGTCGTGATTGATTGAGCAATCTAGGGGATGTGACAG GGGTTTCATGCACCTGGTACAGAACACACAGGGAGTTTCACAAATTTTTTATACAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---			ACAACATGCCTGTTACAGGGGGAAAAATCCTAGGNAATAACTTATGTGTACTTCTTG[A/G]TTTCA TCATAAGACAAAGACAAAAGCACCACCCATGCCTCTGAGGAACATTTGGACCATGCACCCCTTGAAA AA
WI- 18829b	35 T A ---			ACAACATGCCTGTTACAGGGGGAAAAATCCTAGGTT[A/A]AATAACTTATGTGTACTTCTTGATTTC TCATAAGACAAAGACAAAAGCACCACCCATGCCTCTGAGGAACATTTGGACCATGCACCCCTTGAAA AA
WI-20964	87 G A ---			AGCCAACTCAAGGCCCAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGGAAGCAAGGA GCACAGGTAGTCCACAGAAAT[A/G]A/GACACAAGAAACCTCAAGCTGTGAGGTCAAATTTGTAAATTA AAGAATACTAAGATTAGATGAACACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAGAAAGAAC AGATGTTAACAAAACAAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---			CTCTGAACATAAGGCCGTGAAAGGCATGATTGGTTTTTGGCACACAGAGTGGATAACCAAT/AJACAT TGGCTGGAATGAGGTGGTCAGGAAAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAAGTGTAAATAATTACAAAAGACTGACATGCAACTCTTTACCTTACATTAAT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGCCCTTAGGT
WI- 22130b	165 C T ---			TGTTTTGAGGGCTGTAGCAGACTACATAATGAGCGGTGAAAGCGGTGCTTCCCTCTCCTGACAC CAGCAAGGGGGAGGCCACCATACCGGGCCCTGCCCATCATGCATCCAATGATTACTAGCACTAGGAA GCCAACGGAANAGGACCCCGCGCTTGCT[C/T]GTGTTTAAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCAGTCCCTGTGATGGGAATGAC



WI-21661	117 GC ---	---	GCCTAGTCTCCACCCCTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGT CTTTCCAACTTTAGAAATGTATAAATAAGAAATGACATTTTAAATAAAATAG/CJTJTAGTCACAGTC ACACAAAACCTACCTTCTAAGGAAAACGTCCAGTGAAGCCGTTAAATTTGTGCTTTCAGCTATGAAG GA
WI-21980a	25 TC ---	---	TCAGTTTAAACACATTCATCAAGGAT/CJAGATTAATTAATGTGTCAGGTGAGCATAAAAGGGAGATTAT TAAACCAGAAATGTGTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTATTATTAATTTTCAT GGGTGAAGCCCTGGGATAAAG
WI-21636	71 AG ---	---	TGCTTGATTAATGTGGTGTTCATATTATCCTATTTCACAGATGGAACAGAAAATACCAGCTTTTTT AAAJAG/JTAGCAATATCTATTATTAATAAATATTGAAATAACACCATAATAATATCAGCTAAAGGA AGTAATCTAATTGTGTGTTTTCAGAGGGGAGAAAACATTACCTCTAGAGCTGAGGCTATTGTGC TCATGCAAACTCCAATCTGAAGGTGGTAGAACTAGGAAGGGACAGGGATTTC
WI-22457a	112 GA ---	---	TTGCTATAATTTCTTAAAATGCAAAAGAGTACATCACAGCAGAGTATAGCCAAATCACTCATTAGA CAACAGTAAACATACTGGACACGGTTTCAGGCATGAAGGATACA/GAJCAGTTAATTAACATAAAG GAACAGAGTCCCTGCAATTCCTGAAGCATAGGATGGGGAACAGTAATGCAGATTAACTGCGGCC AAAACCCACTGAACCTACCCAGCTGAAAACACTGAAGGATACTGGGTAAGGA
WI-21524b	97 CT ---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTGATGACGACCTTCGCGTCATACCTAT AATGGTTAATAACAGCATTCCTGTCTACCC/CJGATGATGCTTCTCTGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-21524a	35 AC ---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATJACJGCTGATGTACGACCTTCGCGTCATACCT TATAATGGTTAATAACAGCATTCCTGTCTACCCGATGATGCTTCTCTGCAATGGACTATTTGCC CAGTTGCAACAGGGCTAAGATTGTGCACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTC CTGTCAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCAGGGGATG
WI-22652a	32 GT ---	---	TTACCTTCCAAACCCAGGCCACTTTGGAGAAAAG/GJJAAGAGAAATGCTATTAAATCAATAAGCCAAAGAC AATAGGGACTACCTGGGGTAGACCAAGATGGCAGTCACCATACACCATCTCCTGCCACAGAACC TTTGACATGCTGCCCTCCCTACTCCGCACTCACCTGTCTAAATGGGACCTGAAGCTTCAGCATCCCTT CTTAGGG
WI-21703d	197 AG ---	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGTGGTGGTGGCAGGGCTC TGCAATCCCTTTCTCAGCAGCAGCACCATCTTCAACCTCCTGGGAAAGCAGCATTTGGAGCTACACCA CTTGCTCTTTCTCACCAGGGTAAGAAATGCAGGTATTTCAGAGGGGAGTGAGTCTGGGAAJAG/GJ TGGGCAGAGCAGACTAGGGGCAAGGACTTAAGGAACTTGTGGGGGAAGAG



WI-21703c	134	A	G	---	CAACAGGCTCATGGAAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTCTGGGCGAGGGCTCTGTCATCCCTTTCTCAGCACAGCAACCATCTTCACCCCTCCTGGGAAAGCAGCATGGAGCCTACACC[A/G]CTTGTGCTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAAAGTGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGAACCTTGTGGGGAAGAG
WI-22663c	139	G	A	---	CCCTTGTCAGTCTGTGCTCGGCTTCTCACTGCACCTGGCGAGGTAGCCGGCTGCTGCTAATCTTATTCACAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACCTGGTGCACCTACAGGC[G/A]GAAGAGCTTCTCATTTGCTGAGGGCTTTCTCTGAATCCCGTGTGAATGTGGGT
WI-22663b	55	C	T	---	CCCTTGTCAGTCTGTGCTCGGCTTCTCACTGCACCTGGCGAGGTAGCCGGCTGCTGCTAATCTTATTCACAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACCTGGTGCACCTTACAGCGGGAAGAGCTTCTCATTTGCTGAGGGCTTTCTCTGAATCCCGTGTGAATGTGGGT
WI-22663a	38	C	T	---	CCCTTGTCAGTCTGTGCTCGGCTTCTCACTGCACCTGGCGAGGTAGCCGGCTGCTGCTAATCTTATTCACAGTCTCGGTGAACATGGGCTCAGTCTCTCCGGCTCAGTGTGGGTTGCACCTGGTGCACCTTACAGCGGGAAGAGCTTCTCATTTGCTGAGGGCTTTCTCTGAATCCCGTGTGAATGTGGGT
WI-22668	99	A	G	---	TCCTTTATCCTGCTGCCTGCCTGAGTATCTGGGAATCCTACAAGGATTTGAGGGAGCCCTTGGGATTCCAACCTAACAAATTAGTTTCTGTAATATTA[G]TCTAGTCCATTAGATTGTGTAATGATCTAAATGNGTAAACCATTTAATATCAAAAGTATAACAGCATTTAAGTCAGCTTTTCGAAGAAACCTTTTATT
WI-22631a	52	T	C	---	AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCTGCTCAGTCTGATTCAGTGTGATTCAGTGTGCAAGTTTAGGCAAGTATTAACCTCTCAGGCTCATTTCTCTTTGTAAATTTGTGATAATGGACCTATGTACCATCATAGGGTACTTTGGACAAATCAACTGAAATTTTT
WI-20258	157	G	T	---	AATCCACACTTTCACGAGGGGACAGCCTGCCATGTCGTCCACAGGCTCACAGCAGCGCGGCTACTCTGTGGTGGTTTGGTGGCAGGTGGAGATGGTGACGGGCATTTGGAACCGTAAGGCATGACAACGGAGGCGCGGGGTGTTTACAG[G/T]GCGTTGACGCAAGGTGCATGGCTGGCAGCGGCGCTCTACAGAAGGAGGAGCGCAATTCACAGCCTTTGACGTAGTTTCGGGGGAAGTACG
WI-22714	212	C	A	---	ACTACACATATGCTGATTTTCAACAGTAAAAATAACATTTACATTTGTAGAGAAAAATCTAGGGTCTACTAAATAATCTAGTACTTGTTCACCTCTCCTGCTAACTCTGACAGGAGTGTGTGGGAAACGAAAGTCTGAAAAGGATTCAAAGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTTACCAACCCCA[C/A]TGAGTAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI-22734a	44	G	A	---	TGGGGCTACTTTAGATGGATGGGCTCAGGGTCTGGGAAGCCCT[G/A]TCTTAGAAGACATTACCCAATGATGAGAGGCAGCCAGTCGTCGAAGCCATAGTTTGGATGGCGAGACTTTCCGGCAGAGGAAATAGCAAGTGCAAGGGCCTGAGGAGAAATGAACCTTGGGCTTGTCTACAGGGTGAAGGGCGGCGGCTNTGGCTGAGGTTTAGTGGATG



WI-22724	117 A G ---	---	---	TGATATGATGCTGAGATTGCTTCCAAATATGCCTAGGAAGGGAAGAGTGTAGAGATATAGGA CAAATCAAGATTGTCAAATGTATAGTAACGTGTTAAAGCTTGCTAAGGGT[A/G]GTTATTCTATTTT TGGGATATGTTGGGAATT
WI-22750	48 G A ---	---	---	TGTAACCTGTGTTTCTCTGAAAGTTGAGGGAAGCTGAGGCAGCTAAT[A/G]GGCTCATACAAAGGT TTGGAGACCCATTCTGACTACCTAAAGGAGAGTCAGCATTCTGACCATTCTGACTGTGCT
WI-22775a	60 A G ---	---	---	TGCTGTTCTTTAGTTTCATGACGTTTATCAATGTGCTACTGTTTCCATTGTTTACATC[A/G]TAGTA GGAAAGGGAATAAATCCCTAAGGCGCAGCAATAATTTCTGCTTTTGAATCCTTCATTGAGGCAAA TAATTTGTTGAGCACCAAGGCCAGATGGGAACCTGAGGTATGAGGTGTTGGGAGCCAGGAAGGAAG GGT
WI-22808	143 C T ---	---	---	CTTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAAAGTCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCCAGGA GGATGAAGA[C/T]AGCAAACTGATTAAAGAGAGTAGGTATAAGAACCCAGGGAGAGTGGGGTCCAAAT ATC
WI-21016	207 G A ---	---	---	TCTCTGCTGCTTGAGCCCTCATCCCCACCCCTCCAAAGCCTCATGCCACACACCCGTGTCCACATT CCCCATCTCCCTGCTGCTCCCATCTCAAGTCCAAATCCAAAGCCAGAGCCCTGGCAGCTTTTCTG GGAGACAGCATGAAAGAGGGAGTGAGATGGCAGAGATGGGGTGAGCCAGTGCCTGTGGGTC CT[G/A]TTGGCTGTGATGTGGGGGCCAATCTGAGGCCAGAGTTCA
WI-21031	31 C T ---	---	---	TTGAACACCTGACCTGACCTCTGACATGGG[C/T]CTCTGGTCCCATTTGTCTCCAACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAAACACACACA
WI-21314	122 A T ---	---	---	CCATATCCAGTCTCTTTGAAGCTTCTATTGACTTTTAGGGTTGAGTTATTATATCCTTTATCACTAT GACTTTGATTTGATTTTATTTGTTCTCCATTTCTCTGTCAAACTTTTC[A/T]TTTGTATAA ACTGTTTCTAAACTTCACTTAATCTCTATCTGTATTNCTTGTAGTCCCTGAACCTCTTTTAGAGG
WI-21186	95 G A ---	---	---	AGCGAGCATCAGAAATCACCTAGAGGTTGACTAAACAGACTCTGGACCCAAACCCAGAGCTTCT GATTCAGTAGCCCTGAGGTGGGCTTAC[G/A]AATTAGTATTTCGAAGACCTTCTTAAGTGTGCAG ATGCTGCTGTCCCGGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCTCTTTTAA GGAGAGACAGGAATCCAGAGAAACTGCTAATTTAAGCATAATGTATTGAAT
WI-21187a	94 A G ---	---	---	CCACGATAACTATAAAGCAGAAAATTAGCTTTGAAAATCAATTAACATAATTTAGTAACACACATT CATTTTATAACACACATAAAGACACC[A/G]GGNTCTCAGTAATGCTCTAGTCCAGGGTTCTCAA AGTATGGCTTCAGACAAGCCCCATTTCATCACCTAGGGGAATTGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAAACTCTGAGGGTGAGACCAAGCAACCTGT



WI-21190	39	T C	---			TTTCCCACATACCAATGCACCTGTTTGTATAAACTATT/CJGTGGGTAAGCCCTCTTTGGAGAC CAGTGACATAGACATGATCCCATTTATATTAACAATAATTTAATAATCTGTACTATTACTGC TTTAGTTATCTAGTGTATTGAGAAAGGAGAAGTCAGCATAGTTTATTTTCCATGTAATAAAGCTT AACACA
WI-19937d	186	G A	---			ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGAAGGAAA GAACTATTGCACAACCAACATTTACATATCTGATTTAGACAAGCAAAAGCAGCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTTGGTGTCTCCTCAGCAAGTC/GATCCAAACCTTC CAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-19937c	185	C T	---			ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGAAGGAAA GAACTATTGCACAACCAACATTTACATATCTGATTTAGACAAGCAAAAGCAGCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTTGGTGTCTCCTCAGCAAGTC/GATCCAAACCTTC CAAAAGAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-21117b	227	C T	---			GAAAAAGGGGTGCTAAACAAAGAAAAAGTCTCAGATCCCAGTGAATACTGTTTCAGTTTCACAGGCTC TCTCCAGAAAAATGCATATGTACCAATTTGCATGTACATTTTCAGAGCCTTCAAAATACATTTCTGGGG TCCAATCACATACTTCAGGTTTCAGACTCCTAGCTCCCAATATTCTACAGTTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGATTTC/JTJTTCTACTGAATCTTGGGTGGGAG
WI-21122a	42	C T	---			TCACCTTTGATCATAATCCCCTGTAAGCTAAAGTTATTCATC/JTJTAACAGGAAGTCTGTTTTTCC TTATCAATGTACAAAGCCTGACGCGTTACTGTACATATTGCTAGCAGGAGACAAGTGGAAATACT AAACAATACTGGAATTCACATTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCCTATTGTGGGTGCT
WI-21254	53	A G	---			CAGTTTGGTACAGGAAGGGCCCATGAATGTGGGCGGAAGTATCCACAGGAG/JGJCAAGGAGAAG CTGTTCTCTGG
WI-21054	23	G T	---			AAGGAACTGCATGGGTACAAATG/JTJCCAATTCATACTTAACAAGGTGGGAAACGGGTCAATTCT TGGCTGCTCCAGAACAGGGCGAGTCTATGCACTCCTG
WI-21059b	181	T C	---			GGGACCAGGGTAACACCATTAAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGGTGAA CTACAGCTGCCAGCATTTCTGGGCTGCAATTTCCCACTTCGTCACATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTCT/JJATTTAGCCAGGGGCAAAA TGAGATTAGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT
WI-21059a	63	C T	---			GGGACCAGGGTAACACCATTAAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGG/JTJ GAACTACAGCTGCCAGCATTTCTGGGCTTGCATTTCCCACTTCGTCACATCTTAATTTCAAGCTG AAAAATCCTGGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCTAAT



WI-20442	37 T C ---				TCCACGTGAAGGAAGAAAAAANGGGGGGGGCTT/CJTAAGGTGGCACAATTTTAAAGAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAAACAAAAGTGCAAGTGATGAGACGAA CA
WI-21235	43 T C ---				GTGACAAGAGGTGAAGCAAGGGACAAGGGGACAGGGGAGTCT/CJCTCGGGCGCATGTTCACAGG CAAGCTACGTA
WI-22012a	57 T C ---				ATCAGAACTGCAATCTGCACATGAAAGACCTGGGGGAATGCCTACATCTGGAATTT/CJCATTAAC ATCAACGTTAAATTTGTCCGACCACTTCTCATTTGCTGATCATTGATAATGACAGATCCAAACAT GAAACTCCTGAAGCAATGAATATTACCTTGCTTTTCATGCAAAATTTAGGACCAAACTCAAAGG TTTCATCCATGCTGGGACACCATGATCTAAGGAATTTGACAGGGATCTTCT
WI-21149a	167 G A ---				AGGACCTGCTCTCACACGTTCCCTCACCCACCAGCTTTTGCAAGATAGTTGACTAAATACCACT AAATAGTGGCTTTTTTTTTTAAACAATGACCTTATTTTATCTTTTAACTTTAACTGAGTCTTATATA CAGACCTGCCCAACTGGAAAGCTTTTACAC[G/A]TGCTTCAGAATGCGGCGATATTGCACAAATGGTT TGGGCGAGGTTCTGTGGTTAAACATGGGATGGATGGAACCCACAGGCTCTACTG
WI-21376b	188 A G ---				GGTGCAACTTGGAAATAATGGTTTAAACACAGGATAAGCATTAAAGGAAAAACACTTTCAATGTGTC TTCCATTTGATGAATTTGTTTTCTCTTTATCCCGCAAGTGGAGTTTCATGCTCGGTGAAACCA GACAGTGTGAATCTGTTCCAGCCCAATCTGCAGCATTAGGGATGAGTTCTC[A/G]GAAGTGATTCT GAACTGAGCACGCACATCATGCTGTCATGGGAACTCTGGGGAGAAGAGCCT
WI-21382d	125 C G ---				CCATTGCAGTCCAGAGATGAGAACTGGACCAGAGGCAATCATGAACAGACGGGAGTCAAGAGA AGGGTTTCTAAGATGGAGAGTGGGGGGGTTGGATCCAGTGGGATNGGCTTCCQ[C/G]AGGTT GCAACCCCAAGGAAGTCTCTGGAAGCAGCACCAGTCTGATGGGGAGCAGAAGAGCTGCCATCCTC AGTCAGGTCCGAGTCAGGTCCGAGGAGAGCTGCTGCTCCATAGTCTCGCAC
WI-21437a	201 G A ---				TCCCTGAGGTTGGAGTCTAGCATAGCTCCCTCCCTCAAAGAGGGACAAGGGTCAAGGGGCAGAGC AAAAATCCAGTCTGCTTCAACCACGAGAGTGCCTTTGGGATGGAAAGTTCTGGAGCTCCCTCCATT CTATTCTGTGGGGCAGGAACATCCAGGGCTGCTGGTAAATGGCAGGGGTACCTTTACCAGGGQ[G /A]CAGGCATAGTGTGGCCCTGCTGCTGCTGGGGCCACCCCTGGGAACAGT
WI-21202b	156 A C ---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATCT GTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTTTAAGTTAACTGATTTATTGAGGG AGGAGGAGAGAGTTGACCAA[A/C]GTCTACATGCATAGACAGTCTCTAAAGCGTATCTCTCAAAACATG A
WI-21202a	61 T C ---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGTA TCTGTTTTATGAACATGATTTTATAAAATGGTCACAATATATTTTTTAAGTTAACTGATTTATTGA GGGAGGAGGAGAGAGTTGACCAAAGTCTACATGCATAGACAGTCTCTAAAGCGTATCTCTCAAAACATG A



WI-21627b	153 A G ---			GCATGAAVGAACCTCCATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCATTTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAAJAGJTCCAAAGTCATCTAATATTAACCATATTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAATGTGTTGCTTA
WI-21627a	106 A G ---			GCATGAAVGAACCTCCATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCAGJTATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATATTAACCATATTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAATGTGTTGCTTA
WI-21399a	75 C T ---			GGATTTGAGTCCCAACTGATCTCAATTCACCTCTTGATGTAAACAAGCTCATCCCTCTAAAGTT TCAGTTTC/JTTTACCAGTAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATTGCTTGGTAA CTGCCCTCTGCATTTGCTCTGAGGTTGTGTGCCCTAGGACTAGGATCTCTCTTGTCTTCTGCC TTACCTAGGCATAGTGCTGATAGCAGGCTGAAGCCCAATTCATCTGT
WI-20329a	68 G A ---			CGATGCTGCTAAGATAGGAGGTTAATCTTTACATGGTGAGTGGGTCACAGAGACAAGACATCAAT CJGATJCTGTTAGCAGCGAGAGAGACACTTTAAGTTGCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTGTGGCTTCTTAAACACAGTAAACCAATCAAAAGAAAGATTTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACAGAGCCCTTGAAGGGAAAGGCCCTCACT
WI-21249	155 T C ---			TTCTGGCATTCAAATGTACATGTAAATCCCAATTAACAGATCAAAATGTTACACTAAGTTTCAC TAGTATCTAAGTATCCAATCACAATGTATCTAAGTTTCACITTTAAGAAACATTATAAAGGTAAT AAACTCTAGGTGTACTTAT/CJATGGAACAGTATTTATCCNATTTAACTACTGTTTCATTGCGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTAAAGGAATTAATAAACATTGAGA
WI-21504	147 C T ---			TGACACAGCATCAATTTTCATGAATACITTTGAAAGGGCCATTAGAAAAATAAGAGCCAAITTTGGGTC ATTTGAGAAACATTTTCAGCACAATTACAGTGGGGGACGGGCCGCTTCCAGCTGGGTTTTCOC AGATGCAACAAT/CJTGCGGTTCTGGCTTCTCCACTGGTGGGATGGGATCGCGCCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---			CTGCACAGGGAGGACAGCTGCTGGCAGGGACTAATAAACCCCTTCACCTGGCCATGGTGGTGTGT CTCTATGGACCGAGGCCCTGAACCGGGCAGGGAGGGGACAGAAAC[G/A]CACTAGCTTGGGGGTG GGCACCAGCTTCAGACCCCTT
WI-21475c	181 A G ---			TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCAGGCTTCTCACTTGTACTAAGCACAG CAGTCTGAAGCTTGGACCTGGGACGTGCGTCTTTTGGAGAAAGGCAJAG/AAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCCGTTCTCCACCCTATTCTCTCCCTCGAAG



WI-21475b	117 A T ---	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGGTGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCAGGCTTCTC[AT]CTTGGCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGGCAGTGGCTTTGGAGAAGGCAAAAAGCCACAGCAGCAAC ACTTAGGAGGAAGACCCCTCCCGTTCTCCACCCTATTTCCTCCCTGAAAG
WI-20893d	207 A G ---	---	TGTTTGTTCCAGCCACATCTTCCAAAGGAACCCACCAAGCCCGTGTGCAGGCTTGCTGCAGGG CTGCTTCGGCGTTAAAGTGCTACTGAGGAATACAATCATTTGACGTAAAGTTTCATCCGCACTCC AGCGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAGT TTC[AG]ACATAACATTGGTAGAGTAACAAACAAACCCACAAAGCCTAAATG
WI-20893c	179 T C ---	---	TGTTTGTTCCAGCCACATCTTCCAAAGGAACCCACCAAGCCCGTGTGCAGGCTTGCTGCAGGG CTGCTTCGGCGTTAAAGTGCTACTGAGGAATACAATCATTTGACGTAAAGTTTCATCCGCACTCC AGCGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGC AGTTTCAACATAACATTGGTAGAGTAACAAACAAACCCACAAAGCCTAAATG
WI-19941c	71 C G ---	---	GAGCTCAAGGAAGACCTTACCAGATAGGGAATACTGGAGGGTGAAGGAACAAAGGTGAAA GGTATC[CG]GGTCTGGTGAGACAAAAGCAGGGGGCCTGAGAACACAGAGCAAGGTGGTTGGAG GGAGCACAGCAGGGTGCAGGAAGGAGATGGGGACATTTCTATTCCAGTGATGTCCCTTAAAT AAACTGGGTACAGGAGCATNTGGAAGGAGAACCAAGGACAGAAAGCAAGCG
WI-21552b	166 C A ---	---	TGGGTACATGGACAGATGTATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATGCGATCTCCTTCACCTCAAGCATTTATCCATAGTTACAAAGAA TCCAAGTATACTCTTGATTATTTAAAATGTAC[CA]AATTAATTTATTTGAATTTAGTTACCCC ATTGTCATCAAAATTCATCTTATTCATCTTTGTAACATTTATTGTA
WI-21552a	66 G A ---	---	TGGGTACATGGACAGATGTATGTTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG /AJTAATAATTACTTCAGAGTAAATGCGATCTCCTTCACCTCAAGCATTTATCCATAGTTACAAAG AATCCAAGTATACTCTTGATTATTTAAAATGTACAATAAATTTATTTGAATTTAGTTACCCCA TTGTGCTATCAAAATATTCATCTTATTCATCTTTGTAACATTTATTGTA
WI-21512	54 C G ---	---	TCCTCGTACTTCATGCTCCCTCCCTGCCCCAGAACCTTACAAAAATATTTCTGTC[CG]TAGAGAGGA AAGAGCTGGTGCTGCTCTGGAGGCAACGTCAGGTCGGGAAAGGCACGTCGTGCTGTGATCTGTC TCAGTGATGGGAGGTCCTCACTCGCCCCACAGGCAGCCTCGGGGCCAGAGATGAGAAATATGCTGTA TCAGTACAGGGGCTGGCTGCTGGGGTCCCAACAGCTCTCTTTGGGGG
WI-21513b	192 G A ---	---	CACATAGTTTCTCAAGAGAGGATGAACCTGAAAACCTCTAAGGCAGGACAAAGCAACTTCCATT ATTCTAGTTTAGACCAGAACTCTTTAATTTTATATTTCTCTTTAATAACTGTCAAAATACACCAATA CTTAGAGGAAAATATTCACAGTATACCAAAACATTTTAAAGTAAAGAGGCGAGTAA[G/A]AGTAG TATTCTCTACATACCACAGTATACAATGATGCCCTTCTGCGAGGTTTAGGAAC



WI- 21514b	133	C T ---				TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAAACCCCAATCTTCAAGGAAAGGAGCACATTACCATGGAGC[C /TJACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGACAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGGTGATTGTCAAGGGTCAATAAGGAACT
WI- 21514a	100	A G ---				TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAGTATCTCAACATTACAAAACCCCA[AGJCTTCAAGGAAAGGAGCACATTACCATGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGACAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGGTGATTGTCAAGGGTCAATAAGGAACT
WI-22020	27	C G ---				ATGAACATGTTGCAGTGGGATGAATTC[GJTTATCATGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGTATCATTTACCTGTATGAGGGTACTT
WI- 19576a	113	A G ---				TTCATCGGTTCTTAATACAGTACAATCCTTTTGTGTTGAACAAAAAGTCACACTGGCAATGATTATTACA GATCCAAAATAGACTCAGGCTTCAGACATAAAAAATTTAACATTC[AGJCTAGTTCAGTGATTAGT CACAGAAANTAAACATCTGCCAGATGTACACAATTTGGTAAAAAAGTACAGCTTCTCTCCACGGGGA G
WI- 21695a	141	A C ---				ATACACAGGCCACAATTGCAGGATGGAAGGAGTGGGCACTTGGAAAGTGAACATACACATGGCAATA AGCAGCCTATCTTTTACCAACCCAGAGTTTCTTGGGCACTGTGATGGTAGGCCAGACCCCTTTCCAA GGGAATA[AGJCTACTACACTAAGCCTACACTGTACTGTGAGAGTCATGTTGGAAACAAGGCCACAGGC AGTGGGAGGAAATGTGATGACTTCACTGTGTTCAGANTTCTAAGGCCAGCAT
WI- 21574a	235	C T ---				AAACCCAGAAATTTAGGTACTTTTGTATTATGAGGAACTCACTATAGGAAGCAACTTATGAGTG TGTAATATTTGATCTAGCAGCAACTTTCCACTGATCCTGGCAGGTGACAGCTCTCAGTGAACAGCGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTTGTGAATGTCCTCAGAGTCACTAGGAGGCCATT GGGCAGGCCAGGGAACCTTACTGCTACTTCCCT[CTGTCTGTGAGGTGGGA
WI- 21644c	151	T A ---				TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGTCACCTTAACCTTTTCAGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTTACCANTANTATTTAACAGACTCAAGTGTACATACAAGCTTG TTTCATAAATAAGGGA[TAJTTCAATCAAGATCCATGGAATGATGCAGTTTAAACATGTGTTCTCAGC TTGCCTACTGACCCTTCCCTTTTCTAAATATGGCAACAGCACAGCAAGTC
WI- 21614b	55	G A ---				TGCTCTTAACCTCAAAAGTCCAAATAAACATATAGACATTTTGANTATAGCTATC[G/A]TTTTAACA AACCTCATATTATGATCACTGTGCAATTTTCAGTCACCTAAATACGGAACCATGACTATTAAATAACA TTTACTGTGTGGGTTTGTGGGACTGAACATAAACCATACGTGATTTCTAAGGTACTAGGGAGTT GGAAACAGCTACTACGGGTCAATGGTATTTTGGGCAAGTGGCTGTGTGTGGG
WI- 21615b	151	C T ---				GACCGAGAAAAAAGTCAAGGCATATGATGTTTGTGCAAGTATACATGACTATTTCAAGCTTATAGA GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTCATACATATTAAAGATAAGGATGGACT CTTCACTGAGTATTATC/TJAGGACACAATCGACGGATGTAATCTATTTGANTTATACCATAGGCC TATTCTATTGGGCCAAAGGGAAGGATGGTACTGTGGAACGGA



WI-21981	61 T A ---			TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATATTCTTGAGAAAAAAATTAJGT CTCCCTTATGGGTACTGTGATTTCATAGGGTGGGATAAGTACATGACAACATGCATGGGATAGA CACTCTGTTCTCTACAGATCCGTGCTTTGGGAATTACAGGAACATAAAGATATATAATGGATGGT ATTACTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAAGTTAAATTTGG
WI-21660	120 C T ---			TCCCACTAGCCTCTCAGTATTAGATGAGGATAGAACAGATACGGGTGAACAGCCTCTCCACTGCT TACTGTGTACCAAGAGGAGGAGGAGCTACCCCAAGCCTAACCTGGCC[C/T]GTGCTTTTTCAG GCTTCTCAGGATGCCACAGACATCTGGGGAAGTGGGATGCAGGAGAGCCAGGGTCTGTCTTC AGGAGGGTCAAGC
WI-19105c	211 C T ---			TGAAAGTAGCCCTCTGGACAGAAAGAAATATTGTGGTCCATGTGGTTGAGTCTGTTAAGAAGGA CACTAAGGCACATGGCTGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTCTT GTCTGTAGGTTTCCAGGCTGGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCCAGTGGATCCTCC ACAACCTTC/TTCAGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCG
WI-19105a	33 T C ---			TGAAAGTAGCCCTCTGGACAGAAAGAAATATT/TGTTGGTCCATGTGGTTGAGTCTGTTAAGAA GGACACTAAGGCACATGGCTGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTC CTTGTCTGAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCCAGTGGATCTC CCACAACTTCTCCAGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCG
WI-21760c	81 C A ---			CAACCTAGTCACTCTACTGATGCAATGATTTGGAGGTGCTTCTCCTAGCTTTACAATAAGNGAGG GACCTCTGACTGCA/C/A/CCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35 A G ---			CAACCTAGTCACTCTACTGATGCAATGATTTGGI/GJGGTGTCTTCTCCTAGCTTTACAATAAGNGG AGGACCTCTGACTGCACCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 T C ---			TCTGCCATATTGTTCCAGCACCACTATTACTGTTATTATTCTTTTGGAGGAAACCAAGNATTAAG AAATCTGTTTGAATTTCCATGATGCTAACTCTATGTTTAAATCCTTTTCTTACCAAAAGGA ACTTCTTAATCACAGAGAAACAGAGGGAAGACTGAGATATGTTGCAGAAATTTATCTCTAC[T/C] AGAGACAATTCATAGTTCATAATCTTTCAGGGTTGTGCTTTACTTGGGGGC
WI-20934a	72 T G ---			CCAACATGCAACATAGTCTTCATTCTTAAAAAGTACATAGTAAAGGTATGAAAAACATTTGTATTCA GAGAA/T/GTCTAAGACAAATGGTCAATATTTCAATGGCTGGCACTAGTGGTAATTCAGCAGAC AAACAGCATGAGAAAAGGCCGGGAGACAGTAATAATACGTGCCCATTTGCAATGAGTTACCCAATC AAGCCCTTTTACCTCCTTAAGATGGCAGATTAGAAGACCCCTNTTCCCCAGGAGA
WI-21561	55 T G ---			TTTCCATTTTATTACGGCGGCCCATCAGAACAAATAGCATCTATACCTTCGAAACCTT/GJCCTCTTAAC CTCTCCAGGCAAGAGGAAAAAGTGATCATATTGAATTCCTCAGAAATGGTGGGATCTCAAGACTT TTTAGAAAGTGCTTATTAAAGTAAAGAGGCTTGAATATATATGATGATAAATGGTAGCCCTTTCTGGA AATAATTTTGTGTAATCTGTTTAAAAAGATTTTTGGATGCATTGTCCCCA



WI-21961c	200 T G ---	---	---	AGCTTTGCTTGAAATTTGGTACTTACTACCTTGCAATCTCTTTATTATTATTATTACTTTTATTTTCCGTAAGTTATGGGTACAGGAGGTATTTGGTTATAAGTCTTTAGTGGCGATTGTGTGATTTGGTGACCCATTACCCAAGGAGTATACACTGCACCATACTCGGTCTTTATCCCTCGCCCCCTTG/CJCTCCACTTTTCCCTCAAGTCCCAAAGTCCATTGTATCATCTTATGTC
WI-21961b	73 G A ---	---	---	AGCTTTGCTTGAAATTTGGTACTTACTACCTTGCAATCTCTTTATTATTATTATTACTTTTATTTTCC[G/A]TAAGTTATGGGTACAGGAGGTATTTGGTTATAAGTCTTTAGTGGCGATTGTGTGATTTGGTGACCCATTACCCAAGGAGTATACACTGCACCATACTCGGTCTTTATCCCTCGCCCCCTCTCCACTTTTCCCTCAAGTCCCAAAGTCCATTGTATCATCTTATGTC
WI-21956	26 T G ---	---	---	CCCCTTTGGGCTCTTTCAAGTGAATTT/GJTTCTTTCGTTCTTAAAGCCCTTTAAAATGAACCTCCATTCTCTGTTCTGAAACTTGCCTTAGTCTGTTTCTGCTTCATGCCCTCAGTCGAATCTTTCTTCTGAGGGCGCAAGGACTGAAGTCTGCTGGACCTGTAGGGTTCGACGCCGTAACCTCAGGGTAACCTCTATCTCTCCACCGGTAAACAGAGGGGTACATTATGGGGTCCAGGTT
WI-21966	148 G A ---	---	---	CAAACATACATTATGGCTGCCCTTTATTTAAGAAATGTTTACTGAGAATCTGTACTGTAAACAACATATTTTGTAGAACATGAGTGAGTGTGTGTGTGTCGCCGCCGCCGCGCATGGCAGTGGCAGGAGGATTCGAATGGG[G/A]AACAGGATAAAAAGGTAAAAAATTTGGTCCGAAATCTTTGCTTATTAACCTTGGCCCTGCTCCTCACAATGTTTCTACACTTAATTCATAAGAGAGGTAGA
WI-21930c	146 G C ---	---	---	TATACTGGTTTTGGTTACATGGATGAATGTCATAATGGTGAAGCTGAGATTTTAGTGTACCCATCACTGAGTAGTGTACATTGTACCCAACTGTAGGCTTTTATCCCTTACCCTACCTTCCACCCCTCCCCATTTTGAGTCT[G/C]CATAGTCCATTATATCACTCTGTATGCCCTTGCATACCCATAGCTTAACTCCC
WI-21139a	165 T C ---	---	---	GCTCTAGTGAAGAAATTCAGGACGGGTCTTCAGAGCAGAGGGCTTGGTTCAGTCCCTGTCTTGCCACTTAACCTGACATGACCTTGAGCAAGCCACTTAATTTCTCTGCTCTCTCTGTGAATGGGTACAAATGTGGGTGAGCAGTAAAGAACTAATACATTC/GJTAGACACTTCAGCACAAAAGCCTGGGGCACACAGCACTGCATGGAATACACAGGTAAACATTTTAAACAGTGGGGACAAAATTTAAGTACGTGGCCAGCTGTGGTGTCTGTGGTCAATTAAGACAATGTTAAGANTCAGGAGTACTTAAGTGTAGTGGTTACAATTTGTTCTCTCAGTCTTTCATTAAGTAAATCTAATAGATATACATATTACTGCAGATAAAACCATCATCAGAAAG[G/T]TAAATTAATTCATATTTTGAGGCTACTCT
WI-20317b	217 G T ---	---	---	CAGGACTTGGTTGCTGCCAACTGCACATAAATGTCCCCTTTTGTGTTGAGTTATGGTTGTGCGGTTTTCTTTTGCAATAAGAAATATGTCCATTATAGTCCAGAGGCTCTTGTCTTATCCGGATGACGGAGGTACACGGGGCGTCCGCTCAGTCCCGCCGGAAGGACGTATTC[G/A]CTGAACCTGGGACGAGTCTACTCTCCCCACAGGAGGCCACGATTTCAAAATCCTCTTTTGTGCAACCTCT
WI-22082e	179 G A ---	---	---	



WI-22082b	67	C T ---			CAGGACCTGGTTTGTCTGCCAACTGCACATAAATGTCCTTTTGTGAGTTATTGGTTGTGTG[C /TGTTTTCTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGCTCTTGCTTTATCCGGATGACGG AGGGTACACGGGGCTCGCTCAGTCCCGCGAAGGACGTATTGCTGAACTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTTCAAATCTCTTTGCTGCAACCTCT
WI-20993	139	A G ---			AACACAACTCCATGCTTTCAAGATTTCCACACCCAGATACTAAGACATAATTAATAATTACAGCAAT TAAACAGTGTAGTTTGGTACAAATACACATATAGCAATGATACAAATTAGGGGAAAAAACCTGG GCTTCTA/GTAAACAAGTGAATATACATTAAGACAGTATTGAGAAATGGCTTCAGGATTAATTTGA TTAATTTAGAGAGAGCCTATTTCAAGGTCTTCCTAGCTCATCCACACACATCACC
WI-21723b	125	A G ---			AAGCGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATAGTAGCTTCAAAAGGGTTAGTCATATTCCCCA[A/G]CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-21723a	82	G A ---			AAGCGATTTTATTAAATTGATTTGGACATACTGTAGGTCAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTC[G/A]ACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTTCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-22132	99	T G ---			CAACAGATGCTTGAGCCAAAAAGCAACATAGGCAGAAATACAATTGAGAAATATCTTCATGTTTC AACCCTTAATCTGACTTGCCCTTTTACTATCCTT[G/C]CCCCATTCTCTAATCTCTTTTGCCCTTACAA TATATTACCTTCTAGGTATCACTCATCCTATAGGAATGCCCTTCTAGTTAATGTCCTGCCCAACA ATACTAACCCATTGAAGGATAACTATGGAAACCTTTAAATGGGACAGTGGG
WI-21006a	106	A G ---			TGACAGATCACACCACATTTTGTGTAACCTTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCTTTAAAGAACACATACACATGTGCACACAC[G/JAGAGGCAAGTACAAAAATGTAACC CCACCAAGTGCATGTGAATGAAGTCAAAAGGCTTCATTTGCAAACTCTGAGGATCATCTCT CTGCTTCAGGAAAAATAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138	C G ---			CTGAGGCCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCTGCTTGGAAATAACTGAAAAGATTCTAT TTTCTCTTTGTGTACAAAGGATTCAAAATATTTACATCTTCTCTGCCAGTTAAACGTGCCGTGG CT[C/G]CAATACACACCAAGCAAGCGTAACCTTGGCTGCCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI-21079c	166	G A ---			AATGAAATGCCACCACAGGTTAACAGCTTGCCATGCATGCAACTGTGTGGCGCAAAATCAAGTTGT TTTAATACCAGTGTGACGCTTGATTCCTCCATGAAATTAAGCTGTGTGCTCACTTGTTTACATAA CTCAGGCCACCCCTGAAATATCTGTAGTGGG[G/A]AATTTACACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT



WI- 21079a	50 GA ---	---	AATGAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTG[AJCGCAAAATCAAGT TGTTTTAATACAGTGTGCAGCTTTGATTCTCCATGAAATTAAGCTGTGTGCTCACTTGTTTACA TAATCAGGCCACCCCTGAAATATCTGCTAGTGGGGAATTTACAACCCACTGACCATCTCAGCTCAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT
WI- 22129a	45 TG ---	---	TCGTAGATTTAGCCATGCCATATATTTAACTTTTAAGGAAAAGT[GJTTATATAACAGTCATTGCT TGTTAGAAATCCAGTCTGTCAATAAGTTAGCTCTAACAGTTAACATTGAAGCTTTATACCTTATATTA AATGTTTAGCAATCTCTACTACATTTTCAAATATAAATAATTTGGTTGCAATTTCCAGNAAAGGCA TTAACCAACATGGGACTGATCCTGGGGCTTCCACTGACTAAGGTTTTA
WI-21941	79 AG ---	---	TGGAGTTAAGTGGGGCTCTGCTATTTCCCCCAAGAGGACTCGGAAGATGTTGATTCAGGGCAGAGT GAGGGGCAGAC[AJGGATGAGGCTCTCTGTAAAGTCCAACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGGTTGGGAGCCTCACCCAGAGAGCCTCACTGCAATGACCCACACCCACTCACCC CAGCACACAGGCACACGCGAGGSCACACGACACAGNTGCACTCACACGC
WI- 18916b	42 CT ---	---	AATGGCATCCCTGTCGATACCAACATCTTCAGCAGCTCAGC[GJTGCTTCCCACCTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTGCCCACTACTGCACTGGACACAGCCTCACCC AATGCCACCTTCATA
WI- 18916a	35 GC ---	---	AATGGCATCCCTGTCGATACCAACATCTTCAGCA[GJCTCAGCCGGCTTCCCACCTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTGCCCACTACTGCACTGGACACAGCCTCACCC AATGCCACCTTCATA
WI- 19828c	200 AG ---	---	TTCCCTTCTCCCCAAGAGTGGGCGAGAAAAGCTTTGTTAACCTCCTTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTGCTGTAGCCTAGTGCCAGGNCCTCTGGCCCAATCTGGGTTCTCCCCAAG CCCATGCTTCTCCACTTCTCACAATCTTTACTTCTCTGACCCCTCACCCACCCCAAAAT[AJG JCTTTTAATCTGGAAGAAACCCAGCTGCACACTGGGCACTTGACCT
WI- 21863b	47 CT ---	---	CACAAGAGTCTGTACAACTTAGGGACACCCAGCCTGGCCCTGCCCT[GJTAGCTGCATGCCACCCCTC ATATCCACCCCATCCCGAGCCTCTGCCCCGACACCCCGAGGCTCCCTGCTGTGTTGAAGTATTTT CTCCAAGGCAGGAATGATCCTTGATCCCAACCCACAGCATCT
WI-19860	51 CG ---	---	TTGACCTAAAGCCTAGCATAAAATTAGCTAAGTAGAATGTTTCAAAGATG[C/GJCTGCATCAGTAT CTCCATCCACACATAATTCTGTTGATTTGCCATTACCCCATAAAATGGTGGGATCTACCTCCCT CCTTGCAAATTTGAGCTGGNCTCTGATCCTGCTAAGGATCTGAAGCC
WI- 19889b	80 CT ---	---	ACCCAGCTCCTCTTACCCTCTGGCTTTCAGTAGGCTTGGCTAATGGCCANTGAAGTGCAGGGCAAG AGGAGTGAGGGG[CJTAGACGATTTATTTCCCTCTTCACTCCCTGTTAGCTTGGTAGTGGCTGTAT TTCTCTACTGATAGTTCCTTGGCCACAGTCGTAACATTGC



WI-19891c	172 C G ---	---	TGTTGGTCTGAGAAATTCACAGCTTACTACAAGGAAGCTGAGAAATTCCTGGTGGCCCTCCCTCCCTCCCG ACTCCTCTGCTGCTGGGAAACGTGGCTTGNCTCCAGACAGCTGTAGATGCCAGCTCTCCTCAGCGG AGTCCCGATCCCTCAATTTGCCATCTGTCTGACTC/GJCGTCTCCCGGGCGTGGGCGTGTCTGT CAGCAGGCGGGGAGGAAGGAAGGAGATCCAGGGTCTGTCTG
WI-20155a	81 C T ---	---	GCACCTGTAGGGGTAGCTTCCATGGTTCTCCAGCACGGGCTGTACATTACCCCTTAGGCTGACCAT TCCCTTGGCGGGG[C/T]GCAAACTGCTTTGAGGAAATNTCCAGGAGGAATAAACTAGAAAGACGC ACCTGCTATTTCACCATACTATGGAGAATACAGCTAATGAAGTGGTGGCAGAAAGCTTGGCCCGTGTGA GTGCCCCAGGGTAAAGTCTCTCTTCTGTCCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91 T G ---	---	AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGGAGCGCTCAGTGACAAAT ACATTATGTCCAGGATAAGGAGCA[T/G]ACACAGGATTTATACCGGTGGCAGCGCTATAGGCA CGATGATACAAAATATAAGTATATTTCCATCTATATAATACACAGCTGGGTGGGGAAGGATGCT GGGTGATCTTGTTCCTCCGAGAGGCTGGGAGGCGGGGGTGGTGGAA
WI-20270a	53 G A ---	---	AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGACGC[G/A]TCAGTGTAC AATACATTATGTCCAGGATAAGGAGCA[T/G]ACACAGGATTTATACCGGTGGCAGCGCTATAGGCA CGATGATACAAAATATAAGTATATTTCCATCTATATAATACACAGCTGGGTGGGGAAGGATGCT GGGTGATCTTGTTCCTCCGAGAGGCTGGGAGGCGGGGGTGGTGGAA
WI-20622	130 T C ---	---	CCACTTTCAATATTTTACAAAATGCTCAGCGAGCAATATGAAAAGCTTCAACACTTTCCCTTTGTA ACTTGCTGCAATAAATGCAACTTTAACAAACATACAAATTTCTCTGTATCTTAAAAGTTGAA[T/C] TAGTAAATTTTATGATGTTACTCATATTTTATTCATATATCTTTAATGACATCATTTGCCAATACATA CATTATTTCTNTAATTTTATTTTACAATAAGCCAAACATCTGTCATGCAG
WI-20768b	190 C T ---	---	TCCCACTCAAACTCCGACCCCAACCTTCTGGAAGGCGGGCTAACAGGACCTCCTGCCTGCCTGC TCACGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTTCTGTATATCACCACCTA CAGGAGAGGTCTATTTCTGGGCAACCCAGAGNTCAGCACACATACTGCTGGG[C/T]CAGGGACTC GTAATTGCGCTTGGTCCAACTCCTCTATGGGGTTTAGCTGCCCTCATTC
WI-20768a	71 C T ---	---	TCCCACTCAAACTCCGACCCCAACCTTCTGGAAGGCGGGCTAACAGGACCTCCTGCCTGCCTGC TCA[C/T]GACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTTCTGTATATCACCACCT CTACAGGAGAGGTCTATTTCTGGGCAACCCAGAGNTCAGCACACATACTGCTGGGACACGGGACTC GTAATTGCGCTTGGTCCAACTCCTCTATGGGGTTTAGCTGCCCTCATTC
WI-21909	153 A T ---	---	TGTTTGCCTTGTCCAGGTACTCTACTGCTTTACATAAATTATCTCATCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAAATAAGGATATTGTTGGTCACTCTTTAAAGAAA TGCTTTAACATACCAAAG[A/T]AGTGGAAATCAATAGAATAAAATATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCCTAAATTTATATTTCTATGTATGGAAAG



WI-22202	128 A G ---	---	TGTTGCTTGGTTGTTTCTGGAACAATATTGGAACACTTGTGTTTTCATAAGCTGTCTGACAGT GGCACAATCCCATCCATCTTCAGGCCCTTTAATAAGTGCAATTAATAATCTGAATTTCTGATTTAAT ACTGTGTGCAATTCATCTGCAAAAGCAACTGGCACAACTCCTTGGCGGTGAGCTCTCGG AGAACATCTAATAATTGAGTCTAGTCTGTGCGGAACTTCTCCAGCTCAC
WI-22189	70 C T ---	---	CCAAGGATGAAATTTCCACATTTATTTTNCCTTTATGTGAATAGAAAATGGCAGTGAAGTGTCTATG AACTGAGGCGAGGAATGGCATGGCGTGGCTGCGGTACCGCTGGACGTTGTGCTTCCAAAAGTACAC TATGTGGTGGAGACAAAGGGT
WI-22283	109 T C ---	---	GGGAGGCATCATAGAAAAACCCTCAGCCAGAAGTTAGGACATTGTGATTCTCAGCCACTAACGA GCTGTAGACCTTGGTCACTAGGCCTCTGCAGGCTCTGGTTGTCCTTCAATTTGCAAAATAAAAACCCA GACCGGTGATCTTTTCACTTCCCTTCCAGCTCTATTATTTATGATTTGCTCTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCACTCAACTCCAATGATGCAAAAG
WI-22290a	136 C T ---	---	GACGTATCTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTATGGGCCTCTAAGCAACCG GCCAGTAGTGGGGAATGCCACATGCAATGGTGAGTGGGGATCTGGGGGGTTCAGGACCTTGTCTTT TCCTTCCCAATCTCTCTTCTAGCCAGAACTTTGCGAGAGCCCTTTNATTTCTCTCCCTCTATTCC CCTCTTTCCCAATGTGCTAAGTCCCAATTCAGACCCCTCCAG
WI-22292	53 A G ---	---	CCAGTGAAGGGTTACAGCCATAGTGAGGTTCCCCCATTTGCTCAGTACCAGAAGTGTTTGAGTAC GGTCGTTTAAAAAATCTTATCTGACCACAGTGGAAA
WI-22387	186 C T ---	---	ACCTTGACACCTGCCATCCGGTGCCATCTCTGGCTGGACATCTATACCCACTCTGGCTCTGAAAG GCTTGTCACCAAAAAATGGCAGCTGGGCTAAGGCATATTTAAACAAGGCTCCAAAGGACCCCTT TCATTGGGTGATGATCCAGCTCTCTCAGCAAAAGGAGGATTGTGGTCTCTCTCTGTTTCTG AACAGGGCCCAAGGCAAGGCATGCCATCACTGCAGCACTCAACCCCT
WI-22395b	127 A G ---	---	GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTTCTTCTTGAATATTT GTAGGGATGGATGAATTGAAAGTGAATTAAGTCAAGTAAAGGGGCAACTCTTTAATTAAGTAAAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---	---	TTTATGGCTCCTGAGTGCCTTCAACCAGCTACACTTTACCTTGTATCTATAAAGTGAATTTAGAGT AAATACATTTGGCTGTAAGTCGACGATCAGGTGCTCTCCACCACCAAGCAAAACAACTGCTGA AATGTGGCAAGTTTCTCAGTG
WI-22419b	67 T C ---	---	CCCTCTGGACAGTTGCTTTATGTGTTCCAGACAAATCAAGGTCGCCCTCCAGGCACAGCCAGTGCCT CTGTGATGGCATCAGCACAGGCTCCCTGCCCGGCCCTTGAAGCATGGCTGTGTGCAAGAT
WI-21342d	59 T C ---	---	ATTTCCCTTTCTGTGTTTCGTAATTTCCCTTTTGTGAGTAAATNAGCAATACACTGATCTCTGGAA ATCTGCATGATTAATAACATTAAACAAGTTTCAACACACCCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCCCTAACCGAATGCAAAATAGGTATCCCTCAAAATGCACATTTCTCCTCCTAGTT T



WI- 21763b	154 A G ---	---	CATACCCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGTAGTCCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATGCGACCCAGATACCTTCCAAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATTGAGCAGACATTGCCTGTGCTTCTACCCAGCAGCTGTCTAGTGCACCTT GA
WI- 21763a	135 T C ---	---	CATACCCCTTTAGGTGCCACATTGATCTTAGTTAACAGTCTTGTAGTCCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATGCGACCCAGATACCTTCCAAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT TTCGCTCTCCACAGCTGATTACAGACATTGCCTGTGCTTCTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-22440	64 A C ---	---	CAGTCCATTTAGTCCCCAGTCGAGGGTGCACTTCTCTTATCTTGTCTTAAGCCACTTTGGGTAA[AC] TCCATTCAGGCTCTGCACCTTCTCCAGTTTCTCATGTGAGAAGTCCCTGGAGGGAGGAGGCTTCTCTGG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGTGGCATATGATTNCCATTGTGTGACAATTTATTAGCTGGCATCCGAATACAGTAC TTCCTTTT[C]GAAAAAATACACAATGGGAACCTGACA
WI- 21965a	112 A G ---	---	CAGGTTCCACCAGAGGCTTTATTCAGCCACTCAGGACCTGGCTTCTGTCTCCAAAGGCACCTGAACA CAGTCAGGCTCTTCTAAACACTGGCAGGACCTCCCCACAGCC[AG]CCCCACAGGGTCTCTGT TCCAAAGTCTGATGGATTACAGCAAGACTTACACATTACCCACTAGCTGCTGGAGAGGAGGCTC ATGAGGCAGCCTGTGTGCCAGCTCAGTGTGACACACTGCCAATGTGC
WI- 21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAACCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGGTTTCTCTAGTCAGAAAGTCTCATGGACTTCTCTCCTAAGC[AG]TGTCTATGATCAGAC CACCTCTAAATGTGGCTTTTACCCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG AG
WI- 22374a	149 T C ---	---	AGCTTTTACAACAAAGCGAGGGTTTAAGGAGCCTGAGAAGAAATTCACAACCTATTGACTATACAGAG TCTTCAATTCCTCAAAACAGTTAATAGTAACTTGGTGGCACATACAACATGCATTGAATACTCTGTAT TATTCAGTAACTAAAT[C]AGGNTCCTGCATCATTCTCTCACA
WI- 22250b	132 C T ---	---	ACTTGTCTTCAGGCAGGCATTTCTGGGATCTAACTAGAAATCCTTGAACAAATAGTACAGCCA CTTTGAGGAATGTGCATTCAGTGTAGTGGTTATTATGGGGTCTCTGCCTCCTGGCTGTATTATGC GGANCCAGGAGTGGAGGAGCCGTGGAAATAGACAGGGGAG
WI- 22250a	89 G A ---	---	ACTTGTCTTCAGGCAGGCATTTCTGGGATCTAACTAGAAATCCTTGAACAAATAGTACAGCCA CTTTGAGGAATGTGCATTCAGTGTAGTGGTTATTATGGGGTCTCTGCCTCCTGGCTGTATTATGC GGANCCAGGAGTGGAGGAGCCGTGGAAATAGACAGGGGAG
UTR- 04932-2b	192 G C ---	---	GCAGCCATCTCTCTCCAAACCTCCAGGCCACCTGGGGCCAGAGCACCTCATGCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCGCTGGCCAGGTTCTCGGCTCTCAGGACGTCAGCAAGTGA GCCAGAGGTTTGTGGGACTCCAGCCAGGGGATAGGCCAGCCAGCCAGAACCTG[C]CJAGTGCTTC TTTGACGGGGCCGCGTGTCTAGCTGCTCTGCTGGAGGTGAGGAAGGAGGT



UTR- 04932-2a	149 C T ---	---	---	GCAGCCATCCTCCTCTCCAAACACCTCCAGGCCACCCCTGGGGCCAGAGCACCTCATGCCAGCAGCAC CTACGTGGCCCGAGTACGACCCGCTGGCCCGAGGTTCTGGCTCTCAGGACGTCCAGCAAGTGGGA GCCAGAGGTTTG/C/JTGGGACTCCAGCCAGGGGATGAGGCCAGCCCGAGCCCTGGAGTCTTC TTGACGGGGCCGCGTCTCAGCTGCTCTCTGGAGGTGAGGAAGGAGGT
stFIBBb	412 G C ---	---	---	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCCAAGGCCCTTGCCACTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACCCAGCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAGATGCAGCCAGGAGCCTCTCTGA AGGACCAGTCTGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
stFIBBa	341 T C ---	---	---	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGCGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCCAAGGCCCTTGCCACTGTCTCTGGCCCTCTCTGATCATGCCAGG TTTGACCCAGCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAGATGCAGCCAGGAGCCTCTCTGA AGGACCAGTCTGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
stGLV2	61 T C ---	---	---	GTGAGGAAGATGGACCTGGAGCGTCTCGGGAGCTCTCCACCATGGCTGGCTCTGCTCCTCACT/CJCTC CTCACTCAGGACACAGGTGACGCCCTCCAGGGAAGGGTCTTGGGACCTCTGGGCTGATCCTTGGTCT TCTGCTCTCAGGCTCACGGGGCCAGCACTGACTCACTGGCACTG
stSG1001 7c	70 T C ---	---	---	GTTCAAGCTCATCTTGAACCTCTGGTGTCAAGCGATCTCCCACTCGACCTCCAGGGTGTGGGAT TA/T/CJAGGCATGAGCCCCACACCTGGACACAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG1001 7a	33 G A ---	---	---	GTTCAAGCTCATCTTGAACCTCTGGTGTCAAGC/G/ATCCTCCACCTCGACCTCCAGGGTGTGGG GATTATAGGCATGAGCCCCACACCTGGACACAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG1002 3	63 A T ---	---	---	TAATGATAATTAGGGCATCTTCCACACGGAAGATGACACAATTGACCCCAATATCATTGAGGC[A/T] AACAGTTTGGGCTGTTTCCAGTAGTATGACAGTGA
stSG1009 6	36 G C ---	---	---	GTGAGGAAGATCGTCTTCTCCTCCCTCCCATGAC/CJGGCTTCCCGGGGCACCTGTGGCTTTTCC ACCCCGAGACGGCTTTGTAGGAGCCCACTGCCCACTCCGCTGTGGGCTGGGTTCCGCTCTCTAG GGCTCGAGTGTTAAG
stSG1011 8	107 C A ---	---	---	TAGGCTTAAACCTGGAATCTACAAGCCAAAGTCCCTCCCTGCCTGAGGGCAGTACCCCTCATTGGGC ACAGTCCAGACCCCAAGTCAAGATGCCCATTCCTTGGG/C/AJCTCAGCCCTCAGTTCCCTTCATTTC ACCAGGCGGTGCTTGTGAGTTTTCCTCCAGTGAG
stSG1012 0	89 T C ---	---	---	TAGTAGGTAAGAAAGCAAGGAGGATGCTTATCGGATGACTGTTTACAGTGGTGTGAGACTATGC CGTGTTCACGAACACITTAATA/T/CJGTGTTGTAATCTGATTTTATCCCTGCTTACAAATG
stSG1017 8	42 C T ---	---	---	TTGAAGCAATATTGTCTAGCACTCTGCTGGACATTAAAGTCCG/C/JTGGAGGAGGAAGTGAACAGGAA TCGATCTTTGTCTTTAACTGCCCTTAGTTAGGAGATGTTAAATACTTGGC



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stSG1019 3	136 GA ---	---	GGAACTACTACCTAAGGACAAAATACTATTATTAATAAAAAAGTCTTCTAGTGATATTGTGTAA CACATTTCTGGAGCTGGTAGGAATAACCAATTTTATTTTCTGTAGTGCCATCTATACAAACATTTTAC T/GA/TTTGAAACTGAGATTTAAGTTGCAAACT
stSG1020 2c	143 GT ---	---	AAGCTAATTTAGTGAATGGTGCCTCAAAAGGCTTTCCGAGGGGAAGCTCAGTCTGGCTTGGGAG AGTCAGCCTTGGTCACTATAACGGGGCTCCAAAGCTAAGCGTCAAGGAAGAGTCCCACTGCTTCT CGCTGTCA/G/TTCAAGACCACAAAGGAGATGCCCACTGCTGCTCTTCTTGTCTACTTCT
stSG1020 9b	75 AG ---	---	TCCTTTCTCTTTTCACTCTCAGTCCACCATGATTCAAATAAACTAAATTCCTTAAAGATCCCACATTTAT TTTTA/G/CTCCAATAAATGTAATTATCAGCTGCTGAAT
stSG1020 9a	34 CT ---	---	TCCTTTCTCTTTTCACTCTCAGTCCACCATGATTC/TAATAAACTAAATTCCTTAAAGATCCCACAT TTATTTTAACTCCAATAAATGTAATTATCAGCTGCTGAAT
stSG1021 8	29 TC ---	---	TACTAGACATGCAAAATGAGAAGATTACA/T/C/GTGAATATTTAAAGAAGTTATATTTGTTGACAT AATATGCATTGTACCCGGGCATAATAAGTTAAAGCCAGTTATTCIGA
stSG1025 2	108 AC ---	---	ATAGTTTCAGGAACAAAATCATTAAATGGAATAATGAGAAGATTCTTTATTTTGGACCAATTTT AGGCACCTTAAGAGTTTCTTTCTCTCTTCCCTTGATCA/A/C/AGTGAAGATATGATAGGGAATTC AGAAATTCCTCTCTTG
EST10915 0	123 AC ---	---	CTGTATTAATTAAGAAAGGCACATTAATGAGGGACGGAAAAATCTACCTGTACACAAAATTTCTGTAC TTTAACAGCATCTTCAAAATAAACCTTTAAAGGATAATGGTTTACGATCATTTTAAAG/A/C/JATTTTAA GAACTGAGTTATTTGGAC
EST11023 1	166 TA ---	---	TTTTTTGTTAAACCAACCCCTGAAAGTTCCACATGTGAAATATAGATACACAGTGAACAAAAT ATGTGGCCTCCCATGTACATTGGTTACCTATGTACAAGTATCTCTATACCCAGTAAACACAGCAGGGC AATTAGTCAATTAATAAAATAGTACATGTTA/T/A/JGTGTAATAAAATTAATTTTACAAAGGCTTT TCCACTCGTGGATTGTATCCCTTTTGGAGGGAGTAACTCTGG
EST14096 8	71 GC ---	---	GGGATGTATATTACAGATAACACAACTCAAAATATACCATCAGACATTGAAAACATAAGGCCATTCT GTGA/G/C/JTTATTTTAAACCTTGGTGTGTTTGCACATAATGATCTTAAAAAAATGAATTACCAA ACCAAGATTCTCTCTAAATGAAAATTTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATC TGAAG
EST22113 6c	125 CA ---	---	TGCAAAATTTGAGAAGGACAGGGGGCCAAACCCCTGGGACCTCATCTCTGTCTAGAAATGTGAGGTGG CAGGGATGCTTAAGTCTTCTCTGGCAGAGACCCGAGGTGCAGAGATGATCTCTCA/C/AJCCCTTC TCTCAGGGTCTGGAG
EST22555 7	60 GA ---	---	TCAAGCATGTGTAAAGGCACCTGCCCGCCAGACCCCTTCACTTCTGCACACTGGAAGGT/G/AJAA CCTGGAGAGAGAGACACTCCCTCCCTAGCTTCTAAGTGGGACCCCTCCAAAGATGAGCATTCATC TTGGAGACC AAAATAAAAAAGGACAAAAGACACCGGGCTCAGAG



EST22917 6	74 C T ---	---	GTAACCTTGCAACGCCATGCTAAATGGAAGCCTGACTGACCAGGGGCTCTGGGCTCTCAATGCA ATAGAAAC/C/TTGACATGGGGCCAAAAGACTTCCAGACAAAGACGCGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---	---	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGTAACTTAACCTCAGGCTGTCTACTCA/A GTTGGTTTGTAGCCTCACTCGCACACAGGAAGCTTGAATTTGGAGGCTCCAAGTCACTCTCCA
EST36745 3	56 A G ---	---	GAGGGGAACCTCAAAGAGGATTCCAACAGTGAAGCAGAAATCATGGGGCAAAAGTC/A/GJCTATGG GGCAGACTGAGGTTGGAACACACACAAAGCACTCCAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGCACGGAGTAGCCAT
STS- R37410c	201 A T ---	---	TGTGACCATACCAAACCTATGCAATAAAAGAAAAGAAAAATCCTCACTTAAAAAAAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCCTTTTGAAGTGTGAATAAAAGTTCATAGCATTTTGGGA ATTTATGTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAAACATTTCTGGTATG T/A/TJATTGTGAGTGGTGCTCTAGTGGCCAAT
STS- R37410b	139 G T ---	---	TGTGACCATACCAAACCTATGCAATAAAAGAAAAGAAAAATCCTCACTTAAAAAAAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCCTTTTGAAGTGTGAATAAAAGTTCATAGCATTTTGGGA ATTTATG/TJTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAAACATTTCTGGT ATGTATATTGTGAGTGGTGCTCTAGTGGCCAAT
STS- R37410a	48 C T ---	---	TGTGACCATACCAAACCTATGCAATAAAAGAAAAGAAAAATCCTCA/C/TJTTAAAAAAAACAA AAAAACCTTTGCAATGCTATCATTTTTCAGGTCCTTTTGAAGTGTGAATAAAAGTTCATAGCATTTT GGAATTTATGTTTGAATAAAATACAAAATGTGTGATCTCCTGAGACACATTTATAAACATTTCTGGT ATGTATATTGTGAGTGGTGCTCTAGTGGCCAAT
STS- R42778	74 C T ---	---	TATCGTGGGAAGTTCCAACTCATACTTATGCTGCTTTTCTACTTGCTAATAATTGGATGCTTCTTGCCA GGCTC/C/TJTTAAATTGTGCTGTAACTGGGAAGAAACCTTCTACTCCACAACCCCTGAA
UTR- 04350	125 C G ---	---	CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTTCAGCAGCTGTGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCTCCCGGGATGGTGAATAATGTTCCGGACCTAGATA/C/GTGCAGCA AGGTAGCACGACACTGTGAGTGCACATAA
sISG1026 6	55 T C ---	---	GAAATAAACTAAACTGCAAGCAATCACTGTTAATAAGAATTGTCTTCTCTGT/C/GACAGTTG AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGGAGCCAATGAGGTCTCAGAAATCGGGGCAAA CTCCTCTGTGAAAATGTAT
sISG1028 2	70 T G ---	---	GTATAATTACAGCATAGCCAAAGCCCTTTTAAAATAACCAATACTATCATTTTATGAAATCTTTTACA AGA/T/GJAAGCACAGTAGTACAATAATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
sISG1031 0	128 C/A ---	---	CACTTAGATATGAGGAAAATGGTTTTAATGGACACAAAGGAGTCAGCCACGTTGGAAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTGTATGCAATAACAGCAATAATTTTTTCACT/C/AJTG TCAATGCCAATGCATTGAAGGCCCCAGAAAATGAGAAAAGGATAACAAACCTTTTGATAAAAAGGTA AGAAATCTGTGTG



stSG1033 1b	116 T C ---	---	TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAGGATGCATTTTCGG GCTCCAACCTGTCTAGGAAGGCTAGACCTCAACACCAACCTCCAT/C/GCATTTCCTCTTTGG CTACTATGCTTTCCCTGACTTCTGCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCCCTCC
stSG1033 1a	107 A T ---	---	TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAGGATGCATTTTCGG GCTCCAACCTGTCTAGGAAGGCTAGACCTCAACACCAACCTCCAT/C/GCATTTCCTCTTTGG CTACTATGCTTTCCCTGACTTCTGCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCCCTCC
stSG1243 b	225 G A ---	---	ATTGGCAATGGGAAATGACACCAATCATTTGATTACAGAAATGGTTTATAATCCTCCTCTTG AAATTATGTTGAGGCCAGCATGGTAGCTTATGCTGCAATCCAGCAGCTTCGGGAGGCCAAGGAGA AGGATCGCTTGAGCCAGGAGTTCGACACCAAGCTGGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATCTGTTT[C/G]A/AAAGTATTTTCAGACCAAAAGGAGGT
stSG1345 b	60 G A ---	---	AACTGACGTATCACAGGGGCAAGTATCTCTGTCATAAATTTGAACCTAGTTTGCCTTAC[G/A]CGCT TCACATTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA
stSG1345 a	54 T G ---	---	AACTGACGTATCACAGGGGCAAGTATCTCTGTCATAAATTTGAACCTAGTTTGCCTTAC[G/A]CGCT TCACATTTAGCATGGGCCAAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA
stSG1385 b	117 T G ---	---	TTAATGTCATCCAGGAGGGGCGAGGATGAGGGAGGGTTGAGGAGCGAGGAGGAGTTATTT TGGGTGGATTACCACTTTCCCATGAAGAGGGAGACTTGGTATTTTGT/GTCAATCATTAAGAA GACAAAGGGTTTGTGAACCTTGACCTCGGGGGGATAGACATGGGTATGGCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTTCTCGTCG
stSG139	69 T C ---	---	TCGTCTCCTTTCCAGTGTCTTCCAGAAAGCATCCCCATGATGTTGTGACCGCACAGCATTGTGTCT T/C/GCTTTGAGCACTTGCCACTCTGGCTGGTGTGCTGCTGCCACTGATTGTGTACTGTCTGTGCTGCCC GATCTGTTCCAGACAAGGCTGATTACAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTCAATCCCT TGGCTCCTCCACTTCCAGTTGGCTTCTGCTCTCCTCAT/C/GAGTCTCTCTCCATGTGGCAACCAAGATGGC TACTGTTGGTCCAGGTTCACTGCTCTCAGCTTGAAATCCAGCAGCAAGAGATGTCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG
stSG1427	103 T C ---	---	CCCTGGAGTTTCTGAACATAGGAAGAGAATGCAAGTCATGTGTAGGTCC[G/G]CTCCCTTGCATGA AATGTGGGAGAGGGAAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA
stSG1471	50 A G ---	---	CAAAACCAAAATCCTTCCCACGATATATTACTATTATGTCGAAGT/CJTTTAATTCAAAGGTTGAGA ATGACGAATTCAGAAATTTCTTCATACATAAATGCTTCTTCTAGTTCTGCAGATGGGTA
stSG1483	44 T C ---	---	CACACCAACAGTTTCATGCTAATGCCAAGTATCAACTCTTGAGGACAAAGGCAAAACCCAGTGTGCA [C/G]AATGTGGAGGATGTCTGTGTCAGCTGTAGTTACTAATGCAGGAAACCCCAATGCAAAAGAGGAA AATGCTCTGA
stSG1696	67 C G ---	---	



stSG1847 b	95 GA ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAATGAAAGAATTT AGAGTTAAATAAAACAAGTGAGAGACC[G/A]TTTACTTACATCAGTTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATACTTGATCACTGTGCT TCAAACACAACCTG
stSG1847 a	49 CA ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACC[C/A]CTAAATGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACCGTTTACTTACATCAGTTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATACTTGATCACTGTGC TTCAACACAACCTG
stSG1897 a	83 AG ---	---	CTTAATGCCCCCTTCTCTCTCTGCACAGGAGACACAGATGGGTAAACATAGAGGCATGGGAAGTGG AGGAGGACACAGGACTT[AG/G]CCCCACCACCTTCTCTCTCCCGTCTCCCAAGATGACT
stSG2022 a	86 TC ---	---	TGCTCTGAGGTTTCAAATCTGAGATATCTATGGCAAGTTTATAAAAAAGTACATTGATCAAGGTACAA TTTTTAACATTAAATATACA[T/C]ATTCATAATCTCATCTATTTAACATTAAACACAGGCCCTTTGTTGT TGTTATTTTCTCCCTACAATATTTCTGACTCTGTAGGACAGTGGCCCTCAGTTGGGGGTTGAC T
stSG2076	104 CG ---	---	AAACGTTGTCCCAAAATTTGTTTCAGTTTCACAAGTATAAAATAAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAAACACTTAAGAATATATTTGACATT[C/G]ACATCACAGTGGGCATTTT
stSG2108 c	71 AG ---	---	TTGAGCAACAATGATTCGGAAATGGGCAGCTCCAACCAAAAAATGATT[C/G]AGGGGCTCCACAG GAG[C/G]TAAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGCTTATTTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2108 a	49 TC ---	---	TTGAGCAACAATGATTCGGAAATGGGCAGCTCCAACCAAAAAATGATT[C/G]AGGGGCTCCACAG AGAGAGCATAAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGCTTATTTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2141 b	173 AG ---	---	TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGTAATAATCTCAGAAATGGCAGCACCCTGGCATGGCGATGGTGCAAGTGGGT GCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAAG[AG/G]AAGTCCCTATTATTATTTAAGGC AGTTTCAGAGCACTGGCATCTTGTGCTG
stSG2141 a	113 CT ---	---	TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGTAATAATCTCAGAAATGGCAGCACCCTGG[C/T]ATGGCGATGGTGCAAGTG GGTGCAAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAAGTCCCTATTATTATTTAAGGC AGTTTCAGAGCACTGGCATCTTGTGCTG



stSG2148	50 A G ---	---	---	TGGGAACAACCGGCTATAGTCTGAGTCATATTTTTAGACCGTGATTTC[A/G]AAAGAAACAATAA ATGTGGATTAGAAAGGAAACATCCATTACTGTATTTTCGATACTTGTGATGTTCCACAGACGAGCTC ATCAC
stSG2175	68 C T ---	---	---	CTCAATGAGGACTCCATCAGCCAAAGCGTTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGCT [C/T]GCCGCGTGACTCAGCTAATGCTACCGGGTTGGAGCGCACACCGAGCCAGCCACCTTTTCCAT ACCTGGCAGAGGAAGGAGTGAAGGACCA
stSG2189	41 C T ---	---	---	CAAGTGTGAAAGCTGGGATTGAGCCTGATATTCACACTA[C/T]CTACATTCCCTCCAGTATAATA GGAACATCGCTAACTTTGAGCACTTAGTGTTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTC CAGCTTTGCGAAC
stSG2200	49 T C ---	---	---	TGTTGATGACCATAGAGGATGCAAAAGCTCCGGGCTGTTCTGTATGATG[T/C]TTTATATTTATGTAT AATGTCTTACCTGATGATACCCCAACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85 G T ---	---	---	CATTTCTGCCTCCTGCTTCCAGTACTACCCCGTCCAGCAACTGCCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAG[G/T]AGAGCATCTCTCAGCCCTGGAAGACAGTGTGGAGCTTCAGCT
stSG2257	65 A C ---	---	---	TCAGTGATTGAGGAGCTGGCTAAGTCATGCTAACTCTGTGAGGCAGGCTATCAGAAGGGCAG[A/ C]CTGTAGGAACTCTCGCCAAAGCACTGGGCTGCTCTCAGGCAGAAATTTCTCCT
stSG2306	67 A G ---	---	---	GTCATCAGCGTAGAGTCACTGGTATAAACAACAGTAGCTATATGATATTTGGAACTATTTTACA [A/G]TATGCTCCCATTTGGGTTTCCAAACTGATACAACCATGAGGTGAACACTTTCACCTGTTTCACAG TTCCTCCAGAGA
stSG2334	70 T G ---	---	---	GAAACTACCCACAGCATCATGTTAAAAGAAGAGAGATGAAAGAAAAAATCCCGCAAAAAACA AAAA[T/G]TCAGTGGAGGGGCTGTGGAGGGGTGAATG
stSG2339	63 T C ---	---	---	AGAGCAGAATGGTGAATCAACAAGACCTCAAATTTGCTTGAAGTGCAGAAAGTAACTGCTGCAC[T/C] GTTCTCAGAGTCACCATACGGTGACTGTGCTATTCTGGCTGCTTCTTCTATTCATCA
stSG2465	76 C T ---	---	---	CAAGACTAAGAAGCCGCCAGTGGTCCCACTCAAAAAGAGATTTCTGATTCTACCTCAAAATG CAGAAACCA[C/T]TACAGATTAAAGAGAAACACACACACACACTTTGAGAAACTCGCCCTTCCTC ATCTCAAAGTGGGGTATGCA
stSG2549	140 T C ---	---	---	TTGCAGGCTTGATTCCACAATAACAAAGTCATGTATAGAGAATGTGAAATGATACTTGAAAAACCAA GATATATAAATAATTGAAGTCATTATGCCCTTTTATGACTGGGTTAAATATGCAAGCAGCTAAAG GAATA[T/C]TACACCACCCACCCCTTTTAACT
stSG2577	123 T G ---	---	---	AATTGCCAAATGGAAATTTCCAGAGGATTTTAGACCAACTTTGCCCTGTTGCATCCCAGTTTGGT CCCAATATAGGCCCTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAGCA[T/G]GAACAATC CCGGCCCGAGATTAAATTAT
b				



stSG2577 a	121	C T	---	---	AATTGCCAAATGGAAATCCAGAGGATTTTAGACCAACTTTGCCCTGTTGCCATTCGCCAGTTTGGT CCCAATATAGGCCTTCTGCAAGAGAGATCAATGCCGAACCGAAGTGTAAAG[C/T]ATGAACAATC CCGGCCAGATTAAATTAT
stSG2700	58	G A	---	---	ATCTCCTCGACTGCTTTAGTGGGAAAGGAATCAATTATTTATGAAGTGTCCGGCCCC[G/A]AGTCAC TCAGCGTTTGGGGAAATAAACCACTGTCCAGAGAGAGGAGGCTACTTGAGCCGGACACCA
stSG2724 b	101	T G	---	---	AAACAAGCTTTGTCATTTTCCACTACATTTTGTGTCTTTTATATTAATTTGCAATGCTATAAT TTAATACTTATATCCAAATGCTTGCATAATCA[T/G]TTTTTAACTCTGGGTGTTGAAAGAAC
stSG2776 a	65	G A	---	---	GTGGCCGATCTTTACTTTCCAGAAAGGCGGTAAATAAAACCTGTAGAAAGTCTCGAATATGC[G/ A]TATTGGCCCTTTGGAGTTAGGCCAGGAACCTCAACAAGGGACACTGCTGGCCAAACCACAAA ATATCCACTAATCCCGAATATAGTAACCTGTCTTGTCCGAATG
stSG2791 b	109	G T	---	---	AAGGAAGGTGGAGGGAAGGGAAGGAATACAATGGTTAGAAAAGAGCAACTAAAGATTATTC TATTACTTCTGAACGGTAACTAGCAATTTTAAATAATTT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2791 a	100	A G	---	---	AAGGAAGGTGGAGGGAAGGGAAGGAATACAATGGTTAGAAAAGAGCAACTAAAGATTATTC TATTACTTCTGAACGGTAACTAGCAATTTT[A/G]TAAATATTGGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2826	85	C T	---	---	CCGCAATTTCAACACACATCTATGAAAACTAAGGGTGGATCATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAAAACA[A/C/T]GAACAAAAATAAAGAAAGAAAAACCCATGAAATGCCAGGTTTA ATTTTTTTC
stSG2850	88	G A	---	---	ATGGTGCATTGTAAAGGCAATTAATACTTTTCAGGCAGGGGCTGGCAATTTAATGAGCTGA TGTGTCCCAAGGGAGACGGCC[G/A]GGCTCACACATCCCAATCAATCTCTCCCAT
stSG3031	71	T C	---	---	ATACTACGGGGGCTGAAGGCAATGTGAAGAGTGAAGTCAAGTCTGGCATTTTCTGTGGTGCAGC AA[T/C]GCCCCCTTATTTAATGATCCAGACATCTGGGCAGCATAGCT
stSG3058	81	G A	---	---	GTCCCAACTCTCTCTCTTAGAGAAAAAACTGTGATTACCTCAACTTGAATATGAAACTGTGATTG AAAAAGTCAAAAC[G/A/T]GAAGAGCATCAAGGCCAAAAAGGCAAACTGGCTGAGGC
stSG3092	94	T G	---	---	CAGCATCTCCAGAACATTCCTAGAACTGAACCATTCCTGTCACTATTGAAAAACAAGCCAAAGTTC CAATCCAAAAATAATAATGAACGTGC[T/G]GATAAACATTCCTTATGGTTCAGCCCCCTACTTT AGTT
stSG3230	95	A G	---	---	AAGAAGTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTCGAGATACGAGCACCTG CATCTTTTAGTCAATTGTCAGTGGAGT[C/A/G]TGGGGTGTAAAGTGTCTGAACCTGAAGTAG
stSG3245	160	G C	---	---	ACATCTCATACCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGCAGCCCTGCTCCAGGGGCC CAGGTATGTGAGAGGCCAGTGGGGTGGCCACTTGGTGTCTACACACCCCTGCCATCCAGTCTG GCCCCAGTACCTACCTGGGAGGT[G/C]TGTACTTGGCTTAAGTACTTTCATGCTTTAT



stSG3265	42	T C ---	---	AGGTGAATGAGTTACTAAATGTAGCAATTTATTTATAAGGAAAT/CJGCAATGTGTAATAGTTTCTCAG TTTTCAATATGGAAGATGATGATTTTCAGCCACATTCAGTGTATGTTTCTAAATAACACAATCGAC AGGACTGTCTGTTCAGTACAATGGAGGACAGCTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA ATCTGTCTTGTCAGCTGAATTTCTTGGGCTTTATGTGGCAGTGTGGTAAAAA
stSG3269 b	141	C T ---	---	TGTACTTACTGTGTCATCCTATCCATTCCCTCCCTGAGCCTGGAGTGTCTTCCAAAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAAGTTACCCCTTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA/C/TTGTAGATCCCCAAGTCCCTGACACATTTCTTCTAAGAACT
stSG3269 a	24	A G ---	---	TGTACTTACTGTGTCATCCTATCC/CJGTTCCCTTCCCTGAGCCTGGAGTGTCTTCCAAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAAGTTACCCCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCCAAGTCCCTGACACATTTCTTCTAAGAACT
stSG3284	130	C T ---	---	TTAACTCAAGAACTTTCAGTTACAGGAAGATTTATCTAATATTAATAAGCTAAATACAAAAAGC ATAAATGTTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCCA[C/T] TCCCTAACTTTTGTAAATGCTGTAATGGGACATTTGTTGTTGATCTACCC
stSG3292	99	A T ---	---	GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAATCGGTACATGAGGCTTAGACATA CACATCATTTGGACAAGTGACTTAAATATCTAA/JTTCACAAATCAAAATAGCATTTTCTAACTTCAA TAAATGTCATATCTTTAGCTCTCACT/CJCCAGTGTATCCATTTCCCGAGCCGTAGAGCTTTCTG TTCTGTAGATTGCCGTGCTCGACATTTGATAATAAGGAGTGTGTATCATGTGACTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGGTCACTGCTTCTTCTTAA
stSG3323	26	C A ---	---	GATCCCGAGTATTATTTCTAAATGAACCTGTTTGTGGAATAAAAAATCTGAGGACCACCTCAGAG GG/C/TJATAAGGGAACCCCTCTTTGTCTTAGTTCATAAGGACTTTCT
stSG3369	69	C T ---	---	CAAGACTGTAAGAACGTAGGCCCTGTGAGAGTGAAGGAAGGATGCTCGAACTTGCCCAGGACTCAGG CTTCAGCTTCACAATCCGAGGAAGGAATGACATTTCCAAACTGTCACCTTTGTAGC/G/TCTGGGT CAAAGTCTAAAGAGGACAAATAAATAGAGACT
stSG3398	125	G T ---	---	TCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCAG/JGJCTCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCCTCCACCTCAGCCAACTGAGTAGCTGGCCTGCAGGACAAGTCACCATGCCTA CCTAAGTTTTGTAGAGACAG
stSG3416 a	43	A G ---	---	GTAAGACAAGGTTTGCTATGTTGACCAGGCTGGTCTTGAACCTCTTGGCTTCAAGCGACCGTACCA CCTGGCCCTCCCAAGTTGCTGATATTACAGGTGTAGCCACTGCCCCCGGACTTTTAACTGAAT GTTGAAATCAATCTGCTCTTTGCTGGGTAACTGAT/JCAAGTTGCTTAACCTTTGTGAAACCAC TTTCTTATCTGTAAACAAATGGACAAACAGAACCTTTTCTTCTCTC
stSG3424	173	T A ---	---	GTTTATGTTAAAGATTAGGAAAGCTGTGGATGTGAGGGGTGAGGTGATGTGAGGCGCTCAGAGA ATGAGTGGCAGAGAGGGCCCCCT/AIGAAATAGCTTACTCTGTTTCTCTATC
stSG3436	88	T A ---	---	



stSG3463	103 C T ---	---	GATACAGAAGATAGTGTGGTATGGATGGATAGTATGAAGGACAAATAATACAAATATATTTATTG AAATAAACAATAATGCATACACAGCTCAATGGGTAC[C]/TTGGAAACAACTTGCTTGAATAATTA CTGA
stSG3491 b	71 G A ---	---	CAAGATACTTCATTGTCTAAGTAGTGCAGTGTGGCAATATTTCTACGAAACAGGACGATTG AAG[G]/AGTGGAAATTACTGTGAAGGAGTACTTTACCTCCAAATAGCCTGCAATTAGCAGTCTGA ACAATCTCTAATCTTTTACTGGCACCTGTGGATTCTATAAAGTCAATTAATACTATTTCTGTGATG ACAGAAATAAGTTAAC
stSG3523	33 C T ---	---	TAGCCATCTTACTCTAGTCTTTTGGGTTT[C]/TGCATATATGTGTGTAACAACACACACACC CCTAATTCCTCAAATGCTCTGGCATAAGTTTATCTTACTGGTCTC
stSG3536	213 A G ---	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGTACAAAAACCAAAATACAGAATGGCTTC TGTGATACTGGCCTTGCTGAAACGCATCTCACTGTCAATCTATTGTTTATATTGTTAAATGAGCTTG TGCACCAATTAG[G]/TCCTGCTGGGTGTTCTCAGTCTCTGCCATGAAGTATG
stSG3583	112 G A ---	---	GAAAAAGCTTAACATACGATCCATGTGCAACCCCAACAGGATCTACGAACCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G]/ATAACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586 a	60 G C ---	---	CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAATCAGGTGGTGGT[G]/CJACG CCTGTAGTCCCTACTTTGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAA
stSG3589	101 T C ---	---	ATATAGTGTGGTAGCATTATAAATCCTTTAAAAAGCAATCTGGCCATATCAAAGGCAAAAAAGT GTATATACCACTGGCACAACCAACCCCAATGAT[C]/CCTATTCCAAGAATGTATCCAGATGAAA GTATCCAACAACAAAAGCTATATACAC
stSG3590 a	70 A T ---	---	GAGAGATGAGCTATTTATTCTTTTACTTAATGAAGATGTAAGAAATGATCTTCTGTCTAAAAAAA AAA[A]/TTTTCTGTGATGCTCTTGACCTGTAGGAAACACATTCAGTTTCTACACT
stSG3619	78 A C ---	---	CAGTGAGACTTCTCATTTTATAGCAATACATTTTTCAGCTTAAATTTCTGAATTCATACGCT TCTGTCAATT[C]/AACAACTCCAGAGAAAACCTGGGCTCTATATTTAAG
stSG3644	40 T C ---	---	ACATATGTAACGCCATTAGTAGCCATATTAGGATGAGAT[C]/GGATTGAGAGGATGAACCAAGG ATGCGTAATAATCATTAATAAAGTTATCTGGGGAACCGGCCATTTGTCCAACATTTACTAA GTGCTACTA
stSG3646 c	70 G A ---	---	CTCATAATTAGATTGAGATTGTCATTTTGGCAAGAAATATATGATGATAACAATAATATGCTTACT GGT[G]/ATAATTAACCTTGATACTTGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTGTA



stSG3646 b	55 A G ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATAA/GJ/TATGTCCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3646 a	43 A T ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATG/A/TJTGATAACAATAATATGTCCTT ACTGGTGATATTAACTTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3693 b	85 A C ---	---	ATTGTTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAACCCCTGGACTCACCT GAAATATCTACGAGGC/A/CJTCGCCCTCCGAGACTGACGATTATTAAACCACCCACACGGAAAAAGG
stSG3693 a	30 C T ---	---	ATTGTTTCCCTGAACATTCCCGTGGTCTCC/C/TJCTGAAAGCCGATGACCATCCAACCCCTGGACTCA CCTGAAATATCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCACCCACACGGAAAAAGG
stSG3698 b	145 G A ---	---	TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCGAGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG[G/A]AGAATACCCACCCACCTTCCCTCACTGCAGA
stSG3698 a	51 C G ---	---	TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCCGAGGTTG/C/JTCTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTATTGGGGAGAAATACCCACCCACCTTCCCTCACTGCAGA
stSG3724	107 C T ---	---	ACCAGCCTCATGTGCAGAGGGTCTCCTGCTGGATCCCCAACTGGAGCCATCCCTGGCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGTCTCAGTGATGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
stSG3725	104 G A ---	---	GCCAAACAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTAA ATCAAATATATTATTACCAGCCAAACAGCAACAGCCCC[G/A]AGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGTAAATAACGGCACATTTA
stSG3751	128 G A ---	---	CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGGTTCTATACCTTTTGTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGAGGATATGGTCCC[G/A]TT GCTGACTCCATGTGTGCAAGAG
stSG3787	49 T A ---	---	TTCTGTGCAAAAGAAATCCACATCATTGTTGGTAGCAGAGGATCTCTTAT/AJAAAGTTCCCTAAGA CACTGAGGGCATAAACCAACAAATAAATAAGGAGTGATAGGCTAAAGCAGTATCTTCCCT
stSG3880 b	115 G C ---	---	GACAAAGGGAAGAGATGCGCCAGAGACCCAGGGCTGGGGCAGCTGGGGTCCCTGAGTGCACGGCGC CACCACAGTCTCTGTGGTCAAGGCCCTCTCTCTGGGAGCAGGCTA/G/CJGGCACGGAGGATGCAG GGCTGGAGGGGACCCACCTCTGGGGACCC/AAAAGGAGTCCATTCTGCCCC



stSG3880 a	36 G C ---	---	GACAAGAGGAAGATGGCCAGAGACCAGGGCTG[C]GCGCAGCTGGGGTCCCTGAGTGCCAGG CGCCACCACACGTCCTGTGGGTCAAGGCCCTCCTCTGGGAGCAGGCTAGGGCAGCGGAGGATGCAG GGCTGGGAGGGGCCACCTCGGGGACCCAAAGGAGTCCATTTCTGCCCT
stSG3895	44 A G ---	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTAGTGTG[C]G/CJTCTTTTCCATTAACTAA TACATGCCCTCATAGATATATTCAATTAGTGTATCACCATGGGAACAAGATGCTGATTCGTCACACTG AAAA
stSG3902	104 T C ---	---	TCTGTTGAGACTGGAGAGACCAGGTACCAAGCACCAGCTCTGGTGGGAACCTGGCTTCCTGATAACA TCATCTATTTACACCTAAATGTGAAGTCTTTCTTTT[C]G/CJTCAGCTCAATAGCTTAACATCTAATTC ATGTTGCTCCCTTTGCTGGACAAT
stSG3935	50 G A ---	---	GGGTGCTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTCC[C]G/CJCTAGTGTGCAGGC TCCTCCCCAGTTTCCACAGGCTGAGTACTATGGGTCAACCTTCCTGGACGT
stSG40	25 A G ---	---	GAGGAAGAGGTTGAAGAAGTGTG[C]G/CJAAATATATTTAAGATTTCTTTGGGAGAAATCTCGTGC CCAAACCTGGTATGATCCCTTACTATTAGAATAAGGAACAAAAATAAACCCCTTGTGTATGTATCA CCCA
stSG4009	32 A G ---	---	GTGTGGGCTGCTGATGATGAATGGCGGCT[C]G/CJGACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATCTCTGATGGCTTTAAGGGCTGAACCATATCTGAAGGTTTTCACACTGCTTACA
stSG4033	123 T C ---	---	AGAAGCCTTGGGGACAATGGCAGTGCCTTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAAACTACAGTGCAGTAACCAAGAACCTAATGTTTCAAGCATAAAGGACTTTT[C]JGTGAAC AGGTGGGCAACAC
stSG4038 a	29 G A ---	---	GCTGAGAGCAGTGTACAGCCACGCCTG[C]G/CJGAGGCCCACTCTGTCAATAAACATGTTCTGCGC CATGTTCTCAGTCAGGAGGTTGAGGCTCCCGGAGAGCAGCTGAGGGTTCCATCACT
stSG406	53 T C ---	---	ACTGTGGTTCAACAGTATTGCGTTGTCAGACTAGGAAGCTAAACGAACAAA[C]G/CJGGTTTAGTT TTGCTGAAGACTGGCCTTATTAAATGGACAGCTTTCCTAACAGAGATTATTAACTTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
stSG4095 b	55 G T ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGTCTGTAGATGTATTAG[C]G/JATAAAAA GTTTGCTTCTGTAATACCTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTTGAGAATCAAG CCTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4095 a	27 A C ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTC[C]G/CJGATACTATTGTCTGTAGATGTATTAGGATAAAAA GTTTGCTTCTGTAATACCTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTTGAGAATCAAG CCTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4120	65 G A ---	---	TGCATGTTCCACATCTTTCATAACAGCAAAATGTATAATAAACTTACGTACTTATGGATAATCAC[C]G/ A/CJTCTTTCCTCAGAGAGCCCCACAGTTAAACAGGTTCCAGCACACCATTAATCCACCGAGCT



stSG4128	54	A	G	---	CTTGGCAGATAAGGGACTGTTTGCAGATATGACTTTCCTTTGTGTACATTCT/GJATATATTT TACTTCTTGAAATGCCACATAATTTGCAATAATGATTCACTCCTTAGCTCCAAAGCAAGTCC TTTATCAAATGCAAATGTTCCAGAGGG
stSG4209	128	G	A	---	CACGAAACAGATGCAGCCTACACAGTGTCTGTAGGACCGAGGCTCACAAACATCCACATGGCACAAGC AGGCCGGCCACTCCAGGCAACGAAAGCCACCCCGAACCTTGCAGAGCCGCACTCCCTC/GA/GC AGGGGACCACGGAGGCGACAGGTGCTTTTGATGCTCCGAAAGAGCTGAGCTCCATTCCA
stSG4209	65	G	A	---	CACGAAACAGATGCAGCCTACACAGTGTCTGTAGGACCGAGGCTCACAAACATCCACATGGCACA/G /A/CAGGGCCGGCCACTCCAGGCAACGAAAGCCACCCCGAACCTTGCAGAGGCCGCACTCCCTCGGC AGGGGGACCACGGAGGCGACAGGTGCTTTTGATGCTCCGAAAGAGCTGAGCTCCATTCCA
stSG4254	31	G	A	---	CATTACCCAGAACGCCATGGAGGACCAGAGC/GA/CACCGCCGGGACTCCCGCATGGCTGGGGGG GCTATGGCTCTGACAAGAGGATGAGCGAGGGCCGGGGCTGCCTCCTCCCCCAGGGGCAGACGTGAC TGGGGGACCATTGGCCGAAGAGAGGATGACCGGTGATG
stSG4301	81	T	G	---	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCACACTTTCCCAT TTAAGCAAAATAATTT/GAGCTTCTGAGTAGTTGTTCCAGTTTCACCCCAACATTTTG
stSG4331	71	T	G	---	CTCAGAAAGGCCAACACAGAAAAAGATACAAATACATTCACAGCTAAATATTTAGTTTTATGACAC AGAGT/GJTTTTCAACAAGTTTAAAGTGTCACTGAAAGCATGTTAAAAAGTTTAAAGTTATCACTT GGAGAGCAGATTCTTTGGCTCGCCCTTGATTTGTTGAGGGGTGTGC
stSG4340	76	G	A	---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTG/A/TAAGTGGGAGATAAAACAATGTGTACACCTGGACGTGGAGAGCAGAA
stSG4361	109	A	C	---	TTCGCAACCATTTGAGTGACAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTTCTTGAAATTTCCATAAGGGATAACTGCATCTTTTG/C/A/CJCTTCACAACTAGAAAACGACTC AGCGACTTTTCTGTGAGCAAATGTCGAGG
stSG4361	24	T	C	---	TTCCCAACCATTTGAGTGACAGAGCT/C/CAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGG CACAAAGTTCTTGAAATTTCCATAAGGGATAACTGCATCTTTTGACACCTTCACAACTAGAAAACGACTC AGCGACTTTTCTGTGAGCAAATGTCGAGG
stSG4376	73	A	G	---	TTTCACTGCTACTGGTTTCGGTGTCTGAGTCTCAAACCTCTGCTTTGCAAGTGTCTCTCCAAGGGGAG AACAG/A/GJCTGGAACCTGCGGCTCTGCAAGAAGCCATTCTTCCAAAGCCATTCTCTCAGCTGC
stSG4381	50	T	C	---	GAAGGCCACAAACACTCCATAGCCAGAGAAATGACAACATACGATTTCTTT/CJTCAGTCTTGATG ATCCACAGTAGTGATGCTGTCCATGTACAAGTGTCTGTCCAGAACACCCATTAAATTCATGCC
stSG4410	79	A	G	---	ACCAATGGTTCTGCTATGTGCATCCGATATTTTTGCCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAACACCCG/A/GJTGACAAACGAAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGTGT CAGCTGGGT



stSG443	65 C T ---	---	AGCAGATCAGTCAGCCCACTTGTCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA/C/
stSG4430	54 A G ---	---	TJGTATGCAATGAGAAAATAACCAACTGGTAGGATGGGGAGGGGAGGCGAGGGAATAGGCAC
a			AAATGGAATTCTATCTCTGGCTGTCTTCTCAGGTC
stSG4448	99 G A ---	---	ATGCACATTAAATGAATGGCCTAACTACTGGGAACTTTAGTAGTTCTATAAGGT/A/GJATTAACATA
stSG4449	92 T C ---	---	GGTAGGATCCAGTTCTATGACAGGCTGCTGAAGGAAACAGATATGAGGCATCAAGAGGGCCATTTT
			CCTCCCTTCCCTTCTTCCCTTCCAGTCTTTCCATAGTGTTCCTCCCTCCCGCCCCACCCAGGCTCT
stSG4448	99 G A ---	---	CGCTAGCCCTGCCCTCTGGGGTCACTGC/GJATGGGTTAGGCCCCCCAAAAA
			ATTAGCCATTTCATTGCAACAATTGCTTTACTGTAACTAAGAGTACTGTACTGATGATGTTTACAAT
stSG4449	92 T C ---	---	TAACTTTGGACAACCTTAAACCTTAT/CJTAGTGACATTGCTGTCTAATAATCAATACTTCATCATA
			GGCTGAACATAATTATTAAGAGCAAAAGTTACCCCTCCC
			CAGACATGAGGGATGCCCTGTCTCTCTGGACAGAGCCCTCA/CJAGATGATGTCCATGTTTGTGT
stSG4467	42 C A ---	---	GAATGAACTCAACACTCTTCAGTTTTAGAGTCATTTTCTGGTATCGAGCGACACACCGAGGAG
			CACACCTGCTTCCAAGGCTGCTGCCCTCTGACACAGT
stSG4475	21 A C ---	---	ACATGTCAATTCCTGACCAGG/ACTJATTAATAATAGTTTATTTAGAAGAAATGAGTTGAAGTGAGCGA
			TTAAGAGACACAACTGGACTTTTGTTTTCTTTACTGTAGCACCCAGGTTTCATG
			GTAACTTCTGGGGGTGGGGGTGAGACAAACA/A/GJATGAACCAATAATTAATTACAATTATACATT
stSG4477	32 A G ---	---	TCAAGGAGACTTTTAACTAGGTTAATGTGAACGCAGCCATCAATGGTTTGTCAAGGAAAAGGGAGA
			TGAAGTCTTGCTCTGGGCAACGTTTGGCCTCATTCAGTCAGACTTGCG
			TGAATCAGAGCTGGGTGGGAGCTGCAGCAGGGGAGGCTGGGGCCAGATGAGCCGGCCGGGA
stSG4531	79 C T ---	---	CAGCAGGCGTCG/CJGCCACGTCCTGGCGTTGGTAGAAGAGGACATAGGCTGCCCTTGGACTCGATCT
stSG4550	86 G A ---	---	GATTCATTGACAGGGGAGACGCTGTGTGTCATCAA
b			TGCATTAAAGGAATGATACGGCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
stSG4550	85 C G ---	---	AAAAGAGACAGTGGCACCC/G/AJCAATTGGAGGGGAAGCGGGGCAGGGTTTTAGAGAAC
a			TGCATTAAAGGAATGATACGGCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATTT
			AAAAGAGACAGTGGGCAC/CJGJCAATTGGAGGGGAAGCGGGGCAGGGTTTTAGAGAAC
stSG4590	47 A G ---	---	AATCAGGCACAAAGCTCGGGAGAGAAGCCAAACAAAGCTCTCTGCACJAGJATGGGAGGGAGACAC
			CATTGAAAAAGGCATGTTCTCTTTCATGCAAGCGAGGCGCTGGCTCCACAGGCATGGTCTCCTTG
			AATCTGTATCACCCAGCGCTGGT/CJCAATGTACTAGTAGCTTTCCACAGGGATTTTTTATACTATTC
			CTATAAGGTTTTATCATGAATAAAAAGCTCACAACCTCTTTTCAGCCATTGCAGATTTCACATTTATCT
stSG4623	22 T C ---	---	TAATATCCTGTTCAAGATGCTCTGGAG
			TAAAAAAAACAACCCCCCAAAAAACACCCAGAAAGTTTTGAGTTTTATGTTTTTCAGATTTTAAAG
stSG4843	102 A C ---	---	GTAATTTCTTTCTTAGCTTCTAAATTTTGAGTCAT/AJATCAGAAAAGTCTCCCTACTCACAAGGTGA
			GAAAGGA



stSG4850 a	38 C T ---	---	GGAACTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC/CTGTGCACCTTGACAGGCCACGTCAGGAG AGCCAGCGGTGCCTGTGCGGGAGGTTTCCAAGGTCTCCGTGAAGAGCATGGGCAAGTTGTCTGACAC TTGGTGGATTCTGGGTCCC
stSG4879	86 A G ---	---	AACTCTGAAGGGGGTGACCTCAACCCAGCCCTTGTTCTGTGAGTGCTCTTTTGCAGAATGGCCTG CCCCTGGGACTGGAGCAG[A/G]CTTGGGTGAGCTCTAGGTGGAGGGTGTGGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104 G A ---	---	ACTGGACTGGCTCGCTTGCTGAGCCGGCTGAGCGGGCTGGGGCTGGGCTGACCCACCTCGCTCTTCAG AGACTGCGCCGCGGTGACCACGACTACGCTCTGCC[G/A]GTGGGAAAGCAGAAGCAGGACC
stSG4896	112 C T ---	---	AAACAAATCAAAACCCAAATCCCAGCAGTCTATGTACAGGGCCACTCCCTGCCTCTCTGCCATAGAGA GGTTGGGGGCAGCTGAGGAGTGGTGGGGCTGGCCACCTTTCTCTACGCCACAGGCCCTTGAGG AATTAATTGACTG
stSG4932	22 G A ---	---	ACAGTCCGATGGTTACACAAT[G/A]TTGTAATGTATTTAATCCCACCTTACGAATGATTAAATGA TAAATCTTATGTTATTTATCATCACTACCAAAAGGCTGTGGTGCAAGGGTCTGTTCTGGTCT
stSG4950	24 A G ---	---	TCATGACTCCAGGAAAGGTCCTA/GTCTTAGCTTCCTCTCCCTACTTTCTCTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCCTACCCCTACACTTCAAGG
stSG4957	136 G A ---	---	AGATACGGGCAAAACACTGGGATGGCTTCCTGACAACCTTAAGAGGTCTCCGAGTTATATTCTGGTT GGGAAACACTGACCCAGCCCTTATTCTTCAAGGACTCTAGTCATTGGCAAGGAGGATTCATGAGCC CC[G/A]GTGACACAGATGGGGCCCTGCTCTATATTCAAC
stSG4961	91 C T ---	---	GAAGGTGCTCTGAGGAGGTGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGATGAAAGGAAAGT[A/C]TAGAGAGGGCATTCAGGCCAAGTCAGCAACACAGACAA
stSG4967	72 A G ---	---	ACTGGTGCTCTCAGCAGATTCAAGGGTGTGCGAGGGCTGTTACCAAACTCAGTAGGAGTGCAA GGGCT[A/G]TACCCCGGAGCTAGACAGCCTGGGTTTGAATCTCAACTTCTCCCTTTCTTGCTGTGC AACCTTG
stSG4997	22 T C ---	---	CAAAGGAGAGTAGGAGCCCCAA[T/C]TTTAAATGGTTTCTCTCCCTCATGCTATTGATCCAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATTACACATGTTTAGAAGGGAGGAGGCAAGAA GGGATAGGGGAGATGGTGATCCAAAAT
stSG6312	37 C T ---	---	ACAGGTCTCACACTTTGAGCCCTTAGTGCAAAAAACA[C/T]TATGCCATGCGGGGAAATAAAATGCTT ATCCAGTGGAGCGCTCCCTGTATGCATTGAAATATTAGGATACTCAAGCAGAAGAC
stSG6345 a	107 G A ---	---	GCTCTGGTCAAGCAAAATCTCCAGGACAGAAAGCAAGGACAGTAACACACATGTATGACCCCTTA CAAGTGCTTTAAGATTTTAAAAATGTGATGTTTGTCCAC[G/A]TAGTTTCAGGCAATTAAGAATAT GCAACCCAGAGAATTTCTGTGAAAACATTTTGTCTTTGGCCTGGTGTGGACAGAAAGGGTGGCCAA ATGGATTGAGTGATGAGCAGCATG



stSG6362	88	G C ---	---	TGTGAATGTACACTCAGGTCTAACAAATACCTATTATTTCTCTGGTTAAGAAGGTTTAGCAGGAGC CTCCAATGAGCACTGTATGTA[G/C]AGAAAAGGGAAGGAGCAGGAGGAGGAACAGATCTGCACAGA AT
stSG8010	62	G T ---	---	CACATCTGTGTTTCTGGAGCAAGGGAAACCACAGAAGGCCAGGAGTTGGGTGTGCACTGG[G/T]T GTCTTTCAACTGGGTGGAAACCAACTGAGTCCTTGAAGTCTGCTCCTGAGGCTGCAGAAGAATAGA TGGCTT
stSG8022	53	G A ---	---	AGCTCCTGACTCCCTGTTGAGTCAGTCAGTCATGTTGGTAGCCTGAAATGGACCAC[G/A]GTGGGAGTTAT TTACACCATGGAAACTGGAAACTCTACAAATCAATGCGTTTATTTCTTTATTTTTCAGAGGGCAGGTT TATCAGCACACGCTGTATCTCC
stSG8032	67	G C ---	---	TGATTGTTAGGGATAAGTGGGCATTGTGTTTACAAATTTACTCCAAAGAAATTCAGAAAATTTGTGTG[T] G[C]TGGAGGCAGGGTAGCAAGATAAAAAGAGGGAGGACAGCTGGGGTTGGTAAAA
stSG8064 b	46	C A ---	---	AGCTGGCTCTTCTCTGTCGT[G/C]TCGGGAGGCTTACGTCTCG[C/A]CCGTGGTCCCTGGGTGGCC TGCAGGACCAGGGGTGGGAAACAATGCCAGGGAGAAATTCCTGTACATCAAAACAGGGAACA
stSG8064 a	23	G C ---	---	AGCTGGCTCTTCTCTGTCGT[G/C]TCGGGAGGCTTACGTCTCG[C/A]CCGTGGTCCCTGGGTGGCC TGCAGGACCAGGGGTGGGAAACAATGCCAGGGAGAAATTCCTGTACATCAAAACAGGGAACA
stSG8072	59	A G ---	---	CACCATCATCATCGAGTAGGCTGAGGAGCAGGAGGGGTGGGTCTTGTCTTAGGG[A/G]TGGC AGAGGCAGAAAGGAGTCGAGTATTAGTGGCCGATGCAGTTCAGGCTGTCTGTCTCAAAA
stSG8100	40	A G ---	---	ATACCCACACACCCCACTCAACCTTGATCAAAATCC[A/G]AAGTGTAACTAAAGTATAAGAAT ATCATGACTAGTTAAAGATAGCAATACCATAAGGTACAAGTTCAAGTTAGTATTAGTATAACCAAGTAT CTGAGTAACAAATGTCTTGGAAATGGG
stSG8102	138	T C ---	---	AAGGCTCCTTTGAAAGCATGGTTTATTGTTTCCATTAACTTGTCTCAGCTATACTGAAGTATGATT GACAAATAAAACCTTGCATATATTGAGATGTACAGTGTGATGATACATGTATGTATACAATGTGAAA TGAT[C]GTGCATAATCATAATCAATAATTGGTATATTGGTTTAGGAAATGTGATGGT
stSG8105	110	A G ---	---	CAGTGGTTCTCAAACTCCAGCTACACGAGGATGGTCTTGTCTTGTAAACACAGATGACTAGGCC CACCTGGGAGTTCTCTGTTGGAGTCTAGGCCCTGAGAAATATTC[A/G]TTCTAACAAAGTTCCAGGTGA CCCTGAGGCTCTTGGACTGGGGAACAATGCTTTGAG
stSG8130 b	96	T C ---	---	GTGTGTACATCATTTGGGAATGGAGGGAATAAATGACTGGATGGTGGCTGCTTTTAAAGTTTCAAAT GACATTCAGACAAAGCGGTCCCTGAGCCT[C]GTGCCCTGTCTTCAGATCTTCACAGCACAGTTCC
stSG8130 a	36	C G ---	---	GTGTGTACATCATTTGGGAATGGAGGGAATAAATGAGTGA[C/G]TGGATGGTGGCTGCTTTTAAAGTTTCA AATTGACATTCACAGACAGCGGTGCTGAGCCTGTGCTCTTCAGATCTTCACAGCACAGTTCC
stSG8145 b	124	T A ---	---	TTGTGGACTTCAAATCTTTCTTCAGATTTTAAATGACATTTATGATGTACATATTTTAAATTT AGACACATTTTAGAGAACACAAATGTGAACACAAATCTAAGAAATGAATGAGATGT[T/A]CTGAAA TCTGATTCAAACACATTATCTTAAACTGACTTCTGTCAATCCTCTGCTCTGTGAAGG



[illegible]



ESTD-AT3a	..	--	---			AGACCTCAGTTTCTCTGTAAAGGGAAGTTTGTCTTGGATCTCCATGGGCCAGCCAGCACTG GTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACCAAGGTGGAGAGAAATTTGAAAGGGCATTG GAATTCAGAGCAAGAGACAGATATTAAGAGCTGGGGAATGTGG
ESTD-B3AR	--	--	---			GGCTCCAGGGTTCCGTGGAGCGGCCCTAGCCGGGCCCTCTCTGGCGCTGGCGGTCTGGCCACC GTGGAGGCAACCTGCTGGTTCATCTGGCCATCGCCCGACTCCGAGACTCCAGACCATGACCAACGT GTTCTGACTTCGCTGGCCGACCGACCTGGTGATGGACTCTGGTGGTCCGCGCGGCCACCTTT GGGC
ESTD-BA511	--	--	---			GGGCAACATAGTGAAACCCCATCTCTACAAAAATACAAAAATTAGCCAGGTGGTAGCAAGTGC CTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGAGGTGGAGGTGCAG TGAGCCAAAGATGGTGCCACTGCA
ESTD-BCL2	--	--	---			AGCTGGATTATACTCCTCTTCTCTGGGGCCCGTGGGTGGAGCTGGGCGAGAGGTGCCGTT GGCCCCGTTGCTTCTCTGGGAAGGATGGCGACGCTGGGAGAACAGGTACGACAAACCGGAG ATAGTATGAAGTACATCCATTAAAGCTGTCGAGAGGGCTACGAGTGGGATCGGGGAGATGTGG GGCCGCGCCCCCGGGGCGCCCGCCGACCGGCGATCTTCTCTCCCA
ESTD-BCR	--	--	---			CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCGGAGACTCATCTGCGCAAGA GACCAAGAGGTGAGCTTCTGTGTCCCGGAAAGGGAGGCGAGGTGACAAGCTAACTCTGCTTCAAA ATCAACCATCGGTGGACACTGTGTGGTGCCTGCTGCTGCGCACA
ESTD-BRCA1a	--	--	---			AAGAAGAGAAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGTTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTAC TGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAAGTTAGCACTCTAGGGAAGGCAAAACAGAA CCAAATAAAT
ESTD-BRCA1b	--	--	---			ACTAAATGTAAGAAAAATCTGCTAGAGGAAAACTTTGAGGAACATTCATGTCACCTGAAAGAGAA ATGGGAAATGAGAACATTCCAAGTACAGTGAGCAACAATTAGCCGTAATAACATTAGAGAAAAATGTT TTTAAAGAAAGCCAGCTCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD-BRCA1c	--	--	---			ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTAGATGATGGTGAATAAAGGAAGATAC TAGTTTGTCTGAAATGACATTAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGAAAGGAGAG CTTAGCAGGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCAAGA AATTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	--	--	---			ACACAGGTGCTGGCACTGGGGCTGGGATCCTCTCTCCCTAATTTGCTCCGGGAAGCACATTCATCAA CCCAGTCAAGTTTGGGGACAGCCATGCACCTGAGCCTCTGGTAGCCCTTTCACCAATGCATTCCTCTAA GCTCTGCAAAAT
ESTD-C6	--	--	---			



ESTD-C7	--	--	--	--	---	---	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	--	--	--	--	---	---	---	---	GGCAAGTTTTTATTGATAGAGAGGAAATCAAATATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCTTAACCTGGGGATGGACAGACAATGGCAGTGCCAAACCATAGGGCGGATACAAAAGAC AGGCAAGGAAGGGGTAGAACCATCAAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCTAG TAACATAATTGTGCTTCATTATGGTCCTTTCCCGGCCTTCTCTCACACAC
ESTD-CB23	--	--	--	--	---	---	---	---	TAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGGTCCTTTCCCGCCTTCTCTCACACATACAGAGCCCTACCAGGACCAGACAGCT CTCAGAGCAACCTAGCCCAATTACCTCTTCCCTTCCAGAGGACCTGAAAAACGTGTCCACCCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAA
ESTD-CB24	--	--	--	--	---	---	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGGTGCTGTTTGAGCCATCAGAGCAGAGATCTCCACACCCAAAAAG GCCACACTGTATGCTGGCCACAGGCTTACCCCGACACGTGGAGCTGAGCTGGGTGAATGG GAAGAGGTGCACAGTGGGGTCAGACAGACACCCCGCAGCCCTCAAGGAG
ESTD-CB25	--	--	--	--	---	---	---	---	GTTTCTTTTACAGACTGTGGCTTACCTCCGGTAAGTGAGTCTCTCCTTTCTCTCTATCTTTGCGCGTC TCTGCTCTCGAACAGGGCATGGAGATCCACGGACACAGGGCGTGAGGGAGGCGCAGAGCCACCTG TGACAGGTACCTACATGCTCTGTTCTTGTCACAGAGTCTTACCAGCAAGGGTCTCTGTCTGCCACC ATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGATGCGGTG
ESTD-CB27	--	--	--	--	---	---	---	---	TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTTGGGCTGGTTGCATTTACGGAGTGTCTGTGGAGTTCTGCTCATCACTGACCTATCTTCTGA TTAGGGAAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCAAATGCTGCT TTCTCCTGTTTCATCCTGATGGAAGTCTCCTCAACACCACTTCCATACC
ESTD-COL2A1c	--	--	--	--	---	---	---	---	AGAATGTATATAGTCTCAAACTGGCCATCTCCATTTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTGCTATTTATGCTCTCTTTCTGTCACCTTTCAGGGTGTCAAGGTGGAAGGT GAACAGGTCCCGCTGGTCTCCAGGCTTCCAGGTAACTCAAGCATATACAATACTGCGCTTTG GTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD-COL2A1d	--	--	--	--	---	---	---	---	TGAGAGAACACCTAGTCTCCTCCTCCTCTCTCAATGGCAAGAAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGGACCTGGAACACTGGACTTCTTCTACTGCAGCAGACAAGACTTACCC AAGAGAGATTAAATGGCAAGATATACAATACAATTTTATTGACCAACACACTATCATGGAAACAGC ATT
ESTD-CPT2	--	--	--	--	---	---	---	---	GCCGCAATGCCCCGGGAGTTCTCCAATGTGTGGAGAGGCCCTTAGAAGACATGTTTGTATGCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCACTTCTCATCATGAAAAC TGGAGGCCGGGCATAGTGTCTATGCTGATGCTGTAATCCAGCATTTTGTAGAGGCTGAGCGGGTGGATCAC TTGAGGTGAGGAGTTTGAGACCAACCTGGCCAACAT



ESTD- CTLA-4	--	--	--	---	---	ATGGCTTGGCTTGGATTTCAGGGGCACAAAGGCTCAGCTGAACCTGGCTACCGAGCCTGGCCCTGCAC TCTCCTGTTTTTCTCTCTTCATCCCTGCTCTCTGCAAGCAATGCACGTGGCCAGCCTGCTGTGGT ACTGGCCAGCAGCCGAGGCATGCCAGCTTTGIGTGAGTATGCATCTCCAGGCAAGCCAC
ESTD- CYP2D6	--	--	--	---	---	CAGCCAGCGTGGTCGAGGTGCACCATCCCGGCAGAGAACAGGTGACGCCACCACTATGCACAGGT TCTCATATTGAAGTCTCTCAGGGTCCCTTGGCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	--	--	--	---	---	AAAAAACATTTAACACCTTTTCAATCATATACACCATAAAATTTCCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTCCAAATTACTTGCAATCTAAATGTCAATGATTAATGCAAGTTCAACAGACA ACTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATTTATGCCCATAT CTGCATGTC
ESTD- D17S33	--	--	--	---	---	CATCCCAAGCCCATCTCTTAGCCACTGGCATTTTTTCCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCCCTTTGTAGTCCATGGGAAGGCTCCTCTGGGGCGGTG GGTGTGTGGCTATGTGGTCTTGTGTAGACGGGGCTTTGGTTTCAGTTGCACATTTGGCTTATT GCAGATTGCTTTGCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	--	--	--	---	---	TTTGAGACCACCTGGCCAAACATGGCGAAATCAGATCTCTACCAAAATTACAAAATTAGCTGGGTGT GGTGTACATGCTATCGTAATCCAGCTACATCGGGAGGCTGAGCAGGAGAAATGCTTGAACCCA GGAGGCAGAGCTTGCAGTGAGCCAAAGATCACACCCTGCACCTTACAGCCTGGGTGACACAGTGGAGA CTCTGCTCAA
ESTD- D3S11	--	--	--	---	---	AACTGATTAGAACCTGAAATACATATTTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAATCCAAATAAAGTACACTGTAATAAAGAAATTAACAGAAATATCATTTGT TTATCAAACATTTATCACTTATTTTATTGGTAAGCCATACTAAATTTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	--	--	--	---	---	AGGTTCCACATTATTGCTGATGTTTGTGATGTTTCCAGGAGCCTTGATGTCATTCGTATCTCCTCAG GTATCCACCTTGAGACGTACTTTTCAAAAACCTCTACAGCCGTTGTTGTTAATTAATCAAGGTTGA ACATAAAGTA
ESTD- D3S2	--	--	--	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCAGACCTGCTAGCAGAACATTCCTGC TGAGTCTTATTCAAAACCTGACAGCAATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGATTCCC AGAAGTGAACATACTGCTCTAGAACGCCAGAGTCATAGTATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGCTCTTATTTGGAAGGATGCCGGTATGT
ESTD- D4S338	--	--	--	---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATGAAATGATTT CTTAACAATAAATCTGAAAGTCCAAAATTAATCTCTGATCCATGGACTGCAGAAATAAATGTTATTT TAGCTGTCAGAAAAACAATACTAATCTTGCAATGTTTATCAGAGCCCTTGGGTGACCAGGTGTTAT GCCAATAAGCAGTAATAATTTGAGAGGAATCTTGTTTCAATGCAGTAG
ESTD- D4S95	--	--	--	---	---	CTTTCATGCAGATAGGCTTCTCTACTAATCACAGAAATTTGAGAAAGAGCAAAACAACATTTCAAGG ATAATGGGCAATCACTTCTCTCTCTTTAGAGTCTACCGG



ESTD- D7S399	..	--	---	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCTCTTTCACAAACATTTTCATCCATGGACTCCATACTAG AATATTTGAAGAAACAAACATGACAAAACATTTTC
ESTD-DM	..	--	---	---	---	GTGGGACACCGAGGCTCCAGGCTGGCGCTTGACAGTGTGGCTCAAGCAGCTGCTCGGCTCCACT TCCATGGGTGTGGGCTGGACCTCACTGTCCTGGGAGAGGAGGAGTGGGAGGAGACA GAATGCTGATTATCTGTGGAGAACAGAACTTCTGGCTGTGGTAGGGCAGCTGCTTCCAAAGACC TCCTGATTTGAGGAAGGGAGCAGAGCGAAGAGAACAGAGT
ESTD- DRD1	..	--	---	---	---	TCCCAGCCCTATCGGTGATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCCATCAC ACAAAACGGTCAGCACCCAACTGAACCTGCAGATGAATCCTGCCACACATGCTCATCCCAAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAGAACTAAGGTAC
ESTD- DRD2	..	--	---	---	---	TCTGCTTTGGTGCAGGAGGCTGCCGGGAGCCCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCCCCGAGAGGACCGGTACAGCCCCATCCACCCAGCCACACAGCTGACTCTCCCCGACCCCG TCCCACACCGTCTCCACAGCACTCCCGACAGCCCCGCCAAACCCAGAGAAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	..	--	---	---	---	AAGCAGATGGCCAGGATGAGCGCGCAGTAGGAGAGGCGCATAGTAGGATGTGGCGGCGCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTCAAGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCAGAGGGAGGTGCGTATGCCAAGGGGCTTCTGTGAGGAGA
ESTD- ER882	..	--	---	---	---	TCCTTTCAGGATCCGCATCTGCGCCTGGTTGGGCATGCTCCGCTAGGTGTACGGCTCCACAGCTGG GGTGAGGGGGTGGTGGTCACTGCGGGGGCGGTGCAGACCCCAAGGGCTGGGAGGACTTCACCC CGCTCACCTCCGTTCTCTGCAGCAGTCTCCGCATCGTGTACT
ESTD- ETS2	..	--	---	---	---	ACTCACAGTCTTTAAGTGAAAATGGTCGAGAAAGAGGACCCAGGAAGCCGCTCTGGCGCCTGGCA GTCCGTGGGACGGGATGGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGCATGTCTGGACACACAC AGACTATTTTAGATTTCTTTTGGCTTTTGCACCCAGGAACAGCAATGCAAAAACCTCTTTGAGAGG GTAGGAGGGTGGGAAGGAACAACCATGTGATTTTCAGAAAGTTAGTTG
ESTD-F2	..	--	---	---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCTAGTAGCCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCTCCAAAGGCCCGTAGGGGAACCTGGGGGATCTAGGGGATGGGTGAGGAATGGCCG AGCCAGTCCCGCGGTGCTGGTCCCAAGAGGAGGCGGTGGAGGAGGAGACAGGAGATGGGC TGGATGAG
ESTD-F9	..	--	---	---	---	AGATCCTGATGATTTTTTCTATTTTTTCTAAATGTTTACAGTTTGAAGTTTATAGATTTATGCCCA TGCTCCATTTTGGTTAATATTTGTGTAAGATGATGTTTAAAGTCAAACTTCATTTTTTTTTTCCATA GGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAAC



ESTD- G0DH	--	--	---	----	---	CGCAGACGGTCAAGTGTGGGTGCGGAGTGTGGAGGAAGGAGGAGGAAGAACTGGGGTTTAGGGACTTTCGGGGTGACTTCCCGTTCTGTGCTTGACAGAAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGGACCTCTGGTGGACCGTGTGTTCTGCTGCCCCGTGTTAGCTGTCTGTCTGCGCGCAGTCTGCTGTCCCGGAAATTCGAGAGCT
ESTD-GCK	--	--	---	----	---	GTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCTCTGGTCAACCATGAC AACACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACACTGGCTGG AGCAGGAAATGCCGAGCGCGCCTGAGCCACAGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAAGCTGTCCCGAGGTCACAG
ESTD- GNAT2	--	--	---	----	---	GACCCCTGAGTACCTCCCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACACAGGCATCATTTG AACCAAGATTTCCGTCAAAGACTTGAATTCAGGTAAGTCATGGTTCCCTAGG
ESTD- GPPK2L	--	--	---	----	---	AGTCTCATCTCGGTGCCAGGTAGATCCCTTTCACCGCCGAGAACTGCTCGATATC
ESTD- HRAS	--	--	---	----	---	CTGGCTGCCCCGACAGCTGCTGGCACTGGACGCTGGCGCGCCAGGCTCACTCTATAGTGGGTGCTG TATTCGTCACAAAATGCACTCGGATCAGCT
ESTD- HSD3B1	--	--	---	----	---	TTGGAAAGTTCTCCACTGTAAACCCAGTCTATGTTGGCAATGTGGCCTGGGCCCCACATCTGGCCCTTG AGGGCCCTGCAGGACCCCAAGAAAGCCCCCAAGCATCGAGGACAGTTCTACTATATCTCAGATGACA CGCCTCACAAAGCTATGATAACCTTAATTACACCCCTGAGCAAGAGTTCGGCCTCCGGCTTGATTCC AGATGGAGCTTTCCTTTATCCCTGATGTATGGATTGGCTTCCTGCTG
ESTD-HT2	--	--	---	----	---	GGGCTAAATTTCCGAGCACTTTCATAGACTGTTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTTACAGTTTTCAGAGAGATAAAAGGATAACCTGGGTTTTCTGTGC TTTGCTTTCACATCCCTGGGAGTTAATAGTGCATTTTTTCAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAACAAGACACACCTT
ESTD-HT4	--	--	---	----	---	ACCAACGAGCCGATACAGACACTCTTAAGTTTGGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAACTAGGTTCTTGGTGCTCTCTATCGGCAAGATCGTACTTATTTGAATAGTAGAGGTAA ACCACAGCCCCCAAGAGTCACTGAGACTGGCAGCTTCTGCAGCAGGCGTGAACCCCGTAGCCTAAA TGACAGCCGAAGAGGCGCCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	---	----	---	AACACAAAGCCCCCAGCGAGAAATTGAACCTCGGACCCCTGGTTTACAAGACCAGTGCTCTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTTGGTTTTCTTCTTCTCATCTATAGATTGATGTTATGCTCCTA GCATTCGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATCTCCTACAAAATGAAA ACATTTTCGTGCTCTGTAATCCCTCGAAAGTTCT
ESTD- IGFBP1	--	--	---	----	---	ACCCAGTGGAGCCCGCTCATTTGCACGGTCTTGGCAGGAGTGCCCTGGGAGAAGAGGAGATGTTG CAGGGCACACATAGCTTAGTGGAGACTC



ESTD- IGHV4-6	--	--	--	---	---	---	TTTACTATTCAATGGATACAGAATTGTGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCCTACATTGTGTGAGTGACGGGCGAGTGGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGATACGAACCTGAAAGT ATGTAAATACTTCACAAAATACTAATAACGGAGTTGAAATATAAAACCCCA
ESTD-IL1A	--	--	--	---	---	---	CAAAGTAAGCACCCCAATAATGTTAGCTATTACTATCATTAATATTATTTATTTTATTTTGG AGATGGAGTCTGGCTCTGTCAACCCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAAGCTCTG CCTCTGGGTTTCATGCCATTCTCTGCCCTCAGCCTCCCGAGTAGCTGGGAATACAGGCCACCCGCCACT GTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCAACCGT
ESTD-IL1B	--	--	--	---	---	---	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGCTGTATTGAGGGTGT GGGTCTACCTTGGGTGCTGTCTGCTGCCTCAGGAGCTCTCTGCTCAATTGCAGG
ESTD- KRT10	--	--	--	---	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTAAAGTAACTGCTAAGGTTTTCATTAAACCAGCTATTACTTCTAAG AGAACTGTACATGACAAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCCAGTATTGATA
ESTD- KRT8	--	--	--	---	---	---	ACCCTCACCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTTACCACGTCAACATTGACACA
ESTD- LF79	--	--	--	---	---	---	GGGTGATTTGAGGCTCAGTTAATTTCAAATTTGTAACCGTAGCAAAACTGCATTGGTATTTAGA AAAATAAAAATTTCCAATATGTAGTGTGTATTACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCCAGGAGGGCTCCCTTACCACCCAGA
ESTD- LMP2	--	--	--	---	---	---	TACACACTTCTTACCCATTCACTGAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	--	--	--	---	---	---	TGTCAGTGTCCCTAGGGGCACTCACCACCTCCAGCTTCTTCAGCTCTGGCTGTCTGCTGCTGCA AGGGTTTGTAAATCTCAATTCATGTCTCTTCATCTTTTAGGAGCTGTGGGTTTGTGTGTTTC TTCTGTTTTGCTTAGTATCTGACTACTTTTAAATATAAAAGAGATGTATCTAAACAAAATAGAG ATTGTTATCAGAAAGTTCACAACATTTATTAAAAATTTTTCACCTG
ESTD-MCC	--	--	--	---	---	---	TTGTCAGGAGTGTGCTGATGCTGCCTCCCGAGCTCTGCTCCCTAGCCGAACCTTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGCTTCCCAAGGGTTTGGTCTAAGTTGCTGATTACCCGGATTCTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTTCCTGTTTAGCATGG
ESTD-NF1	--	--	--	---	---	---	ATTATCCAGATGAATTTACAAAACATAACCAGATCCACAGACTGATATGGCTGGT



ESTD-NFKB1	--	--	--	---	---	---	AAATGGAGCTTGATATTTGTACAAAAAAGTTTTATTTTCTAAAAAAGAAAAAAGAGAAA AAATTTAAAGGGTGACTTATATCCACACTGCACACTGCCTAGCCCAAAACGCTTATTTGGTAGG ATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTTGTAGGGACGAGAAAGATCATTTGAAATTTCTGAG AAAACCTCTTTTAAACCTCACCTTTTGTGGGTTTTTGGAGAAGGTTATCA
ESTD-NPPA	--	--	--	---	---	---	TGTCCTAGGCCAGCCCTGCTTGTCTCCTCCCTGGCTGTTATCTTCAGTACTGCAAAAGAGAACACAGAC AT
ESTD-NRAMP	--	--	--	---	---	---	GGAGGAGGAGGTGGGAGGGGGTCTGTCTGCTCCAGGTCCACAGACACAGAGAGCGGCGCTCAGTG TATCCCCACCCCCAATGTGGGCGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-NRAS	--	--	--	---	---	---	GTGTTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTTCTGCAGGCATATAGAATTTGGT GGGTTTTCTTTATGTAGGGTGATATTGGATACCTTTTGTGTTGTGATTATATATTAGCAATTTGAGGG ACAAACAGATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTGC ATTCCCTGTGGTTTTTAATAAAAAAT
ESTD-OTC	--	--	--	---	---	---	GTGACCTTCTCACCTTTAAAAAATTTACCGGAGAGAAATTAATAATATATGCTATGGCTATCAGCAGA TCTGAAATTTAGGATAAAACAGAAAGGAGGTATGTAAACA
ESTD-PAI1	--	--	--	---	---	---	GCCACCACACCCACCCAGCACACCTCCAACCTCAGCCAGACAAGGTTGTTGACACAAGAGAGCCC TCAGGGCAGACAGAGAGTCTTGACACGTGGGAGTCAAGCGTGTATCATCGGAGGCGGCGGGCAC ATGGCAGGGATGAGGGAAGACCAAGAGTCTCTGTTGGCCCCAAGTCTCTAGACAGACAAAAACCTAG ACAATCAGTGGCTGGCT
ESTD-PAR	--	--	--	---	---	---	CTCTCAGGAACCCAGCTCTTCTTACCAAACACGACTTATTGCTGTCGAGAGGTACAACCCGTAGA ACTTCTCTTAAGTAAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTCTTCTTCACTTTCTGTGTTCTAGAACGTTTTCTAG GACTGGCAGTTTAAAGCTTTCACCTTAGGCTTTCTGTATACCCATGCC
ESTD-PBDA	--	--	--	---	---	---	CCTTCTCATGCCAGATGGAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAAATCTCTACCCGAGCTTGTCTGCATACAGACG GACAGTGTGGTGGCAACATTGAAGCCTCGTACC
ESTD-PS-1	--	--	--	---	---	---	GGGAGTAAACCTTGGATTGGGAGATTTCATTTCTACAGTGTCTGTTGTTAAAGCCCTCAGCAACA GCCAGTGGAGACTGGAACACACCATAGCCTATTTCGTAGCCATATTAATTGTTTGTGCCCTTACATT ATTACTCTTGCCATTTCAAGAAAGCATTTGCCAGCTCTCCAAATCTCCATCACCTTTGGGCTTGTTTT CTACTTTGCCACAGATTATCTTGA
ESTD-PXIPI	--	--	--	---	---	---	ATGAACATGGTCTTTAATTTATGATATGTTTATAGCTATCTTAAAGGGCTCTTTTTTTTA ATGCAGAAAGAGGGGAAAAAGAGCGAGCTGTGGTGACAAGGTGTTTTCTCAAGGCTCATACAGA TTCTGAAAATCATGGTCCCTAGAACATTTTGAAGAGGTAAGCTTATGAAATTAATCTT
ESTD-Per/RDS	--	--	--	---	---	---	ACCTACAGACGTGCTGGATGGTGTGTCCAACCCCGAGGAATCTGAGAGCGAGAGAGGGCTGGCTG CTGGAGAAAGAGGTGCGGAGACCTGGAAGGCT



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ESTD-PDS	--	--	--	--	CCGAGGAATCTGAGCGAGAGCGAGGGCTGGCTGTGGAGAAGAGCGTGCCGAGACCTTGAAGG CCTTCTGGAGAGTGTGAAGAAGCTGGGCAAGGGCAACAGGTGGAAGCGAGGGCGCAGACGCAGG CCAGGCCCAGAGGCTGGCTGAGGGCCCTGGGCCCCCTCCCTCCCGAACACTGAGAAATAGTGCAT CCAGAAGCGTGGATCTCCCCCTCATCCAACCTCCGAAAGTCTGAA
ESTD- FVR1	--	--	--	--	CTTCGTACGGGAGGTACGTCCTCCGCTCTTTCATGGACATATGGATGAGTGTGACCATTTCCOC CTGCTGACAGTATGACACGCGCAGACTTGTCTACTATGAGAGGGAGCTGTGTGCACTCATGCCGCG TCCCTCTGAGGCTGGAGCCACTGAGATCAGCTGGAGTGGAGCCACTGCGCTGGGGCCAGCCACT CCGAGTCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	--	--	--	--	TGAACACCCCTGTGGTCCGGAGCCAGGTGTGTTCTCCTGGGAGCCTGAGGAGTTTGTGTGTGTG CAGTCCCCCGCGCCACCTGCTGGTTGAGCCTGGACATACACCTTCACCTCCTTTGGCCGGAGAAGAC ATTTACCCACCTGGCCATGTCCCTGGCCTGTTGTGCACACCTCTGTGAAGACCCCAACCCCTGCCTCC CCGACCCCAAGCCAGTTTCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	--	--	TTACATTTGTGGATTGTTCTTTGTGTGCAGCACCTTTTCAACATGATGTATCCCATTTGTCTCAAG TTTGCTTTGGCTGGCTGTGCTTGTGGGATATTGAAGAGATCTTTGCCAGTCCAATGTCTAGAGAG TTTCCCAATGTTTCTGTATAAGTTTCATAGTTGAGGCCCTAGATTTAAGTCTTTAATCCATTTTG ATTTGATTTCTGTA
ESTD-TAT	--	--	--	--	AAATGGTCAGGACCCTGATCCACAAGAGTGGTACCATTTTCATCAGGGCCATCAGTTCATTCAGCTC CCATGACTGGATGCTAAGTCAGCAACTGAGTTCATTCATCTTAAATGACTTGTGGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTACAACCTTTCTCCAGTATGGATGGATTATGATGGGGGG GAGAAGCAAAATTTTAAATAGGACCCCATGAGACACATCA
ESTD- THR8	--	--	--	--	TGGGGCTTTCCTCGGCGAGGTAGACTTCTTACTGGCTGTGATTTCCAGAGAAAGAGTCCCAAG CACACGAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATCACACAGGATCACTTCATCCA CACTGGATTGGCCCAACAAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCCCTGTAGATGGG
ESTD- TNFA	--	--	--	--	TTCTGCATCCTGTCTGGAAGTTAGAAGGAACAGACCACAGACCTGGTCCCAAAAGAAATGGAGG CAATAGGTTTGTAGGGGCATGAGGACGGGTTTCCAGCTCCAGGGTCTACACACAAATCAGTCAGTG GCCAGAAAGACCCCCCTCAGAAATCGGAGCAGGGAGGATGGGAGTGTGAGGGTATCCTTGATGCTT GTGTGTCCTCAACTTCCAAATCCCCCGCCCGGATGG
ESTD-TYR	--	--	--	--	TAGTGAAGTTTTCATCTCTCTGAGCTTCTGGAATTTCTGTCCACCGCAACAAGAGTCTATGC CAAGGCAGAAAGCTGGTCTTATGGGCAAAATCAATGTCTCTCCAGATTTCCAGATCCCCCAAGCA GTGCATCCATTGACACATAATAATGATCCAGACAAAGAGGTCAATAATTTGATGTGCTTAAACAT GGGTGTTGATCCATTTTTCATTTGGCCATAGTCCCTATGGGATGACA



ESTD- TYRP1	--	--	--	---	---	AGTAGTGATGAAGCTAACAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAACTCCTAATCAGCTGTGGTCTAACAAATGCCCTACTCTCTTATGCAATAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTATAACTGTATTTCTTTACACTTTATTACCTTCTTCT AATACAAGCATATGTTAGAATTAAAGTTCTAGGCATACTT
ESTD- VB12	--	--	--	---	---	TCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCAAGACACAAGGTACAGAGACAGGAACACACAGTG ACTCTGAGATGTCACAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCGGGGCATG GGCTGAGGCTGATCCTACTCATAT
ESTD-VWF	--	--	--	---	---	AGGTAGGAAAAGCAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTTCCACACTGTCTTTGG TCCCCTAGAGTCTG
ESTD-WT1	--	--	--	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCTGCGAGGATGTG CGACGTGTGCTGGAGTAGCCCCGACTCTTGTACGGTCGGCATCTGAGACCAGTGAGAAACGCCCTT CATGTGTGCTTACCCAGGCTGCAA
ESTD- s14544	--	--	--	---	---	TTGGAAGTTAGAGCCTATATTAATTAACGGAATTACTAAGGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAAATGTCTCAGTTCGCTGTGTGGTTAGATGCAGGATTTATATGATCCGTTAACC TCT
EST71770 6	--	--	--	---	---	AGCACCACTCTCAGGTCAAGCCTCAGCACCAAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGAGTTATTTTATCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAAAGAGAAACCACCTGCAGAGTACCAGCTGTTGGTGAAGG AGTGCCCAAGTCCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAGG
EST52418 6	--	--	--	---	---	CAAAATTACAGGGTCAACTGCTATGATGTGTTGGAGCCCCAGTCACCCCTTTGGTGGCTACAAGATGTCG GGGAGTGGCCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACTAAAGTGAAGAACTGTGAGTGTGG CCCACCTCTATTTGCCAGCCCCAGGGACAGAGCTGATCCTTGAACCTCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAGGGCTGGCTTATCAGCCTCCAGCCAGACCCCTGGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTCTGCTGCTGCCCGG GTCACTC
EST13586 3	--	--	--	---	---	AGGCAGAACTGGGCCCATGCGGGGACGTGGAAGGCCACTTGAGCTTCTGGAGAGGACCTGA GGGACAAGGTCAACTCTCTTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAGACTCTCTCCCT CCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGCAGGAGGAGGAGGATGCTGGCC CCTTGGAGAGCTGAGCTGCCCTGGTGC
EST51976 7	--	--	--	---	---	



EST11458 6	--	--	--	---	---	CCACITTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGTCTATCTGTTCTCGAGTTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCCAAGCCAGATGATTTACCATTTTCCACAGTGGT CCCATTAACAAACATTCTATGAGCCAGGAGAGAGATTACGTATTCTCTGCAAGCCGGGCTATGTGTCC CGAGGAGGGATGAGAAAGTTTATCTGCOCTCTCACAGGACTGTGGCC
EST39852 8	--	--	--	---	---	CGGTCTTCTTCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACTCTCTTACGGTACAGAAAGAGATGCATGAACAGCA GGAACACGTGGAAAGGCCCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTATAAT ACAGCOCT
EST62448 0	--	--	--	---	---	ACCTGGTGTGCTGGTGGTGAACCTGGTCTCTTGGCAATTGCCGGCOCTCTGGGGCCCGTGG TCTCTCTGGTGTGGTAGTCTGGAGTCAACGGTGTCTCTAGTGAAGCTGGTCTGATGGCAACC CTGGGAACGATGGTCCCCCAGGTGCGATGGTCAACCCGACACAAGGAGAGCGCGGTTACCCCTGG CAATAT
EST36027 2	--	--	--	---	---	AGTGACTTCCAAGGAAATGGCTACCAACTTGCCTTCATGCGCTGTGGCCAACTATGCCTCTCAGA ACATCACCTACCACTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGGAAACCTGAAAAAGG CTGTCAITCTACAGGCTCTAATGATGTGAACCTTGTGCTGAGGGCAACAGCAGGTTCACTTACACT GTTCTTGTAGATGGTGTCTCTAAAAGACAAATGAATGGGAAAGACAA
EST12274 0	--	--	--	---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGTAT TACATAAAGAAAGTCAAGTGGTTTACTCTCTCATGACCAAAATATCTTCCCTCCTTAGGATGAGGTGA TAGTAAATGACCGATGGGGTCAGAACTGTTCTCTGTCACCATGGAGGATACTATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC
EST76807 7	--	--	--	---	---	ATGCTAAGGGGATCGGACATGAAAGGACCCCTGTGAGCCGATTGTCTCTATCTCCAGCGGCCCTGTCTATC CAGCTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCACCACTGCCCCCT GCTGCCATGTGGACTGGTCAAGTTGAGGACTTCTTG
EST44438 7	--	--	--	---	---	GCAGCCAGGAGCGGCTGCAACATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCTT GCTCCGACCTAAGCGGAGCAGCCCTCAAGAGCCGAGCGGTGGG
EST12839 3	--	--	--	---	---	TGCAAAACACACAAAAATCTTCCAGATGCCCTATGGCTGTGGAGAGCAGAAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAGATCAAGTCCCAAGG CCATTGGCTATCTCAACACTGGTGAAGTACTTGAAGTAAAGGAAACTTGAATGTTATTCAACTGG ATTTCCAGTAGGTTTCACTTACTTATGAATATATGATACTTAGCTTAG
EST54419 8	--	--	--	---	---	CTTCTGCCTAATTTGAATGATATTGTTGCTGTGGGACCTGAGCAGCTTTTATGGCACAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGATTTGGGTTAGCGTGGTCTGATGTTGTCTACTA TAGTCCAAAGTGAA



EST10398 2	--	--	---	---	---	TGCTGGGTGGCAAGGCTGCAACAAGAGGAGCAACCCAGGAGGCTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTTATCTACTTATGATGATGTTACATTTGGGGCTTGACTTCCACACGGAGAAG CATTGTTTCTCGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTG
EST36751 7	--	--	---	---	---	CCAAGTCGTTCAATTTTAGCTTTGCAGGTTTAACTCGATTACTTTTCTATTCAAATCTCTGTAAAA TTGAAATATGAACCTAGTTTCTGATCTATGTTTCAAGTTAAACAG
EST40562 --	--	--	---	---	---	CACGTGAAAGGAGCTATTTTGGAGGCTTAAAGATAAGAACTGTCCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAAGTTTCACTGGATGCATTATAACAAATATTTACCTTTTGAATAAATAATG AAGGATTTGACCTGCTCGCTCTGGAAGAGTATCCGTACCGTCTGACGTTTGAACAATACAGAT GCCTCCCTTGTAGCAGTTTCAGCCTCCTCTACCCTA
EST18288 3	--	--	---	---	---	GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGACGGAGCCAGTGTGG ACAGCACCCCTGGCTTCAACACCTACGTCCACITTCOAAGGTAAAGCAACCTCTCTGCTGCTGGC CCTAGGACTTAGTATCC
EST70523 3	--	--	---	---	---	TTCCGGCAGCCCCCATCTTGGCACCTTGGTCCCTCAGGGGCCACCCCGGCACTCACCCGCTCT CGCTCTCGTTAAACATCCGGCCGGCGCGCTCTTGAGCACATAGCCTGGACCTTCCGTATAGGAGG ACCGTGTAGGCTTCTGTCGCCGGCTTGCCAGGGGCCAGCCCTGCAGAGAGGGGTCCCTGTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGTG
EST58707 7	--	--	---	---	---	CAGTGTATCTGGAAGCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGCTTT AAGTTCAGCATCTTTGGCTACATGAAGGCCAAATCCGAGAGACCTAGAAATACACGAGACCGA ATGTATCAAATGGACATTCAGCAGGAATTCACGATACCTGTCTGTGGTAGGCCAGGTTTATAGCA CACTTGTCACCTACATTTCTGATTGGTGGACTCTTGTGCTAAGAACCTT
EST74167 6	--	--	---	---	---	AGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCCAAGGAGCTGCAGGCGCGCAGGCCCGCTGGCGCGGACATGGAGGA CGTGGCGGCGCGCTGGTGCAGTACCGCGCGAGGTGCAGGCCATGCTCGGCCAGACACCGGAGGC TGCGGGTGGCGCTCGCTCCACCTGGCAAGCTGCGTAAGCGGCTCCTC
EST43211 8	--	--	---	---	---	CGCTGTGTGCAAGTACCGCGGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGG CCTCGCCTCCACCTCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCCGATGACCTGCAGAAAGGCC TGGCAGTGTACAGGCGGGCGCGAGGGCGCGAGCGGCTCAGCGCCATCCGCGAGCGCGCTG GGGCGCTGTGGAACAGGCGCGGTGGGGCGCGCCTGTTGGGCTC
EST36770 4	--	--	---	---	---	TGTAGCCAAAGTCACTGCATCATCTTGGCTGCTGGCAGGCTGGCCAGTTTGGCAGCTATAATCC ATCGAAATGATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTCCATTATGAGTCCCAAAAT TCAACCCCTCCGATAGGCTGGGCTGACCAAAATATACTGGGTTTCTGTTCTCTTCTGATCAT TCTTACAAGTTACTCTTATTGGGAAGGCCCTAAAGAGGCTTAG



EST26021 1	TAATGTAAGCTATCCACCAAGAAGCCTGCACCATGTTTGAGGTTGAGTGACATGTTTCGAAACCTGTT CCATAAAGTAATTTGTGAAGAAGAGGAGCAAGAGAACATTCCTCTGCAGCACCTTCACTACCAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCAATATGTGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTTCTTCTTTTTCGCAACAAAGACAAAGCAAGCC	---	---	---	---
EST51212 0	ATCCTGAGCTCGCCAATAAGCTTCTGGTTCTACTTCTCTTCCACAAGCCCCCAATTCACATTCTCA GAGGAATCCCAAGCTTAGGAGCCCTGGAGCCTTTGTGCTCCCACTCAATACAAAAGGCCCTCTCT ACATCT	---	---	---	---
EST20118 2	GTTCGGAATCCTCCTCCTGAAAGTGGCCGGGTTTAACTGCTCATGACGGTGGGGTGTGGTCCAGCT GAGGTGAGGGGCTTGAAGCTGGGAGTGGGTTTAGGGACGCGGTCTCTGGTGCATCCTAAGCTCT GAGAGCAACCTCCTTGAAGCTGGGAGTGGGTTTAGGACGCGGGTCTCTGCGTGCATCCTAAGCT CTGAGA	---	---	---	---
EST53018 6	ACAATCCAGGTCACACATTCAGAAAGAGGAGGGTGGTCAAGTGCCTGGGTAGGTCCAGTAATCCA AGGATTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC	---	---	---	---
EST68787 5	CTTCTATGGGATTTGACTTTATTTCTCCATTGCTTACCTTTACAGGTGTTAATATAGTGAAG GAAGCTTGAGCTCATGACAATTTGAAGCTGACAATACACAAGAGGAATAAATTCACAGTCAA AGAAATCAAGCACTTTTCGAAACATTTGAAGTTGTTTTGAACCTTGGTGCACCTTTAATACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT	---	---	---	---
EST34088 2	GTGGGGCAACAGTGGGAGAGAGGGGCCAGGGTATAAAGGGGCCACAAGAGACCGGCTCAAGG ATCCCAAGGCCCACTCCCGAACCACTCAGGGTCTCTGGACAGCTCACCTAGCTGCAATGGGTACA GGTAAG	---	---	---	---
EST37382 5	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCAACCCCTCTTCTCTTCTCCCTTGG CTTTGAGTCAAAATGGCTGGACTTGAGTCCCTGAACCAAGAGAGAAAGAGGACCCCAAGAAAT CACAGGTGGCAGCTGCGCTTACCGCCATCTCCCTTCTCACGGGAATTTTCAGGGTAAACT	---	---	---	---
EST74082	TCAGGGTGGCTGGACCCAGGCCCTCAGCTCTGCAGCAGGGAGGACGTGGCTGGCTGGAAGCATG TGGGGTGAGCCAGGGGCCCAAGGCAGGGCACTGGCTTCAGGCTGCTCAGGCTGCTGCTGTCAC CCAGATCACTGCTCTTCTGCCATGGCCCTGTGGATGCGCCCTCTGCCCTGCTGGGCTGCTGGCCCTC TGGGGACCTGACCCAGCCGAGCCTTTGTGAACCAACACCTGTGGC	---	---	---	---
EST45311 0	GGCCTCCTCTCTTCCAATTCTGTCCTATAGTTTCTCTATTAAAGTGAACATGCAATCTTTTAGT GGATAGATGCACACAACACACAGCCATTATGGGGAAGGATCCACGTGTGGCCATATTGTAACA CATTTTCTGCAATCACCTCTTTTCATTTAACAGCCCTATTCAATGGCCCTTTTCTTTTCAGTAGTA CATACACATCTGTGTCATTGTGAAT	---	---	---	---



EST65258 8	---	---	---	---	---	TGCCCCATACGCGGCGGAGACATGGCTTGCCACAGCTCTGAGGATGTCACCAATTAACCAAGAAAT CCAGTTATTTCCACCCTCAAAATGACAGCCATGGCCGCGGGTCTCTGGGGGCTCGTCGGGGG ACAGCTCCACTCTGACTGGCAGCTTTTGATGGAGACTTGAGGAGGAGGGCTTGAGGTTGGTGAG GTTAGGTGCGTGTTCCTGTGCAAGTCAGGACATCAGTCTGATTA
EST38216 3	---	---	---	---	---	ATGCAAGATGAAGGTGGACAGGGAGAGAGGGCCAACTGTATCCAGGGCCTGCAGATGTCGCTG GACTATGGGTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 --	---	---	---	---	---	ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCATTTGTTTAGCATTAACCTAA TTTTTTTCTGCTCCATGCAGACTGTTAGCTTTTACCTTAAATGCTTATTTAAATGACAGTGGGAG TTTTTTTCTGCTCGAAGTGGCAGTATCCAGAGTTTTGGTTTTTGAAGTACATGCCTGTGAAAAA GAAACTGAATACCTAAGATTCTGTCTGGGGTTTTTGTGCATGCA
EST35879 9	---	---	---	---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGCGTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGCACCCAGGCTGACCCAAATAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCCTGGAAGACAGACGCGGGATGGGGCAGGAGAGCTGCCTGGATGAA GGAAGAGATTTAAGAAGCTTGATTTGGACAATCTGGTCTTTGAGTGTGGAAGATTGATGCTCT GCCTGAGTTACAACAGAAATCCTTAGTACAGCGAGTAATAGATATATTGCACACAGATGGGAATGGA GAAGTAGACTTTAAAGTGAAGAAAGTAGTATTTTTTA
EST68308 5	---	---	---	---	---	GGAATATTAATAATATTTAAATACCTCCATTTTGCTTATCCTTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATGTCATGTTGGCAATTTGTTCTTACAAAATCGGATGGAAATCT GTTAAGTAAGTACTGTTTTGCTTGGCTTGGAAATGGATTTTAAATGTTGACTTTATCAT ATCACAGGTCTCTGGTCTCTGGCCATCATTTCTGGGAGAGATGGTGGTCTGCAAGCCCTTTGG CAATGTGAGATTGATG
EST54045 6	---	---	---	---	---	AGGAGAAGCTGAGGAGGGGAAGAGACACAAGAAATGACATTGATGAGTGAAGATGTCGGCTCAGGAT GCCGGAAATGAC
EST52908 0	---	---	---	---	---	TGAAGCTTCTGCCAGCTTGCAATGTTTCTAGGAGAACCCCGCTACACCTTATCTATAGCCTTCCCC TAGGTCTT
EST19590 --	---	---	---	---	---	CTCTGGATGGTTACAGGTGGCAGGCACAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAGGACAGCCACATGCGCGGGATGGCCGGGAGTCTGGT TGCGCCACGGCTGTGCCCTGTTGTGAACGGTAGCCTTGCGGTTGCGATGCCCTAAACCTTGTCT TGCCCAAGGAGGGGGGGTGCATGCCCTGAGATGATAGCGGCC
EST76136 --	---	---	---	---	---	Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence



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## EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.



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## CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,  
or a portion thereof which includes a polymorphic site,  
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is  
biallelic.
8. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is the reference base  
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is an alternative form  
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a  
20 segment of a fragment shown in the Table, column 7 or  
its complement.
11. The allele-specific oligonucleotide of claim 10 that is  
a probe.



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12. The allele-specific oligonucleotide of claim 10,  
wherein a central position of the probe aligns with the  
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is  
5 a primer.
14. The allele-specific oligonucleotide of claim 13,  
wherein the 3' end of the primer aligns with the  
polymorphic site of the fragment.
- 15 10 15. The allele-specific oligonucleotide of Claim 10, which  
is selected from the group consisting of the nucleotide  
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which  
is selected from the group consisting of the nucleotide  
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the  
Table, column 7 or the complement thereof, wherein the  
polymorphic site within the sequence or complement is  
occupied by a base other than the reference base shown  
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising  
obtaining the nucleic acid from an individual; and  
determining a base occupying any one of the polymorphic  
sites shown in the Table.
- 25 19. The method of claim 18, wherein the determining  
comprises determining a set of bases occupying a set of  
the polymorphic sites shown in the Table.



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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method  
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.